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54 **GENE SIGNATURE.**

57 A 3'-directed cDNA library which accurately reflects the abundance ration of mRNA in a cell has been prepared from various human tissues, and sequencing of the cDNAs contained in the library has been conducted to examine the incidence of each cDNA in each tissue. As each cDNA has expression information with each tissue corresponding to the mRNA concentration, these cDNAs are usable as a probe or primer for detecting cell anomaly or discriminating cells. The cloned gene can produce proteins utilizable as a medicine or the like.

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Fields of the Invention

The present invention relates to purified single-stranded DNA molecules, purified single-stranded DNA molecules complementary thereto or purified double-stranded DNA molecules consisting of said single-stranded DNA molecules, which can specifically hybridize to human genomic DNA, human cDNA or human mRNA at particular sites. The DNA molecules of the present invention can be used for detecting the overall or individual expression status of mRNAs coding for the corresponding cellular proteins, detecting and diagnosing cellular abnormalities due to disease and viral infection, or distinguishing and identifying the cell type, and efficiently cloning genes expressed in a tissue-specific manner. The present invention further includes cloned DNA molecules which can be used to produce proteins useful as pharmaceutical products or the like.

Related Arts

Recognizing the importance of the most fundamental attribute of mRNA, that is, "the nature of the cell is determined by the expression pattern of genes as reflected in the population of mRNA", the inventors of the present invention have proposed "body mapping" as a unique approach to their objective. This is an entirely novel attempt to prepare "the information on gene expression" for presumably about 200 different kinds of cells and tissues present in the human body and elucidate when, where and to what extent a certain gene is expressed, and map genes to the respective organ or cell type in which they are expressed.

While a variety of cells in the living body express various proteins depending on their respective biological functions, the intracellular concentrations of these proteins vary according to the cell type, stage of development and differentiation, environment, etc.

In general, genes are classified into "genes encoding proteins essential for the life of the cell" and "genes encoding proteins responsible for functions specific to the cell". Of these two, "genes encoding proteins essential for the life of the cell" are expressed constantly in all types of cells and also called "housekeeping genes", while "genes encoding proteins responsible for functions specific to the cell" are often expressed specifically in a particular type of cells or a particular group of cells, and also may be specifically expressed at a particular stage of cellular development and differentiation. Furthermore, they are often "inducible genes" and the amount of their expression varies depending upon the environment to which cells are exposed. In other words, cells may grow as a result of the expression of "genes encoding proteins essential for the life of the cell" and display their specific functions as a result of the expression of "genes encoding proteins responsible for functions specific to the cell".

However, under abnormal cellular conditions due to disease or infection, the expression of genes within individual cells is altered as compared with that under the normal conditions. Especially, during viral infection, RNAs encoding virus-specific proteins are synthesized in large amounts within the cell, leading to the production of said protein in large amounts. In other words, the alteration in the expression level of genes within the cell, especially as reflected in the concentration of intracellular mRNA, can lead to such abnormal cellular conditions as seen in diseases.

Thus, the function of each cell in the living body is closely related to the expression status of genes within the cell. Accordingly, in order to elucidate the function of each cell at molecular level or to investigate the pathogenesis of a disease at molecular level, it becomes necessary to comprehend the expression status of cellular genes, especially the intracellular concentration of each mRNA.

A theoretically possible approach to this objective is the extraction and analysis of all cellular proteins for determination of expression status. However, although it may be possible to isolate a specific protein, in most cases it is almost impossible to completely isolate all of these proteins, because a great variety of proteins are expressed within the cell.

Another approach is to directly estimate the concentrations of cellular mRNAs corresponding to all intracellular proteins. However, although it may be possible to isolate a specific mRNA, it is practically impossible to completely isolate all of these mRNAs and directly estimate their amounts, because a great variety of mRNAs are synthesized simultaneously within the cell and furthermore they may be unstable and susceptible to enzymatic degradation during their extraction.

This invention aims to provide DNA molecules which can be used as probes or primers required for detecting the overall or individual expression status of mRNAs coding for the corresponding cellular proteins, detecting or diagnosing cellular abnormalities due to disease or virus infection, recognizing and identifying various cell types, and efficiently cloning genes expressed in a tissue-specific manner. Moreover, the present invention aims to provide cloned DNA molecules which can be used to produce proteins useful as pharmaceutical products.

Summary of the invention

In general, the genetic information flows in order from DNA to mRNA and to protein (F. H. C. Crick, 1958). That is, "the information for the amino acid sequence of a protein" is first transcribed into mRNA and then translated into protein.

To explain this in further detail mammalian genes commonly comprise a region encoding a protein and a region regulating the expression of said gene. The regions of a gene encoding protein (called "exons") are often separated by intervening sequences (called "introns"). When a gene is transcribed into RNA, the introns of the precursor RNA (pre-mRNA) are excised and exons are connected in tandem to form a contiguous structure coding for a particular protein (this process is called "splicing"). On the other hand, the region regulating the expression of gene comprises, in addition to the regions directly regulating transcription such as a promoter and operator which are present upstream of the transcription region, untranslated regions are located both upstream (5') and downstream (3') of the coding region. In particular, 3' untranslated region (3' UTR) is important for regulating expression, since it contributes to the transport and stability of mRNA. During the processing of pre-mRNA, a methylated cap is added at its 5' end, the 3' untranslated region is cleaved at a specific site, a poly(A) tail is attached by adding 100 - 200 adenylate residues to the cleaved end, and the coding regions are spliced together to form mRNA. The protein is then synthesized after attachment of ribosomes to the mRNA.

The inventors of the present invention have elucidated that, in general, when the intracellular level of a particular mRNA is high, the expressed amount of the corresponding protein is also elevated, and also that it is possible to estimate the relative concentration of each intracellular protein by estimating relative intracellular concentration of the corresponding mRNA [DNA sequence 2, 137-144 (1991); Nature genetics, 2, 173-179 (1992)].

Basically in the present invention, mRNA is extracted from a particular cell and cDNA is synthesized by conventional methods using reverse transcriptase. However, in the present invention, cDNA is synthesized using a method developed by the inventors of the present invention so as to reflect the relative intracellular concentration of mRNA. A cDNA library is constructed and a group of cDNAs representing the population of total mRNA are cloned and sequenced.

An approach which appears to be similar to the one used by the inventors of the present invention but is entirely different, is the method of cloning of a cDNA library constructed by the random priming by Venter et al.

Venter's group randomly cloned cDNAs from commercially available cDNA libraries derived from brain cells (catalog No. 936206, 936205 or 935, Stratagene, California) and determined their base sequences [Science 252, 1651-1656 (1991); Nature 355, 632-634 (1992)].

While the method used by Venter et al. involves sequencing of cDNAs obtained by random priming, this method has the following drawbacks:

- 1) Since random cloning of various regions of a single-stranded mRNA may often lead to the formation of many cDNA fragments without any mutual overlapping portions, it is difficult to determine whether these cDNA fragments are derived from the same mRNA or a different one,
- 2) The longer a mRNA strand, the higher the chance for said mRNA to be reverse-transcribed into cDNA, and
- 3) Since the availability of each primer to be used among random primers differs depending on their base sequences, the relative frequency of cDNA synthesis is variable.

From aforementioned reasons, the relative frequency of appearance of cDNA does not reflect the relative concentration of cellular mRNA. Consequently, it is impossible to determine the relative concentration of each mRNA and the actual population of intracellular proteins by using the method of Venter et al.

However, with the method developed by the inventor of the present invention, it is possible to construct a cDNA library which precisely reflects the relative concentration of mRNA without any of the aforementioned complications. Since, in the present invention, cDNA is synthesized using only "poly-T" as the primer, the 3' ends of the cDNA have "a poly A tail". Therefore, the synthesis of cDNA with "poly-T" as the sole primer is initiated from the 3' end resulting in the formation of 3'-oriented cDNA. Since the 3' untranslated sequence is unique to a particular mRNA species and not present in other mRNA species [Birnstiel, M. L., et al., Cell 41, 349-359 (1985)], almost all the 3' end-oriented cDNAs hybridize with specific mRNAs. Digestion of the resulting cDNA with a restriction enzyme MboI which recognizes the specific four-base sequence GATC results in the formation of cDNA extending from the 3'-terminus to the first MboI restriction site. In the present invention, each cDNA thus cloned and included in "a cDNA library faithfully reflecting the relative intracellular concentration of mRNA" is called a "gene signature" (abbreviated as GS hereinafter). A GS includes not only the double-stranded DNA but also each single-stranded DNA thereof.

The present invention relates to a purified single-stranded DNA, purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under the sequence identification number (SEQ ID NO) 1 - 7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA. The present invention also relates to probes and primers consisting of said single-stranded DNA. The present invention also relates to a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1 - 7837 (wherein T is read as U) or any portion thereof at its 3' region and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA. The present invention also relates to probes and primers consisting of said single-stranded DNA.

The present invention is explained further in detail as follows.

The DNA of the present invention not only includes a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under SEQ ID NO 1 - 7837 but also includes a single-stranded DNA containing a portion of said single-stranded DNA (or said single-stranded DNA complementary thereto) if it hybridizes to human genomic DNA, human cDNA or human mRNA.

Furthermore, the DNA of the present invention not only includes a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a mRNA containing any of the base sequences listed under SEQ ID NO 1- 7837 (wherein T is read as U) or any portion thereof at its 3' region but also includes a single-stranded DNA (or a single-stranded DNA complementary thereto) containing a portion of said single-stranded DNA (or said single-stranded DNA complementary thereto) if it hybridizes to human genomic DNA, human cDNA or human mRNA.

In addition, the DNA of the present invention not only includes a single-stranded DNA or a single-stranded DNA complementary thereto but also includes a double-stranded DNA consisting of said single strands.

Obviously, the term "contain" as used herein does not necessarily mean that the DNA of the present invention contains at a single site without interruption (1) "a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under SEQ ID NO 1-7837 or a portion thereof" or (2) "a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a mRNA containing any or any portion of the base sequences listed under SEQ ID NO 1 - 7837 (wherein T is read as U) at its 3' region or a portion of said single-stranded DNA." In other words, the term "contain" is applicable also to the case where one or more exogenous bases are inserted in the base sequence of the DNA (1) or (2).

The hybridization to a particular site of human genomic DNA, human cDNA or human mRNA can be achieved under standard conditions (see e.g., *Molecular Cloning: A Laboratory Manual*, Sambrook, J., et al., Cold Spring Harbor Laboratory Press, 1989). In the following preferred embodiment, there will be described methods for constructing a cDNA library which reflects precisely the relative intracellular concentration of mRNA, cloning cDNA groups which correspond to total mRNA, and determining the base sequence of each cDNA.

First, cells from specific tissues, for example, cells from organs, for example, cells derived from human liver (HepG2) are grown, and the total mRNA is extracted by standard procedures. mRNA thus obtained is attached to a vector to construct a cDNA library.

For example, mRNA is attached to the vector plasmid pUC19, which has the M13 sequences flanking the cloning site, as follows.

pUC19 is cleaved by HincII and PstI and poly-T of 20 bp - 30 bp is added to the PstI-digested end to which the 3'-end poly-A tail of the mRNA is hybridized (Fig. 1a). After the DNA strand is extended with conventional methods using reverse transcriptase, a double stranded DNA is formed with DNA polymerase (Fig. 1b). The double stranded DNA thus obtained is cleaved with the restriction enzyme MboI which recognizes a specific four base sequence (Fig. 1c).

MboI, which recognizes a four base sequence (GATC), cleaves the DNA within a few hundred bases from the poly-A tail. Since MboI is found to digest, without exception, about 300 human cDNAs which were randomly selected from the GenBank data base by the inventor of the present invention, this enzyme cleaves the cDNA to be cloned at a specific site. In addition, as pUC19 is prepared in dam⁺ E. coli, e.g., E. coli JM109 and since its adenine at the MboI recognition site is methylated (G^mATC), it is not cleaved by MboI.

Subsequently, in order to prepare a vector containing the double-stranded DNA which has previously been attached to pUC19 and has the MboI-cleaved end, the pUC19 DNA is digested with BamHI to make termini cohesive with the MboI-cleaved end. Since the recognition sequence of BamHI (GGATCC) contains that of MboI (GATC), the extended portion of the double-stranded DNA is not cleaved with BamHI.

The resulting double-stranded DNA is then circularized by standard ligation methods, and the recombinant vector plasmid thus prepared is introduced into *E. coli*, e.g., *E. coli* DH5 in order to make a cDNA library.

With this method, only a clone containing the base sequence upstream of the poly-A tail of the mRNA is obtained.

Since the average size of the inserted cDNA fragment is relatively small, 270 bp, it is free from biased cloning resulting from variations in the efficiency of cDNA synthesis and transformation that occur in the case of larger sized DNAs. Furthermore, because instability due to repeated base sequences and the like is eliminated, the cDNA library of the present invention faithfully represents the relative concentration of mRNA in the cell.

Furthermore, when the cDNA inserted into the vector is relatively short, it is possible to accurately amplify the cDNA fragment using the sequence of the vector flanking it as a primer. It is also possible to determine the base sequence from the 5' end directly by the PCR without interference from the 3' poly-A tail which will reduce the accuracy of sequence determination.

Amplification of the GS, i.e., the cDNA fragment inserted into the vector, is performed as follows.

The *E. coli* cells in which the cDNA library is introduced are grown using standard methods and lysed. Debris contained in the bacterial lysate are removed by centrifugation and the supernatant containing the vector DNA is recovered. The vector DNA thus obtained is used as the DNA template for amplification by the PCR (Fig. 1d, amplification with PCR primers 1 and 2).

Base sequences flanking both ends of the GS is properly selected for use as primers and the PCR is performed under standard conditions. PCR products thus obtained are subjected to the elongation reaction using fluorescence primers complementary to the vector sequence flanking the 5' end of the GS, and the sequence is determined with an autosequencer (Fig. 1d, sequence determination with dye primer).

Based on the results of the sequence determination of each GS, the species and the frequency of appearance of the GS in each tissue or cell type are analyzed.

As to each cell type not only normal cells but also cells under pathogenic conditions (such as tumor cells, virus infected cells, etc.) can be used without any restriction. For example, liver cells (from fetus, neonate or adult), various hematopoietic cells (granulocytic, monocytic, etc.), lung cells, adipocytes, endothelial cells, osteoblasts, colon mucosa cells, retinal cells and hepatoma cells (HepG2, etc.), and promyelocytic leukemia cells (HL60, etc.) will be used. The appearance frequency for each GS is described for each cell type in Tables 1 through 219. There, patent number represents "SEQ ID NO for each GS", size represents the "length of each GS", and F represents the "sum of appearance frequencies in the cells studied". In addition, hepG2 stands for "hepG2 (a liver cancer cell line)", HL60 stands for "HL60 promyelocytic leukemia cell line", granulo stands for "granulocytoid, HL60 stimulated by DMSO", mono stands for "monocytoids, HL60 stimulated by TPA", 40 w liver stands for "40 w neonatal liver", 19 w liver stands for "liver of a 19 weeks old fetus, adult liver is "adult liver", lung stands for "adult lung", adipose stands for "subcutaneous adipose tissue", endothel stands for "primary cultured aortic endothelium", osteoblast stands for "primary cultured osteoblast", colon mucosa is "colon mucosa", small cell carci stands for "small cell carcinoma of lung", retina is "retina", cerebral cortex is "cerebral cortex", adenocarci (lung) stands for "adenocarcinoma of lung", squamous cell ca (lung) stands for "squamous cell carcinoma of lung", keratinocyte stands for "primary cultured keratinocyte", fibroblast stands for "primary cultured fibroblast", Alzheimer stands for "Alzheimer temporal lobe", cerebellum stands for "cerebellum", visceral fat is "visceral fat", corneal epithelium is "corneal epithelium", peripheral granulocyte is "peripheral granulocyte", neuroblastoma is "neuroblastoma" and taste bud of tongue is "taste bud of tongue".

"Accession number of target mRNA" represents the accession number of the entry in GenBank Release 79 whose base sequence has homology with that of each GS, "match %" represents the percent homology of the GS sequence relative to that of said homologous sequence, "match starts at (GS)" represents the base position counted from the 5'-end of the GS at which the region for homology calculation starts, "match starts at (GenBank)" represents the base position counted from the 5'-end of the GenBank sequence at which the region for homology calculation starts, and "GenBank target size" represents the whole length of the GenBank sequence corresponding to the GS. The columns in Tables 1 - 219 represent the same items as in Table 1.

Based on the data in Tables 1 - 219, each GS can be classified into several groups. A GS, which is expressed at high frequency in a specific cell or groups of cells with similar property, for example,

promyelocytic leukemia cell, granulocyte and monocyte and not expressed entirely or expressed very little in other cells (groups), is a likely GS corresponding to the gene encoding "the protein responsible for functions specific to the cell" (e.g., GS0001553, GS0002047, GS004895, etc.). On the other hand, a GS, which is expressed commonly in every kind of cell, most likely corresponds to the gene encoding "the protein essential for the life of the cell" (e.g., GS0000019, GS0000155, GS000861, etc.). In addition, some GSs are expressed at low frequency (e.g., GS0000013, GS0002399, GS0003155, etc.).

Since the GS with the sequence determined as described above will reflect the population of mRNA expressed in a particular cell, it must be possible to find the relative concentration of mRNA in each cell by determining the appearance frequency for each GS in a cDNA library derived from that cell. Therefore, to confirm the correlation between the appearance frequency for each GS in a cDNA library and the relative concentration of cellular mRNA, the GS thus obtained was labeled with ^{32}P by standard methods and used as the probe in the following hybridization test. mRNA isolated from a specific cell is hybridized to said ^{32}P -labeled probe under standard conditions. The results of this Northern hybridization test were such that, when a GS found with high appearance frequency in a cDNA library was used as a probe, a dense band was formed, confirming the correlation of the frequency of appearance of the GS with the relative concentration of mRNA in the cell (see Example 5).

Similarly, the colony hybridization test of the cDNA library constructed as described above with a ^{32}P -labeled probe prepared as described above showed a close correlation between the frequency of appearance of the GS and the number of colonies hybridized with said GS (see Example 6), confirming the correspondence of the frequency of appearance of the GS and relative concentration of the GS in a cDNA library.

From the above results, by determining the appearance frequency of each GS in a cDNA library derived from a variety of cells, it has become possible to determine the expression status of the gene (or mRNA) corresponding to each GS. This fact implies conversely that each GS may be useful for industrial purposes as a specific probe or primer encoding information about the expression status of its corresponding gene (or mRNA) for each cell. For example, when it is proven that "a certain GS appears at high frequency only in a cDNA library derived from tissue A, that is, the gene corresponding to said GS is specifically expressed only in tissue A", by conventional cloning of the corresponding full-length cDNA using said GS as a probe or primer, it is possible to clone a full-length gene which is expressed in a tissue-specific manner.

Furthermore, for example, when it is proven that "the frequency of appearance of a certain GS is low in a cDNA library derived from tissue B, that is, the appearance frequency of the gene corresponding to said GS is low in tissue B", by examining the expression frequency of the gene corresponding to said GS in a test sample of tissue B from a patient using said GS as a probe or primer, it may be possible to identify the pathogenic gene, wherein an unusually high expression frequency of said gene being a strong indication that said GS may be the gene involved in the pathogenesis. Furthermore, by conventional methods for cloning said full-length cDNA using said GS as a probe or primer, it is possible to isolate said pathogenic gene and elucidate its characteristics.

In practice, the DNA of the present invention may be used as a probe or primer for detecting and diagnosing disease, cloning a pathogenic gene or related gene, cloning a viral gene, identifying and recognizing cell types, cloning a species-specific promoter and gene mapping.

One GS corresponds to one mRNA. It is therefore obvious that any portion of cDNA complementary to each mRNA carry the same "information for expression" as the GS. Accordingly, the DNA of the present invention is not restricted to "the DNA comprising the GS itself or portion thereof", but also includes the DNA comprising, for example, "a full-length cDNA complementary to each mRNA" and "the non-GS region of the cDNA complementary to each mRNA or a portion thereof". They can be used as a probe or primer comprising the same "expression information" as that of the GS and can be used as a probe or primer in a similar manner as a GS. For example, by using a GS or a portion thereof as a probe or primer, it is obviously possible for those skilled in the art to readily isolate "a full-length cDNA corresponding to each mRNA" or "the non-GS region of the cDNA complementary to each mRNA or a portion thereof". For example, as described hereinafter, conventional techniques such as "5' RACE", "nesting" and "inverse PCR" can be used.

An example of the method for detecting disease using the GS of the present invention will be described. As shown in Tables 1 - 219, with the method described above it is possible to detect a GS present specifically in a cDNA library constructed from each tissue by detecting and comparing the frequency of appearance of GS in each tissue. It is also possible to identify a GS corresponding to a protein which is expressed commonly in various tissues or which is expressed at low frequency. These GSs are denatured and then fixed on an appropriate filter, for example, nylon filter or nitrocellulose filter. It is

convenient to use a single filter with many GSs fixed on it. Usage of a single filter on which many denatured DNAs are fixed is well known. An example may be "the Escherichia coli Gene Mapping Membrane" (Takarashuzo, code No. 9035). It is a single nylon filter on which the cosmid contigs of genomic DNA of E. coli are fixed. It is possible to prepare a filter comprising a group of specific GSs corresponding to proteins expressed in a particular tissue, a filter comprising a group of GSs corresponding to proteins commonly expressed in various tissues, or a filter comprising a group of GSs corresponding to proteins expressed at low frequency. The single-stranded GSs fixed on these filters are then hybridized to labeled complementary DNA fragments synthesized using "random primers" prepared from template mRNA extracted from a test tissue, using four labeled nucleotides and reverse transcriptase (labeled mRNA can also be hybridized to the filters). Similarly, labeled complementary fragments synthesized using mRNA extracted from normal tissue as the template are hybridized (labeled mRNA can also be hybridized to the filters). If the profile of hybridization to a group of GSs has been categorized beforehand by comparing the hybridization profile of various pathogenic tissues to that of corresponding normal tissues, it is possible to diagnose the pathogenic condition of a particular test tissue by comparing the hybridization profile of the test tissue with that of the corresponding normal tissue and assigning that profile to a certain category. Virus infection can be detected in the same manner as in the case of other diseases.

Next, an example of the method for cloning pathogenic genes or their related genes using the GS of the present invention is described. As described above, using the filter on which denatured GSs are fixed, the GS-hybridization profile of various pathogenic tissues and that of corresponding normal tissues are compared. A considerable difference in the hybridization intensity between normal and pathogenic tissues will be an indication that the particular GS corresponds to a pathogenic gene. If a filter comprising only GSs specific for a particular tissue is applied to a sample from that particular tissue, the probability for detecting the GS with a great difference in hybridization intensity is elevated. Also a filter comprising GSs corresponding to proteins whose expression is low will facilitate the identification of the GS corresponding to the pathogenic gene by detecting an intense signal, because the hybridization signal for these GSs is usually weak. Once a GS corresponding to a pathogenic gene is found, said pathogenic gene can be cloned by established methods such as genomic Southern hybridization using said GS as a probe and/or a primer.

Furthermore, a method for cloning a full-length gene using a GS as a probe or primer is described in detail. Cloned genes isolated in the present invention are also appropriate for use in the production of proteins useful as pharmaceutical products. mRNA is extracted from tissues by conventional methods and cDNA libraries are then prepared (See Molecular Cloning, 2nd ed. Vol. 2, Section 8 New York; Cold Spring Harbor Laboratory). In this case, it is desirable to extract mRNA from tissues in which the target gene is highly expressed. One method to detect a specific gene in libraries thus prepared is, for example, to select positive clones via hybridization using a whole or partial GS as a probe. In general, since a GS is specific for a particular mRNA, hybridization can be carried out under certain stringent conditions. Probes used are at least more than 25 bases long, preferably more than 50 bases long, and more preferably more than 100 bases long.

Furthermore, if cDNA libraries, in which the cDNA for a specific gene is concentrated, are prepared, they will be preferable for selecting said specific gene. One method useful for this purpose is carried out as follows: 1) preparation of an affinity chromatographic column of resin on which the denatured GS corresponding to the specific gene is fixed; 2) application of mRNA extracted from a tissue to said column and retention of the mRNA species corresponding to the specific gene on said column; 3) elution and concentration of said retained mRNA; and finally 4) preparation of cDNA libraries using said concentrated mRNA species as the template. Another method is the selective amplification of cDNA corresponding to the specific gene by the PCR. Selective amplification of a specific gene is carried out as follows: using a partial sequence of a GS localized toward the 3' end of the specific gene as primer, cDNA is synthesized from mRNA with reverse transcriptase and 4 NTPs. To the 3' end of a single-stranded cDNA thus obtained a homopolymer such as poly-T is attached by the action of "terminal deoxyribonucleotide transferase (TdT)". In addition, using "a primer complementary to the homopolymer" and "a primer used in said reverse transcriptase reaction, or a primer whose sequence is included in the same GS but is located proximal to the 5' end", cDNA corresponding to the specific gene may be selectively amplified by the PCR [see 5'RACE (5' Rapid Amplification of cDNA ends): PNAS, Vol. 85, pp. 8998 - 9002 (1988); Nucleic Acids Res., Vol. 17, pp. 2919-2932 (1989)]. In addition, instead of the attachment of a homopolymer, there is another method comprising the following steps: 1) a single stranded anchor DNA is linked to the 3' end of a single stranded cDNA using "T4 DNA ligase"; and 2) said cDNA is amplified by the PCR using a primer complementary to said anchor DNA [Nucleic Acids Res., Vol. 19, pp. 5227-5232 (1991)]. Said primer is desirably more than 13 bases long, preferably more than 15 bases long, and more preferably more than 18

bases long. Furthermore, in order to enhance the efficiency of heat denaturation in the cycling reaction, said primer is preferably less than 50 bases long and more preferably less than 30 bases long. By linking said amplified DNA to a vector, a cDNA library concentrated with respect to the target gene is prepared.

In addition, it may be also possible to isolate a cDNA clone corresponding to the specific gene directly from the PCR products. Specifically, the PCR products are first separated by gel electrophoresis, subjected to Southern blotting analysis using the denatured GS as a probe, and examined for the presence of a band which specifically hybridizes to said GS. If a GS-hybridized band is detected, it is highly possible to isolate the cDNA clone corresponding to the specific gene by excising said band from the gel and subjecting it to direct cloning.

As described above, in order to further amplify the specific gene previously amplified by the PCR, it may be possible to perform the second PCR of the primary PCR products by replacing either or both primers previously used with a primer having the base sequence internal to said two primers (nesting) (Journal of Virology, Vol. 64, p. 864 (1990)). Nesting may be performed directly upon the products of the primary PCR. Alternatively, if a band which specifically hybridizes to the GS is detected by the Southern blotting analysis of the primary PCR products, nesting may be performed for the DNA obtained by excision of the band followed by extraction. In the case where a band which specifically hybridizes to the GS is detected by the Southern blotting analysis of nested products using the denatured GS as a probe, it is highly possible to successfully isolate the cDNA clone corresponding to the target gene by excising said band from the gel and subjecting it to direct cloning.

The isolated cDNA clone corresponding to the target gene may often correspond to the full-length mRNA, but it may be a cDNA with the 5' end deleted. In the case where the 5' end is deleted it is possible to isolate the full-length cDNA clone by conventional methods. For example, by screening a cDNA library using a probe comprising the base sequence in the 5' end region of the cloned cDNA, since the target position of said probe is shifted further toward the 5' end of the full-length cDNA than in the case of using a GS as a probe, it is possible to isolate only longer cDNA clones as the positive clone. Also by synthesizing cDNA using "a primer comprising the base sequence in the 5' end region of the cloned cDNA" with mRNA as the template followed by PCR amplification of "a single stranded cDNA having a homopolymer or anchor DNA sequence at the 5' end" and using "the primer used for previous cDNA synthesis or a primer having the sequence internal to that of said primer" and "a homopolymer or a primer complementary to anchor primer" as described above for the 5' RACE method, only the sequence toward the 5' side of the cDNA may be selectively amplified since the position of said primer is shifted further toward the 5' side of the full-length cDNA. Even if the cDNA thus obtained has a deletion at the 5' end, the population of cDNA fragments covering the full-length of the long cDNA may be obtained by repeating this procedure. It may be easy for those skilled in the art to obtain a full-length cDNA by suitably linking said cDNA fragments having overlap segments together.

Alternatively, by performing the inverse PCR (Inverse PCR: Genetics, Vol. 120, p. 621 (1988); Molecular Cloning, 2nd ed., Vol. 2, 14.12-14.13 (New York; Cold Spring Harbor Laboratory)), it may be possible to isolate a cDNA clone extending externally from the GS, that is, in the genomic DNA region. Specifically, the target DNA (genomic DNA or cDNA) is digested with restriction enzymes into fragments of about 2-3 kb and then circularized by ligating the cleaved ends. By performing the PCR for said DNA using "a set of primers which are complementary to the cDNA clone isolated using the GS or the GS as a probe or primer, and thereby making the direction of DNA synthesis mutually opposite (outward), it may be possible to amplify the DNA region extending externally from the GS. There is known a method to isolate a full-length genomic DNA of a specific gene by repeating this procedure (Nucleic Acids Res., Vol. 16, p. 8186 (1988)).

In addition, although "Taq polymerase" is conventionally used in the PCR described above, the cloning procedure may be more efficiently performed using the "LAPCR (long and accurate PCR" technique (Nature Genet., Vol. 7, p. 350-351 (1994), Nature., Vol.369, p.684-685(1994)).

Furthermore, needless to say that by linking said full-length gene thus obtained to a suitable expression vector followed by its expression in an appropriate host, it is possible to obtain the corresponding gene product (Molecular Cloning, 2nd ed.).

Next, there will be described an example of the method for identifying and recognizing cell types using the GS of the present invention. As shown in Tables 1 - 219, based on the appearance frequency of GS in each tissue and its comparison among tissues, it is possible to identify those GSs specifically present in a cDNA library constructed for each tissue. These "tissue-specific GSs" are fixed on a filter. It will be more convenient if GSs specific to each tissue are collected and fixed on a filter as a whole (e.g., a GS block specific for hepatocytes or cerebral cortex cells). As described above, to this filter are hybridized labeled complementary fragments synthesized using "random primers" prepared from mRNA extracted from test tissues or cells, "nucleotide containing 4 labeled nucleotides", and "reverse transcriptase". (Directly labeled

mRNA can also be hybridized to the filters.) Depending on the type of tissues or cells, intense hybridization signals will be observed with the GS groups specific to said tissue or cell. Furthermore, a tissue-specific promoter can be cloned by structure analysis of the 5' upstream sequence through the cloning of the corresponding gene using established methods such as genomic Southern hybridization with the "tissue-specific GS" as the probe and/or primer.

These tissue-specific promoters thus obtained are useful for gene therapy in the future.

Gene therapy in a narrow sense aims to supplement the defective protein of patients using gene technology, and in this case it is necessary to express the exogenous gene in a desired tissue in a desired quantity. For this purpose, a promoter which is known to be expressed in a specific tissue in a desired quantity (in most cases a large quantity is desired) is highly useful. Although, at present, a virus promoter is often used, it can be inactivated by endogenous modification such as methylation. Promoters provided by tissue-specific GSs will be ideal substitutes for viral promoters.

There will be described the method for chromosomal assignment of DNA corresponding to the GS of the present invention using the probe derived from the GS obtained as described above.

First, the Southern blotting method will be described.

According to this method, for example, chromosomes are isolated from a lymphoblast cell line of human normal karyotype (e.g., GM0130b), and then a monochromosomal hybrid cell is prepared by introducing each human chromosome into non-human cells, such as rodent cells, and cultured on a large scale by standard methods. Then the DNAs extracted from said hybrid cells are digested with various restriction enzymes and subjected to agarose gel electrophoresis. Then, the electrophoresed DNAs are hybridized to ³²P-labeled GS prepared as described above and used as the probe. By identifying the hybrid cell the DNA of which is hybridized to said probe, it is possible to identify the chromosome in which the DNA corresponding to the GS of the present invention is present. Southern hybridization test of the total human genomic DNA using each labeled GS as a probe formed a single band corresponding to the GS, indicating that the DNA of the present invention can be used as a desirable probe for human genomic DNA. It is obvious that a desirable probe for human genomic DNA can be used also as a desirable probe for human cDNA and human mRNA.

A method similarly using the PCR to determine chromosomal localization of the GS of the present invention will be described.

To prepare most appropriate primers, base sequences are selected from the sequence of the GS in question by conventional methods, for example, by using the computer software OLIGO4.0 (National Biosciences) and the oligonucleotides (20-24mer) having the selected sequences are synthesized. The preferred size of the sequence to be amplified by the PCR is from 50mer to 100mer.

Using the primers thus synthesized and the chromosomal DNA extracted from the monochromosomal hybrid cell as such as the template, amplification by the PCR is performed in a conventional manner. Resulting PCR products are subjected to non-denatured acrylamide gel electrophoresis and stained with ethidium bromide for fluorescent detection. The sizes of these PCR products are then determined.

Chromosomal assignment is confirmed when the presence of a PCR product of correct size is confirmed.

It is evident that a chromosome or chromosomes in which the DNA corresponding to a GS is localized can be identified by using these procedures. It has also become evident that the DNA of the present invention can be used as desirable primers for human genomic DNA since a single band has resulted from amplification of the total human genomic DNA by the PCR using primers designed based on each tested GS. Obviously, a desirable primer for human genomic DNA is also a desirable primer for human cDNA and human mRNA.

Brief Description of Figures

Fig. 1 shows the preparation of 3' Mbol cDNA library.

Fig. 2 shows the results of tests of primers. A shows the location of primers on the vector; and B shows the electrophoretic patterns of DNA fragments amplified using the primers (A). Primers used are as follows: lane 1, FW (-40)/RV (-14); lane 2, FW (-40)/RV (-36); lane 3, FW (-40)/RV (-71); lane 4, FW (-40)/RV (-29); and lane 5, FW (-47)/RV (-48). Artifacts are indicated by arrows.

Fig. 3 shows the electrophoretic pattern of PCR products using FW(-40) and RV(-14) as primers. The lane at the right end shows the electrophoretic pattern of size markers and the other lanes show the PCR products using FW (-40)/RV (-14) as primers.

Fig. 4 shows the mRNA concentration reflecting the frequency of appearance of each GS in the cDNA library: especially, Figs 4A - 4D; experimental results; Fig. 4E, photographs of colonies; and Fig. 4F,

summary.

Fig. 5 shows the appearance frequencies for various cDNAs in the 3'-directed HepG2 cDNA library.

Fig. 6 shows the genetic mapping of each GS (gs) using PCR.

Fig. 7 shows the genetic mapping of each GS (gs) using PCR.

5 Fig. 8 shows the genetic mapping of each GS (gs) using PCR.

Fig. 9 shows the genetic mapping of each GS (gs) using PCR.

Fig. 10 shows the genetic mapping of each GS (gs) using PCR.

Fig. 11 shows the chromosomal mapping of GS001418 (gs001418) using PCR.

Fig. 12 shows the chromosomal mapping of GS001457 (gs001457) using PCR.

10 Fig. 13 shows Southern blotting of human total chromosomes using the GS as a probe.

Fig. 14 shows Southern blotting of human total chromosomes using the GS as a probe.

Fig. 15 summarizes the characteristics of hybrid cells used for Southern hybridization.

Fig. 16 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000152 (clone s14g02) as a probe.

15 Fig. 17 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000041 (clone s650) as a probe.

Fig. 18 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000181 (clone hm01e01) as a probe.

20 Fig. 19 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000055 (clone c13a18) as a probe.

Fig. 20 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000180 (clone s479) as a probe.

Fig. 21 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000094 (clone s173) as a probe.

25 Fig. 22 shows Southern blotting of chromosomal DNA from the hybrid cells using junk (clone hm01g02) as a probe.

Fig. 23 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double cleavage with EcoRI and BamHI.

30 Fig. 24 shows the chromosomal mapping of each GS by Southern-blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double digestion with EcoRI and BamHI.

Fig. 25 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double digestion with EcoRI and BamHI.

Fig. 26 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double digestion with EcoRI and BamHI.

35

Preferred embodiments of the invention

In the following section, there will be explained preferred embodiments of the present invention. However, the present invention will not be restricted to these preferred embodiments.

40

[Example 1]

Preparation of mRNA

45 Cytoplasmic RNA was extracted from a liver cancer cell line HepG2 (Aden., et al., Nature 282, 615-617, 1979) using standard procedures [Sambrook, J., et al., Molecular Cloning, 2nd ed. (New York: Cold Spring Harbor Laboratory), vol. 1, pp. 7.3-7.36, 1989]. Briefly, HepG2 cells grown in Dulbecco's modified Eagle medium supplemented with 10% FCS were lysed in RNA extraction buffer [0.14 M NaCl, 1.5 mM MgCl₂, 10 mM Tris-HCl (pH 8.6), 0.5% NP-40, 1 mM DTT, 1000 units/ml RNase inhibitor (Pharmacia)] by using a
50 Vortex mixer for 30 sec and then left standing on ice for 5 min. Nuclei and other cell debris were precipitated by centrifuging at 12,000 g for 90 sec, and the supernatant was deproteinized with Proteinase K followed by phenol extraction. RNA was precipitated by isopropanol and rinsed with 70% ethanol. Finally, the poly A⁺ fraction was collected by oligo dT column fractionation (Aviv., et al., Proc. Natl. Acad. Sci. USA 69, 1408-1412, 1972).

55

[Example 2]

Preparation of vector primer DNA and construction of cDNA libraries

To prepare a vector primer, pUC19 DNA amplified in JM109 cells (Yanisch-Perron, C., et al., *Gene* **33**, 103-119, 1985) was digested with PstI to completion and a poly T-tail was added with terminal transferase (Pharmacia) to a mean length of 26. This process was monitored by the incorporation of ³H-deoxythymidine triphosphate [Okayama, H., et al., *Methods in Enzymology* (San Diego: Academic Press), vol. **154**, pp. 3-28, 1987]. The product was digested by HincII, and the resulting short fragments were eliminated by chromatography with Sepharose S-300. Then the T-tailed plasmid was purified by an oligo dA column and stored in 50% ethanol at a concentration of 1 µg/µl.

Fig. 1 shows the outline of the construction of the cDNA library. Two micrograms each of the cytoplasmic Poly A⁺ RNA and the vector primer DNA were co-precipitated in 70% ethanol containing 0.3 M Na-acetate and the pellet was dissolved in 12 µl of distilled water. For the first strand synthesis, after heat denaturation at 76 °C for 10 min, 4 µl of 5 x reaction buffer [250 mM Tris-HCl (pH 8.3), 375 mM KCl, 15 mM MgCl₂], 2 µl of 0.1 M DTT and 1 µl of 10 mM each of dATP, dCTP, dGTP and dTTP were added to the sample at 37 °C. The reaction was initiated by the addition of 200 units of reverse transcriptase MMLV-H-RT (BRL), and after incubation at 37 °C for 30 min, stopped by transferring the reaction tube onto ice. For the second strand synthesis, to the aforementioned reaction mixture the following was added: 92 µl of distilled water, 32 µl of 5 x E. coli reaction buffer [100 mM Tris-HCl (pH 7.5), 20 mM MgCl₂, 50 mM (NH₄)₂SO₄, 500 mM KCl, 250 µg/ml of BSA, 750 µM βNAD], 3 µl of 10 mM each of dATP, dCTP, dGTP and dTTP, 15 units of E. coli ligase (Pharmacia), 40 units of E. coli polymerase (Pharmacia), and 1.5 units of E. coli RNase H (Pharmacia). The reaction mixture was then incubated at 16 °C for 2 h and heated to 65 °C for 15 min. Then 20 units each of BamHI and MboI were added, and the reaction mixture was incubated at 37 °C for 1 h and heated again at 65 °C for 30 min. Finally, the sample was diluted up to 1 ml with 1 x E. coli reaction buffer, and 100 units of E. coli ligase were added. The resulting mixture was incubated at 16 °C overnight. An aliquot of this mixture was used to transform competent E. coli DH5 cells (Toyobo). Transformants were selected by ampicillin resistance. The product was named "3' MboI cDNA library".

[Example 3]

Amplification of cDNA insert by PCR

The plasmid-carrier E. coli colonies were picked into 96-well plates containing 125 µl of LB medium (Davis, R. W., et al., *Advanced Bacterial Genetics*. New York: Cold Spring Harbor Laboratory, 1980) in each well and incubated in a moist chamber at 37 °C for 24 h. A replica culture was made for every plate using a 96-pinned replica device (Sigma) and the master plates were stored at -80 °C for future use. After overnight incubation at 37 °C, 50 µl of the culture from each well of these replicas were transferred to polycarbonate 96-well plates (Techne). Bacteria were collected by centrifugation in an Omnispin H4211 rotor (Sorvall) at 1500 rpm for 5 min, resuspended in 50 µl of water, covered with a layer of mineral oil and lysed at 95 °C for 30 min in a metal bath. Debris were removed by centrifugation at 3600 rpm for 30 min in the same rotor.

Five microliters of the supernatant were added to 20 µl of distilled water and kept at 95 °C for 10 min under a layer of mineral oil. Then the denatured lysate was subjected to PCR by adding 25 µl of 2 x reaction mixture [40 mM Tris-HCl (pH 8.9 at 23 °C), 3 mM MgCl₂, 50 mM KCl, 200 µg gelatin/ml] containing 5 pmol each of primers, 5 nmol each of dATP, dCTP, dGTP, dTTP and 1.25 units of Taq DNA polymerase (Cetus) at 70 °C. Temperature cycling reactions were carried out immediately after addition of the reaction mixtures using a thermal cycler either for microfuge tubes (PJ1000, Perkin Elmer Cetus) or for a 96-well plate (PHC-3, Techne); 35 repeated cycles of 30 sec at 96 °C, 1 min at 55 °C, and 2 min at 72 °C without a final extension step were performed.

For this method, the correct choice of primers for the PCR reaction is crucial. Therefore, preliminary tests were performed using the following primers with a predicted T_m of above 60 °C.

The primers tested were a pair of primers, FW(-47) and RV(-48), which are identical to the commercially available 24 mer primers, a second pair of primers, [FW(-40) and RV(-29)], which are a longer version (21 mer) of the well-tested sequencing primers, and the primers RV(-71) and RV(-14), which have a triplet sequence at the 3' terminus identical with that in FW(-40) but is in the opposite orientation (Fig. 2A).

In most of the cases where various combinations of primers were tested, short PCR artifacts appeared, besides the expected major products (Fig. 2B, arrows indicate the PCR artifacts.). These artifacts could be reduced by raising the annealing temperature, lowering the primer concentration or lowering the substrate

concentration but in all cases the yield of the products was not high enough to serve as a template for the sequencing reaction without concentration thereof.

However, since one pair of primers [SW(-40) and RV(-14)] did not yield artifacts (Fig. 3), this pair was selected for further tests, and was found to give reproducible results. Similar results were obtained with randomly selected cDNA clones. Therefore, only this pair of primers SW(-40) and RV(-14) was used as the primers of the present embodiment.

[Example 4]

10 DNA sequencing

The PCR products were drop-dialyzed against TE [10 mM Tris-HCl (pH 8.0), 1 mM EDTA] on millipore filter (VS 0.025 μ m) for 90 min while stirring. Forty-eight samples are easily applied on a single filter of 150 mm diameter. Without further purification the samples were subjected to the Cycle Sequencing protocol (Applied Biosystems, 1991) using dye labeled primers with minor modifications. For dideoxycytidine sequencing reaction, 2 μ l of the dialyzed PCR reaction product (about 0.2 pmol of template DNA) were added to 3 μ l of a reaction mixture containing 0.4 pmol of FAM M13 (-21) Primer (Applied Biosystems) in 160 mM Tris-HCl (pH 8.9), 40 mM $(\text{NH}_4)_2\text{SO}_4$, 10 mM MgCl_2 , 50 μ M dATP, 12.5 μ M dCTP, 75 μ M 7-deaza-dGTP (Boehringer Mannheim Biochemicals), and 50 μ M dTTP, 25 μ M ddCTP, 0.8 unit of Taq Polymerase (Perkin Elmer Cetus), and subjected to 15 plus 15 cycles of the reaction (95 °C 30 sec, 60 °C 1 sec, 70 °C 1 min and 95 °C 30 sec, 70 °C 1 min) according to the manufacturer's recommendation in a 96-well plate using a thermal cycler (PHC-3, Techne). The three other sequencing reactions for dideoxyguanosine, dideoxyadenosine, and dideoxythymidine were performed in parallel (with TMRA, JOE, and ROX primers respectively, supplied by Applied Biosystems) in an identical fashion, except that twice the volume of all the ingredients was added to the dideoxyguanosine and dideoxythymidine reactions. Each sample, from a set of four was cooled to 4 °C, pooled, precipitated with ethanol, resuspended in 6 μ l of a solution of formamide/50 mM EDTA (5/1 by v/v), loaded onto sequencing gel and analyzed by a DNA autosequencer (Model 373A Ver 1.0.1, Applied Biosystems).

30 [Example 5]

The frequency of appearance of each GS of the cDNA library reflects mRNA population.

To confirm that our 3'-directed regional cDNA library was a non-biased representation of the mRNA population in HepG2 cells, the inserts of four cDNA clones (EF-1 α , α -1-antitrypsin, hnRNP core protein A1 and inter- α -trypsin inhibitor) from the clones redundantly obtained by random selection of cDNA were radiolabeled and used as probes in a Northern analysis of poly A⁺ mRNA from the HepG2 cells. (The results are shown in Fig. 4A-D, and summarized in Fig. 4F.) The relative band intensity of the four mRNA species demonstrated that their relative ratios were 52, 24, 1 and 1.2, respectively (lane iii in Fig. 4F). Then the same set of probes was used for measuring the number of colonies hybridizing with each probe in the same cDNA library of 8,800 clones (Fig. 4E).

The clonal frequencies were 307, 128, 7 and 9, or in ratio, 44, 17, 1 and 1.3, respectively (lane iv in Fig. 4F). These two estimates agreed, showing that the cDNA library used is a non-biased representation of the mRNA population. The ratio was practically unchanged when different preparations of mRNA from the same cell were tested.

Fig. 4 shows the proportionality of the composition of the 3'-directed cDNA library and of the mRNA. Fig. 4A, 2 μ g of poly A⁺ RNA from HepG2 cells was electrophoresed in lanes 1-4 of a formamide agarose gel containing ethidium bromide (5 μ g/ml) and then exposed to UV. Lane 5 is the RNA ladder (BRL) used as size markers (kb). In Fig. 4B, the filter was northern blotted using the following ³²P-labeled 3'-specific cDNA probes: Elongation factor-1 α (lane 1), α 1-antitrypsin (lane 2), HnRNP core protein A1 (lane 3), inter- α -trypsin inhibitor (lane 4). In Fig. 4C, one pmol each of the non-labeled cDNA fragments [EF-1 α (lane 1), α 1-antitrypsin (lane 2), HnRNP core A1 (lane 3), inter- α -trypsin inhibitor (lane 4), were electrophoresed in a 2% agarose gel, then photographed. Fig. 4D is a Southern analysis of the blotted filter from Fig. 4C, using the same set of radioactive probes. Lane 5 shows the migration pattern of the reference 1 kb ladder (BRL). Hard copies of these screen images were taken at 8 h for b, and 1 h for d. The radioactivity in each band was counted directly in a scinti-scanner (β -603; Betagen) and registered in (i) and (ii) in Fig. 4F. The observed band intensities were corrected based on the band intensities in Fig. 4D (ii in Fig. 4F), and normalized relative to the value of probe 3 (HnRNP core A1, lane iii in Fig. 4F) as 1 (iii in Fig. 4F). These values represent the relative content of each mRNA species in the original mRNA preparation. Fig. 4E

shows the results of colony hybridization of the membranes carrying 8,800 colonies of the 3'-directed cDNA library using the same set of the four radioactive probes. Positive colonies were counted and registered (iv in Fig. 4F), then normalized with the value of HnRNP core protein A1 as 1. The numbers in B, D and E in Fig. 4 represent the probe No. in Fig. 4F. Fig. 4F shows a remarkable agreement between the values of lanes (iii) and (v).

[Example 6]

Population study of the cDNA library

To analyze further the composition of the cDNA library, 7 and 10 clones were selected from the redundant (group I) and solitary (group II) sequence groups, respectively, and these inserts were used as radiolabeled probes for colony hybridization (Fig. 6). The frequencies of the colonies that hybridized with group I probes were roughly identical to those that were randomly picked and sequenced. These frequencies were about 3.5%-0.1%. Nearly 52% of the cDNA library population consisted of the redundant sequence group containing 173 species. When 8 probes from group II were tested, 18 positive colonies were identified among 26,400 colonies screened, giving an average frequency of 0.007%. Two probes did not hybridize with any of the 26,400 colonies, resulting in the average frequency of <0.004%. Thus, the average frequency of the 10 probes in group II was several orders of magnitude less than the lowest of group I.

The results are summarized in Fig. 5, showing the appearance frequencies of various DNA species in the 3'-directed HepG2 cDNA library. In Fig. 5, seven cDNA probes (a15 through tb042) were selected from the 162 identified genes in the redundant group (group I), and ten (s155 through s632) were randomly chosen from the solitary group (group II). In columns A, B and C, each one of the insert DNAs was radiolabeled and used as a probe for colony hybridization tests of 982 (A), 8,800 (B) or 26,400 colonies (C). NT indicates "not tested". The DDBJ entry names of the 17 clones listed in this table are HUM000A15, HUM000C321, HUM00TB038, HUMHM01B02, HUM0C13A04, HUMHM02D02, HUM00TB042, HUM000S155, HUM000S159, HUM000S639, HUM000S635, HUM000S170, HUM000S154, HUM000S167, HUM000S645, HUM000S647, and HUM000S632.

[Example 7]

Analyses of sequencing errors

All the sequence data presented in this specification were obtained by repeated cycles of enzymatic amplification of the plasmid inserts, followed by cycle sequencing with Taq polymerase. Sequences of 60 clones that showed data bank matches were examined for discrepancies from the data bank entries. It was found that the accuracy in the region 1-100 bp distant from the cloning site was 98.7%, indicating that the primers or probes designed with the sequence in this region could be obtained practically without any erroneous sequences or even if they contain any errors, they are functionally without problems.

[Example 8]

Mapping of GS by PCR

(cDNA sequence)

cDNA library was constructed from mRNA of DMSO treated HL60 cells. The methods for construction of the 3'-directed cDNA library and for sequence analysis of the library components are the same as described in Examples 1-4.

(PCR primer)

Primer design was performed by using the computer software OLIGO 4.0 (National Biosciences) which eliminates possible formation of inter- or intra-molecular secondary structures. In addition to the primer design, transfer of oligonucleotide sequences to the local database and synthesizer were semiautomated using a Macintosh computer linked with a network. DNA oligomers were synthesized on an automated DNA synthesizer (Model 394, Applied Biosystems) on a 40 nmol scale. The synthesized oligomers were used as

PCR primers without further purification.

(Preparation of Genomic DNA)

5 The human genomic DNA was extracted from the normal karyotype lymphoblastoid cell line GM0130b. Mouse and Chinese hamster genomic DNAs were purchased from Clontech. Monochromosomal hybrid cells utilized for mapping panel were commonly used ones which have been described previously. Briefly, chromosomes 3, 4, 9, 11, 12, 13, 15, 22 and Y were carried in human-Chinese hamster monochromosomal hybrid cells, and chromosomes 1, 2, 5, 6, 7, 8, 10, 11, 12, 14, 15, 16, 17, 18, 19, 20, 21 and X were carried
10 in the human-mouse monochromosomal hybrid cells A9 series. The integrity of the hybrid cells were monitored by *in situ* hybridization.

(Amplification by Polymerase Chain Reaction)

15 PCR was performed according to standard protocols (Saiki, R. K., et al., Science 230, 1350-1354, 1985), using 10 pmol of each primer on a whole 20 μ l scale reaction, with 35 thermal cycles of 30 sec at 94°C, 60 sec at an annealing temperature, and 90 sec at 72°C, using a Perkin-Elmer 9600 thermal cycler. Annealing temperature was determined according to the "optional annealing temperature" estimated by the Program OLIGO.

20

(Analysis of the PCR Products)

The PCR products were run on an 8% polyacrylamide non-denatured gel (Acrylamide:Bis-acrylamide = 19:1, 1 mm thick) at 300 V for 1 h, followed by staining in 90 mM Tris-borate, 2 mM EDTA buffer solution
25 containing 0.25 μ g/ml ethidium bromide for 15 min. The size of the amplification products were determined relative to the 10 bp DNA ladder (BRL). Detection of fluorescence was performed by using a laser fluorescent image analyzer (FM-BIO, Hitachi Software Engineering). The image data were transferred to a computer for analysis.

30

(Results of Analysis of the PCR Products)

Among various species of 3'-directed cDNA-GSs obtained from granulocytoid cells, 195 novel GSs which did not match the sequences deposited in Genbank Release 76 were selected and used for designing primers for the PCR. The PCR was performed with these primers using the total human genomic
35 DNA as the template.

Among the 195 primer pairs, 191 (98%) yielded products whose size matched those expected within 5 nt. The results are summarized in Figs. 6 - 10 whose figure legends are as follows: GS, gene signature; CN, clone name; Chromosomal position, chromosome numbers to which GSs were mapped; Sequence of primers, DNA sequences of primers (Sense, sense strand; anti-sense, anti-sense strand); AT, annealing
40 temperature; HO, Observed size of PCR products with total human genomic DNA (nt); HE, Expected size of PCR products with total human genomic DNA (nt); MO, Observed size of PCR products with mouse genomic DNA (nt); CO, Observed size of PCR products with Chinese hamster genomic DNA (nt); G, Number of "hits" of GS in the granulocytoid (DMSO treated HL60) cDNA library after analyzing altogether 1000 clones; T, Total number of "hits" of the GS after analyzing altogether 3000 clones from the three
45 cDNA libraries of HL60 with and without induction by DMSO or TPA. Question marks ("??") indicate that the PCR products did not yield a clear band.

"M" indicates that the PCR products yielded a band which was indistinguishable from the band observed after the reaction using mouse DNA as the template. Similarly, "C" indicates that the PCR products yielded a band which was indistinguishable from the band after the reaction using Chinese
50 hamster DNA as the template.

The overall rate of success of the PCR was 191/195 (98%), although GSs were randomly selected from the cDNA sequences, indicating that the quality of the cDNA library used in this work was reliable, and that the sequence analyses and primer designs were performed appropriately. Thus, the possible chances of failure of the PCR caused by presence of an intron(s) in the relevant cDNA sequences is negligible in working with the GS, as introns virtually do not lie in the poly A proximal 3'-region of vertebrate genes
55 (Wilcox et al., Nucleic Acids Res. 19, 1837-1843, 1991). This is a big advantage compared to the use of partial fragmented cDNA sequences obtained from randomly primed cDNA libraries (Adams et al., Science 252, 1651-1656, 1991) or from 5'-directed cDNA libraries.

(Chromosomal assignments of GS)

The 191 primer pairs that yielded PCR products from total human DNA were used for chromosomal assignments of the GSs with the monochromosomal hybrid cell panel. At least 119 GSs were assigned to a single chromosome. As an example, GS001418, shown in Fig. 11, was assigned to chromosome number 3. With some clones, extra products were obtained, some of which were assigned to the same chromosome, whereas others to different chromosomes. An example, GS001457, is shown in Fig. 12. Sixty-two (33%) clones yielded the expected PCR products with two or more different chromosomes. Thirty-five cases (18%) yielded PCR products whose size were indistinguishable from background rodent genomic DNA. Among these, 21 GSs produced products indistinguishable from mouse and Chinese hamster DNA. Ten GSs yielded no expected PCR products with the monochromosomal cell panel DNA although the expected PCR products from total human genomic DNA were observed. The 10 cases probably arose from a small deletion in the hybrid cells. Five clones obtained from HepG2 cDNA library have been analyzed also by Southern blot analysis. Four out of the 5 GSs (GS000053, GS000120, GS000271 and GS000279) gave consistent results with those obtained by the PCR. One GS (GS000228), which was uncertainly assigned to chromosome Y because of the weak signal detected by the Southern blot method, was assigned to chromosome 11 by PCR.

[Example 9]

Mapping of GS by Southern blot method

(Cell lines)

Total human genomic DNA was isolated from the human normal karyotype lymphoblastoid cell line GM0130b. Monochromosomal hybrid cells used as the mapping panel are shown in Fig. 15. Hybrid A9(neo-x)-y cells as described by Koi, et al. (Jpn. J. Cancer Res. 80, 413-418, 1989) were donated by Dr. M. Oshimura, Faculty of Medicine, Tottori University, passaged 3 times and frozen for storage. The loss or rearrangements of chromosomes could have occurred during this period. The GM series was obtained from the Mutant Cell Repository, National Institute of General Medical Science (NIGMS) (Camden, NJ). To confirm that human chromosomes remained intact in the hybrid cells after storage in liquid nitrogen, metaphase spreads of the hybrid cells were monitored by chromosome staining based on *in situ* hybridization using biotinylated total human DNA as the probe (Durnam, D. M., et al., Somatic cell Mol. Genet. 11, 571-577, 1985). Intact, as well as translocated or fragmented human chromosomes were easily detected by this means. In a hybrid cell mapping panel, chromosomes 11, 12 and 15 were represented by the hybrid cell lines A9(neo-11)-1, A9(neo-12)-4 and A9(neo-15)-2, respectively, and in another panel, they were represented by the hybrid cell lines GM10927A, GM10868 and GM11418, respectively.

(Isolation of genomic DNA and Southern blotting)

High molecular weight DNA was extracted from cells using sodium dodecyl sulfate (SDS) and Proteinase K, followed by phenol-chloroform extraction and ethanol precipitation. DNAs were digested overnight with a combination of two restriction enzymes including EcoRI, BamHI and BglII. About 5 µg of each digest was electrophoresed in an 0.8% agarose gel, then transferred to Hybond N⁺ membrane (Amersham) with 0.4 N NaOH. The membrane was rinsed in 2 x SSC and stored at 4°C for subsequent use.

Clones containing a novel sequence and having more than 150 bp were selected as probes. The cDNA inserts of the clones were amplified by the PCR. The PCR products were isolated by electrophoresis through a 2% low-melting temperature agarose gel (Nusieve : SeaPlaque, 3 : 1), followed by excision. The gel was removed by melting at 65°C and digesting with β-Agarose I (Bio Labs) at 40°C for 1 h. The probes were labeled with [α-³²P]dCTP by random priming using a commercial kit (Amersham). Hybridization proceeded at 65°C in a high salt buffer containing 6xSSC, 1x Denhardt's solution and 0.5% SDS, in the presence of 0.1 mg/ml of sonicated, denatured salmon sperm DNA. The membranes were washed in 2xSSC, 0.1% SDS at 65°C for 30 min, then twice for 30 min in 0.1xSSC, 0.1% SDS at 65°C, and analyzed using a Fuji BAS-2000 imaging analyzer.

(Analyses with Genomic DNA)

Among the HepG2 3'-directed cDNA libraries described in Examples 1 and 2, 160 novel clones were selected and used as probes for Southern blots.

5 Total human genomic DNA was isolated from a cell line GM0130b that has a normal karyotype, and digested with the restriction enzymes, EcoRI, BamHI and BglII alone or in combination. The GS clones used as probes were the 3'-directed cDNAs. Each of these cDNAs covers a region between the poly(A) site and the nearest MboI site (GATC) (Okubo, K., et al., Nature Genetics 2, 173-179, 1992) and thus do not have restriction sites for BamHI or BglII. In addition, because the average size of GS is 270 bp, the chances of
10 having an EcoRI site in the cDNA moiety were not high. In fact, only 7 clones out of the 160 analyzed had an EcoRI restriction site.

Membranes blotted with digested human genomic DNA were hybridized with radio-labeled GS probes and washed at high stringency. Since the 3'-terminal region of cDNA has, in general, a unique sequence which differs from that of protein encoding regions which tend to have conserved motifs, cross hybridization
15 with unrelated cDNA sequences will not occur under such stringency. Examples of the results of hybridization are shown in Figs. 13 and 14. Clones s503 and s632 (Figs. 13a and 13b; junk) respectively represent unique single band producers. As shown below, 67 clones belonged to this class. The positions of the GS sequence relative to the restriction sites were inferred from the band patterns. Clone s311 (Fig. 13c; GS000092) showed a single band with EcoRI -as well as (EcoRI + BamHI)-digested DNA, but two bands of
20 different sizes in other double digests. The double digestion thus helped resolve multiple GSs. Similar results were obtained with clone c13a08 (Fig. 13d; GS000055), in which there were 2 bands with EcoRI- or (EcoRI + BamHI)-digested DNAs, and 4 when digested with (EcoRI + BglII) or (BamHI + BglII). On the other hand, 4 hybridization bands appeared with clone s479 with EcoRI alone, but the number of bands decreased with (EcoRI + BglII) and (BamHI + BglII) (Fig. 14e; GS000180). These results indicate that
25 genomic DNAs should be digested in various ways to reveal the maximum number of hybridizing fragments. The results of the analysis showed that 41, 10, 7 and 19 clones contained 2, 3, 4 and 5 or more bands, respectively. Clones s14f01 and tw1-46 (Figs. 14f and 14g; GS000407 and junk, respectively) contained at least 10 bands in each lane. Since the EcoRI restriction site is not present in the two GS sequences, the multiplicity of bands is likely to represent the multiple copy number of these genes. Clone
30 kmb07 moved as a smear (Fig. 14h; junk), even after intensive high stringency washes, suggesting that this probe has a repetitious sequence which has not been hitherto identified.

(Chromosomal assignments)

35 A set of monochromosomal hybrid cells carrying a single human chromosome in a background of rodent chromosome was collected (Fig. 15). Thirteen cell lines were microcell hybrids established by Koi et al. (Koi, M., et al., Jpn. J. Cancer Res. 80, 413-418, 1989) and the others were obtained from NIGMS. The results of monitoring the human chromosomes in these cell lines by *in situ* hybridization using biotinylated total human DNA are also presented in Fig. 15.

40 The GSs were assigned to chromosomes using hybrid cell mapping panels. Three types of membranes were prepared, each having DNAs prepared from hybrid cells, and digested with EcoRI, (EcoRI + BamHI), or (BamHI + BglII). Among these three types of membranes, the one which should have yielded the maximum number of bands was used for each GS probe, according to the results of total genomic Southern blots. Examples of hybridization results are shown in Figs. 16 - 22. The numeral on each lane represents the
45 human chromosome numbers which is contained in the hybrid cell, and H stands for the total human chromosomes. Clone s14g02 (GS000152; Fig. 16) that showed a single hybridization band with the total human DNA digested with EcoRI (lane H), showed the corresponding band only with the hybrid cell line containing human chromosome 4. Thus, this GS lies in chromosome 4.

The clone s650 (GS000041; Fig. 17) was assigned to chromosome 12 which showed a characteristic
50 7.5kb band in the presence of an (EcoRI + BamHI)-digested membrane. However, with an EcoRI digested DNA, the clone could not be assigned, as the human-specific and the cross-reacting rodent DNA fragments overlapped. The single, but shorter fragment band (1.3kb) which appeared in lanes 3, 4, 9, 13 and 22 represents the homologous DNA sequence in Chinese hamster, and the 3.3kb band in other lanes represents the homologous DNA in the mouse.

55 Clone hm01e01 (GS000181; Fig. 18) exhibited two fragments when hybridized to total human DNA treated with EcoRI alone, and these corresponding bands appeared in lanes 1 and 2. Thus, the two members of this gene family are located on two chromosomes.

Fig. 19 shows that clone c13a08 (GS000055) exhibited 4 bands when hybridized to (BamHI + BglII)- or (EcoRI + BglII)-digested total human DNA, although only 2 bands appeared with EcoRI- or (EcoRI + BamHI)-digested human DNA. Therefore, the (BamHI + BglII)-digested DNA panel was used for this clone. Two bands (12.3kb and 7.5kb) appeared in lane 7, a 5.2kb band in lane 2, and a 3.2kb band in lane 17. Two bands (6.0kb and 3.8kb) that cross-reacted with Chinese hamster DNA appeared in lanes 3, 4, 9, 13 and 22, and a single band (3.5kb) that cross-reacted with mouse DNA appeared in other lanes.

Clone s479 (GS000180; Fig. 20) showed 4 EcoRI fragments with total human DNA. The hybridization to an EcoRI-digested DNA panel yielded in bands of 10.5kb in lanes 7 and 19, 8.5kb in lane 8, 7.8kb in lanes 11 and 12, and 3.5kb in lane 11. Thus, the human specific genes are dispersed among chromosomes 7, 8, 11, 12 and 19, among which the 10.5 and 7.8kb bands in the total DNA both consist of two overlapping fragments. As shown in lane H, the intensity of these overlapping fragments was higher than normal. The 3.5kb band in lane H, as well as in lane 11 was also intense, suggesting that it also represents overlapping fragments.

Clone s173 (GS000094) exhibited 5 bands in EcoRI-cleaved total DNA (Fig. 21). Four corresponding fragments included a 4.5kb fragment in lane 1. Another 4.5kb band was observed in lane 4, indicating that the corresponding band in lane H overlapped. In addition, an intense 3.1kb band was observed in lane 17.

Clone hm01g02 (junk; Fig. 22) exhibited many bands with total DNA, and with those from monochromosomal hybrids. This clone must represent a multiple and closely related family of genes. It also contains a sequence conserved in homologous rodent genes which also give rise to multiple bands. Since most of the human specific and rodent bands overlapped, the chromosomes could not be assigned. Other combinations of restriction enzymes did not resolve the overlap.

The results of the total genomic DNA analyses and the chromosome assignments of 160 GSs are summarized in Figs. 23 - 26. Through total genomic DNA analyses using 4 differently digested human DNAs, 67 clones were categorized into a single band group, 41 in a two band group, 10 in a three band group, 7 in a four band group and 19 in a group that yielded five or more bands. Nine clones did not show any hybridization band under fixed conditions.

Assignment of two band clones showed that the two genes lie in different chromosomes in 15 of them, whereas the gene represented by clone s317 originated from the same chromosome. The three band clones s308 (GS000412) and s401 (GS000224) showed that two of the fragments lie on the same chromosome, and clone hm05g02 (GS000209) and s17a10 (GS000294) showed bands in different chromosomes. Clones displaying four or more bands showed a relatively dispersed distribution among chromosomes. "junk" in Example 9 is the DNA segment cloned by the same method used for GS but is not numbered.

[Example 10 Cloning of gene using GS]

[10A. Cloning of a full length cDNA encoding a human ribosomal protein, homologue of yeast S28. Cloning of the full length cDNA by PCR using a primer comprising a partial sequence of a GS(1)]

Using a primer (5'-TGAAAATTTATTACTACAGTGTTCACCA-3' (SEQ ID NO:7839)) that is a partial sequence of a DNA which is substantially the same as the complementary strand of HUMGS00500 and a primer (5'-TAATACGACTCACTATAGGG-3' (SEQ ID NO: 7840)) complementary to the vector (pSPORT) sequence that is located external to the 5' end of the cDNA, HepG2 cDNA library was amplified by the PCR and a full length cDNA clone encoding a human ribosomal protein, a homologue of yeast ribosomal protein S28 was isolated. (Hori et al., Nucl. Acids Res. 21: 4394, 1993).

[10B. A human ribosomal protein homologous to rat L9 ribosomal protein-Cloning of the full length cDNA by PCR using a primer comprising a partial sequence of a GS(2)]

Using a primer 5'-CTTCTTTCTGTAGCCAGGTAAGTCT-3' (SEQ ID NO: 7841) that is a partial sequence of a DNA which is substantially the same as the complementary strand of HUMGS00418 and a primer (SEQ ID NO: 7840) complementary to the vector (pSPORT) sequence that is located external to the 5' end of the cDNA, a full length cDNA clone encoding a human ribosomal protein homologous to rat L9 was isolated (Hori et al., Nucl. Acids Res. 21:4395, 1993).

[10C. A human protein homologous to bovine phosphatidylethanolamine-binding protein. Cloning of the full length cDNA by hybridization using a probe comprising a partial sequence of a GS]

By hybridization with the probe,

5' - GATCGTTCTTCATGGGGGTAAGAAAAGCTGGTCTGGAGTTGCTGAATG

TTGCATTAATTGTCCTGTTTGCTTGTAGTTGAATAAAAATAGAAACCTGAAT

GAAGGAAA-3' (SEQ ID NO:7838),

that comprises a partial sequence of HUMGS00421, a full length cDNA clone encoding a human protein homologous to bovine phosphatidylethanolamine-binding protein was isolated (Hori et al., Gene 140:293, 1994).

[10D. Human mpl-ligand. Cloning of a cDNA coding for the human mpl-ligand using a GS]

This embodiment employs the 5' SLIC (single ligation to single stranded cDNA) method which is an improved version of the 5'RACE (rapid amplification of cDNA ends) method, and is described in Nucleic Acids Res., 19, 5227-5232 (1991).

① Reverse transcription of cDNA and attachment of anchor

The template was prepared using the reagents of the 5'-Amplifinder™ Kit (Toyobo, Inc.) in accordance with the protocol included therewith. Specifically, 2μg of human fetal liver poly A⁺RNA (Clontech Laboratories, Inc.) and 10 pmol of the primer PA-6, a primer corresponding to the 3' end of the gene signature (GS) sequence HUMGS02342 and consisting of the sequence 5'-TTTTCGGCGCTCCCATTTATTCCTT-3' (SEQ ID NO: 7842), were mixed together and then denatured by heating the mixture at 65 °C for 5 min. The cDNA was synthesized by combining the denatured sample with AMW reverse transcriptase, RNase inhibitor, dNTPs, and a reaction buffer, and then heating the resultant mixture at 52 °C for 30 min. EDTA was then added to the mixture to stop the reaction. Thereafter, the RNA was hydrolyzed by adding NaOH to the reaction mixture and heating the resultant mixture at 65 °C for 30 min. The mixture was then neutralized with acetic acid. A suspension of glass beads (GENO-BIND™) and NaI were added to the neutralized solution and the cDNA was adsorbed onto the beads. The cDNA, adsorbed onto the beads, was washed with an aqueous solution of 80% EtOH, and then eluted in 50 μl of distilled water. Glycogen was added to the solution of purified cDNA, and the cDNA was precipitated with EtOH and resuspended in 6 μl of distilled water. The resultant suspension (2.5 μl) was added to a solution containing 4 pmol of AmpliFINDER Anchor (5'-CACGAATTCATCTATCGATTCTGGAACCTTCAGAGG NH₂-3') (SEQ ID NO: 7843) provided with the Kit, T4 RNA ligase, and a ligation (reaction) buffer. The reaction mixture was incubated at room temperature overnight, and the AmpliFINDER Anchor primer in the reaction mixture was thereby ligated to the 3' end of the cDNA. The ligated product was then used as a template for the subsequent PCR.

② Amplification by PCR

The primary PCR was carried out using the template produced in the procedure described above (①), the Anchor primer, 5'-CTGGTTCGGCCACCTCTGAAGGTTCCAGAATCGATAG-3' (SEQ ID NO: 7846) and the PA-5 primer consisting of the sequence 5'-CTCGCTCGCCCATCCTTATACAGGCTCAGTTTGTCT-3' (SEQ ID NO: 7844). Specifically, 1 μl of the template was mixed with Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-5 primer and Anchor primer. The resultant reaction mixture was diluted with distilled water to a final volume of 50 μl and the PCR was performed in a DNA Thermal Cycler 480 (Perkin Elmer Cetus Corp.). The reaction mixture was subjected to 40 cycles of the PCR, wherein each cycle consisted of incubating the sample in sequence at 94 °C for 1 min, 63 °C for 1 min, and 72 °C for 3 min and, in the last PCR cycle, at 72 °C for an additional 8 min. The products of the PCR were resolved by electrophoresis in a 1% agarose gel and a broad band of

approximately 800 bp in length, representing a product of the PCR, was detected. The detected band was excised from the agarose gel and the DNA contained therein was recovered using a Sephaglas Bandprep Kit™ (Pharmacia Corp.) in accordance with the protocol included therewith. Specifically, the gel was dissolved in a solution of NaI and the resultant mixture was heated at 60 °C for 10 min. Sephaglas™ BP was added to the gel mixture and the DNA was adsorbed onto the glass beads contained therein. The glass beads, containing the adsorbed DNA, were then washed three times with a Wash Buffer provided with the Kit and eluted in 30 µl of TE buffer (10 mM Tris-HCl pH 8.0, 1mM EDTA).

One µl of the eluted DNA was used as a template in a secondary PCR. In order to enhance the specificity of the secondary PCR, the reaction was performed with PA-4 primer which consisted of the sequence 5'-CTCGCTCGCCCATGTATAGGGACAGCATTTCTGAGAG-3' (SEQ ID NO: 7845) and was positioned within the template sequence internal to the PA-5 primer and the Anchor primer. Specifically, 1 µl of the template was mixed with 2.5 units of Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-4 primer and Anchor primer. The resultant reaction mixture was diluted with distilled water to a final volume of 50 µl preheated at 94 °C for 6 min, and the secondary PCR was then performed under the same conditions described above (①) for the primary PCR. The products of the secondary PCR were resolved by electrophoresis in a 1% agarose gel and a broad band of approximately 800 bp in length, representing a product of the PCR, was detected. The detected band was excised from the agarose gel and the DNA contained therein was recovered and purified under the same conditions as described above (①) for the primary PCR.

③ Subcloning into plasmid vector

The purified DNA product of the secondary PCR was subcloned into the plasmid vector pUC18 (pharmacia Corp.), using a SureClone™ Ligation Kit (Pharmacia Corp.) in accordance with the protocol included therewith. Specifically, the purified DNA was added to a solution containing Klenow polymerase, polynucleotide kinase and a reaction buffer, mixed and heated at 37 °C for 30 min in order to create blunt-ended termini and to phosphorylate the 5' terminus of the DNA molecules contained in the reaction mixture. The blunt-ended and phosphorylated DNA was combined with a solution containing 50 ng of a dephosphorylated and Sma I-cleaved pUC18 vector provided with the Ligation Kit, T4 DNA ligase, DTT and a ligation reaction buffer, and the resultant mixture was warmed at 16 °C for 3 hr. One sixth volume of the reaction solution was employed to transform E. coli competent cells using standard methods. Specifically frozen E. coli competent cells (Wako Pure Chemical Industries, Ltd.) were thawed and mixed with the ligated DNA. The resultant mixture was incubated on ice for 20 min, heat-treated at 42 °C for 45 sec, and then incubated on ice for 2 min. A medium [Hi-Competence Broth (Wako Pure Chemical Industries, Ltd.)) was added to the mixture containing the transformed E. coli cells. The mixture was incubated for 37 °C for 1 hr and then spread onto agar plates containing 100 µg/ml Ampicillin, 40 µg/ml X-Gal (6-bromo-4-chloro-3-indolyl-β-D-galactoside), 0.1 mM IPTG (isopropyl-β-D-thiogalactopyranoside) and cultured overnight at 37 °C. White colonies were selected from the colonies which consequently appeared on the agar plates and analyzed by the PCR to determine the presence or absence of the DNA insert. Specifically, a sample of a selected colony was picked with a sterilized toothpick and used to inoculate a 50 µl reaction solution containing 1 unit of Taq DNA polymerase, dNTPs, PCR buffer, 200 µM each of the M13 P4-22 primer consisting of the sequence 5'-CCAGGGTTTCCAGTCACGAC-3' (SEQ ID No: 7847) and M13 P5-22 primer consisting of the sequence 5'-TCACACAGGAAACAGCTATGAC-3' (SEQ ID No: 7848), wherein both primers are comprised of sequences complementary to the pUC18 vector. The resultant mixture was heated at 94 °C for 6 min and then subjected to 30 cycles of the PCR wherein each cycle consisted of incubating the sample in sequence, at 94 °C for 1 min, 55 °C for 1 min, and 72 °C for 2 min. The amplified insert was detected by electrophoresis of the PCR products on an agarose gel and thereby the clone pR02342-2, containing an insert, was selected.

④ Sequencing of cDNA

The plasmid DNA was prepared using the QIAprep-Spin Kit (Funakoshi, Ltd.) in accordance with the standard alkali-SDS protocol included therewith. Specifically, E. coli cells transformed with the DNA of clone pR02342-2 were cultured overnight in Luria Broth medium containing 100 µg/ml Ampicillin. The cultured cells were then pelleted by centrifugation and resuspended in P1 solution provided in the Kit. The resultant cell suspension was mixed with the P2 alkali solution of the Kit, incubated at room temperature for 5 min, neutralized with N3 solution of the Kit, incubated on ice for an additional 5 min and then centrifuged. The supernatant obtained from the centrifuged solution was applied to a QIAprep-Spin column. The Spin column

was then washed in sequence with PB and then PE solution of the Kit and the DNA was eluted from the column with TE buffer. Sequencing of the eluted DNA was then carried out using the sequencing kit PRISM™ Terminator Mix (Applied Biosystem Corp). Approximately 1 µg of the purified DNA was mixed with a solution containing 3.3 pmol of either the M13 P4-22 primer or M13 P5-22 primer and 9.5 µl of PRISM™ Terminator Mix. The M13 P4-22 and M13 P5-22 primer were used to sequence both strands of the DNA insert of clone pR02342-2. The resultant mixture was diluted to a final volume of 20 µl with distilled water and subjected to 25 cycles of the PCR wherein each cycle consisted of incubating the sample in sequence at 96 °C for 30 sec, 50 °C for 15 sec, and 60 °C for 4 min. The excess primers and fluorescent dye present in the reaction mixture were removed by gel filtration using a MicroSpin™ S-200 HR column (Pharmacia Corp.) and the DNA products of the sequencing reaction were precipitated with EtOH. The precipitated DNA was resuspended, sequenced using an automated sequencer, "Model 373A" (Applied Biosystem Corp.), and thereafter analyzed to determine the nucleotide sequence.

The analysis of the nucleotide sequence revealed that the insert of clone pR02342-2, including the PA-4 primer, was 608 bp in length. The sequence of this insert was subjected to a search for homologous sequences entered in the Gen Bank data base, and a 100% match was found to a sequence in the cDNA which encodes the human mpl-ligand (Accession No. L 33410, Nature 369, 533-538, 1994). Further comparison of the insert of clone pR02342-2 with the cDNA sequence of the human mpl-ligand revealed that the cloned insert contained 81 bp of the 3' coding region of open reading frame. In addition, the insert of clone pR02342-2 contained an additional sequence extending beyond the 3' end of the human mpl-ligand cDNA sequence registered under Gen Bank Accession No. L 33410. These findings suggest that, using the GS HUMGS02342, the inventors of the present invention succeeded in cloning a cDNA clone pR02342-2, which could possibly have a different and more desirable property for expression than the human mpl-ligand cDNA represented by the sequence registered under Gen Bank Accession No. L 33410.

25 ⑤ Cloning of the full-length cDNA encoding the human mpl-ligand

In order to find an optimal PCR primer, an appropriate computer program is used to search the sequence downstream of the coding region of the human mpl-ligand (clone pR02342-2) and thereby a primer PA-7 is designed and synthesized. A PCR similar to that described above in ② is performed using the template produced by the procedure described above in ①, the Anchor primer, and the PA-7 primer. Specifically, 1 µl of the template is mixed with 2.5 units of Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-7 primer and Anchor primer. The resultant reaction mixture is diluted with distilled water to a final volume of 50 µl and the PCR is performed in a DNA Thermal Cycler 480 (Perkin Elmer Cetus Corp.) under conditions similar to that described above in ②. The products of the PCR are then resolved by electrophoresis on a 1% agarose gel and a band greater than 1300 bp in length, representing a product of the PCR, is recovered and cloned into a suitable vector in a manner similar to that described in ③. The cloned DNA is sequenced in a manner similar to that described in ④. The sequence is then compared to that of the human mpl-ligand cDNA registered under Gen Bank Accession No. L 33410 to confirm the presence of the full-length open reading frame.

Alternatively, using the Takara La PCR Kit (Takara Shuzo Inc., Code No. RR011) in accordance with the protocol included therewith, performing the 5'RACE procedure using primers similar to those described above in ②, a cDNA of approximately 2 Kb in length, corresponding to the human mpl-ligand, was isolated.

The tables of appearance frequencies for all GSs related to the present invention are followed by "Sequence Listing" for these GSs, wherein HUMGS numbers after the heading 'clone' represent GS numbers. In the sequence table, N in the base sequence stands for "A or C or G or T or U". However, since nucleic acids in the Sequence Listing are DNAs, "T or U" stands for T in this case.

By the present invention, it has become possible to provide DNA molecules which carry "the information for expression" in various cells and can be used for detecting and diagnosing the cellular abnormalities, recognizing and identifying cells and further efficiently cloning genes which are expressed in a tissue-specific manner, and furthermore cloned DNA molecules which can be used for the production of proteins useful as pharmaceutical products.

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1	00001	00001	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
2	00002	00002	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
3	00003	00003	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
4	00004	00004	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
5	00005	00005	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
6	00006	00006	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
7	00007	00007	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
8	00008	00008	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
9	00009	00009	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	00010	00010	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11	00011	00011	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
12	00012	00012	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
13	00013	00013	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
14	00014	00014	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
15	00015	00015	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
16	00016	00016	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
17	00017	00017	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
18	00018	00018	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
19	00019	00019	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
20	00020	00020	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
21	00021	00021	10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AP	AR	AS	AT	AW	AY	BABC	DE	BF	BGBH	BI	BK
22	00023	00021	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	00026	00022	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	00028	00023	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	00029	00024	5	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	00030	00025	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	00031	00026	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	00033	00027	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	00034	00028	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	00036	00029	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	00037	00030	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	00038	00031	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	00039	00032	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	00040	00033	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	00041	00034	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	00042	00035	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	00043	00036	9	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	00044	00037	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	00045	00038	5	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	00046	00039	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	00047	00040	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	00048	00041	10	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	00049	00042	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	00050	00043	16	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
45	00051	00044	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	00053	00045	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	00055	00046	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	00056	00047	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	00057	00048	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	00060	00049	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	00061	00050	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	00062	00051	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	00064	00052	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	00065	00053	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	00066	00054	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	00067	00055	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	00068	00056	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 2

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK			
58	00069	00057	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0M34664	92.4	344	1	1484	2202			
59	00070	00058	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
60	00071	00059	7	1	0	0	3	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
61	00072	00060	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
62	00073	00061	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
63	00074	00062	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
64	00075	00063	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
65	00076	00064	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
66	00077	00065	34	1	3	2	5	1	0	0	2	2	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
67	00078	00066	12	1	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
68	00079	00067	2	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
69	00080	00068	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
70	00081	00069	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
71	00082	00070	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
72	00083	00071	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
73	00084	00072	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
74	00085	00073	26	5	3	1	0	0	1	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
75	00086	00074	4	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
76	00087	00075	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
77	00088	00076	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
78	00089	00077	33	1	3	2	2	0	1	0	1	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
79	00090	00078	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
80	00091	00079	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
81	00092	00080	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
82	00093	00081	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
83	00094	00082	9	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
84	00095	00083	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
85	00096	00084	62	6	5	4	2	0	0	0	1	2	6	5	1	3	1	1	5	3	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0
86	00097	00085	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
87	00098	00086	7	1	0	0	0	0	0	0	2	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
88	00099	00087	9	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
89	00100	00088	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
90	00101	00089	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
91	00102	00090	44	2	4	0	3	0	1	1	1	6	2	1	2	8	0	1	1	1	1	4	0	0	0	0	0	0	0	0	0	0	0	0	0
92	00103	00091	4	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
93	00104	00092	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 3

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
94	00105	00093	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
95	00106	00094	8	2	1	1	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
96	00107	00095	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
97	00108	00096	31	2	3	0	0	1	0	2	0	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
98	00109	00097	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
99	00110	00098	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
100	00111	00099	38	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
101	00113	00100	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
102	00114	00101	38	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
103	00115	00102	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
104	00116	00103	17	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
105	00117	00104	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
106	00118	00105	7	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
107	00119	00106	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
108	00120	00107	5	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
109	00121	00108	4	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
110	00122	00109	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
111	00123	00110	14	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
112	00124	00111	6	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
113	00125	00112	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
114	00127	00113	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
115	00128	00114	6	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
116	00129	00115	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
117	00130	00116	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
118	00131	00117	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
119	00132	00118	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
120	00133	00119	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
121	00134	00120	24	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
122	00135	00121	81	5	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
123	00136	00122	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
124	00137	00123	10	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
125	00138	00124	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
126	00139	00125	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
127	00140	00126	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
128	00141	00127	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
129	00142	00128	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 4

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
166	00179	00165	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
167	00180	00166	7	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
168	00181	00167	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
169	00182	00168	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
170	00183	00169	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
171	00184	00170	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
172	00185	00171	13	2	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
173	00186	00172	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
174	00187	00173	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
175	00188	00174	11	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
176	00189	00175	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
177	00190	00176	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
178	00191	00177	3	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
179	00192	00178	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
180	00193	00179	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
181	00194	00180	34	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
182	00195	00181	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
183	00196	00182	67	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
184	00197	00183	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
185	00198	00184	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
186	00199	00185	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
187	00200	00186	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
188	00201	00187	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
189	00202	00188	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
190	00203	00189	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
191	00204	00190	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
192	00205	00191	5	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
193	00206	00192	7	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
194	00207	00193	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
195	00209	00194	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
196	00210	00195	14	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
197	00211	00196	128	8	24	2	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
198	00212	00197	16	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
199	00213	00198	8	1	0	0	0	0	0	0	0	0	0	0	0	0																		

Table 6

[illegible]

Table 7

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	BAB	BC	BE	BF	BG	BH	BI	BK
238	00254	00237	38	1	0	0	2	0	1	2	1	0	1	0	2	0	1	3	0	0	0	0	0	0	1	3	20	0	0	024096	98.1	214	1	1152	1365
239	00255	00238	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
240	00256	00239	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
241	00257	00240	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
242	00258	00241	6	1	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0	004588	95.4	217	3	1857	2077
243	00259	00242	2	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
244	00260	00243	4	1	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0						
245	00261	00244	17	2	1	0	1	0	1	0	0	1	0	1	1	1	1	1	1	1	0	0	3	0	2	0	2	0	0	065460	99	204	1	1607	1809
246	00262	00245	50	2	7	2	0	1	1	2	0	3	6	0	1	3	0	3	0	1	2	0	0	4	4	0	6	2	0	017885	98.6	211	1	888	1097
247	00263	00246	2	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
248	00264	00247	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
249	00265	00248	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
250	00266	00249	3	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
251	00267	00250	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	055330	99.1	107	83	1	2150
252	00268	00251	5	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
253	00269	00252	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	063679	98.3	116	1	1152	1267
254	00270	00253	9	1	0	1	0	0	0	0	1	0	1	0	3	0	1	0	0	0	0	0	1	0	0	0	0	0	0	004526	95.2	209	1	2887	3088
255	00271	00254	21	2	0	1	2	0	1	0	0	2	0	0	5	0	1	2	0	0	0	0	0	0	0	2	4	0	0	X75683	99	210	1	92	301
256	00272	00255	9	1	0	0	0	0	1	2	0	0	0	1	0	0	1	0	1	0	0	0	0	0	1	0	1	0	0	005262	100	197	1	931	1148
257	00273	00256	119	9	6	4	13	2	11	2	1	12	14	0	6	0	3	1	3	0	0	0	0	2	3	3	15	3	0	X64899	94.8	192	1	626	819
258	00274	00257	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
259	00275	00258	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
260	00276	00259	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
261	00277	00260	36	3	0	0	0	8	14	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	029882	100	191	1	234	424
262	00278	00261	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
263	00279	00262	10	2	0	1	1	0	0	0	0	2	3	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
264	00280	00263	3	1	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	064228	99.5	196	1	6389	6597
265	00281	00264	8	3	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	1	0	0	007395	97.9	190	1	2036	2226
266	00282	00265	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
267	00283	00266	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
268	00284	00267	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
269	00285	00268	89	6	14	1	8	0	3	4	1	4	3	5	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0					
270	00286	00269	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
271	00287	00270	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
272	00288	00271	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
273	00289	00272	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

28

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AQ	AS	AW	AY	B	BE	BF	BGBH	BI	BK						
274	00290	00273	85	5	9	3	8	4	2	1	1	1	1	7	4	1	4	5	0	2	6	5	3	6	1	0	2	0	5	0	X66699	99.5	184	1	163	349
275	00291	00274	8	1	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0
276	00292	00275	49	4	12	1	0	2	1	1	4	6	4	0	0	2	0	0	0	5	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
277	00293	00276	74	6	13	1	6	2	4	3	3	2	5	0	1	0	0	0	0	2	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
278	00294	00277	5	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
279	00295	00278	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
280	00296	00279	8	1	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
281	00297	00280	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
282	00298	00281	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
283	00299	00282	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
284	00300	00283	24	2	1	0	0	2	0	1	0	0	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
285	00301	00284	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
286	00302	00285	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
287	00303	00286	17	2	2	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
288	00304	00287	48	2	1	2	1	0	1	0	1	1	3	2	2	3	1	0	4	2	6	0	3	0	1	0	0	0	0	0	0	0	0	0	0	0
289	00305	00288	46	1	6	0	2	2	3	1	2	1	4	4	2	2	0	0	3	0	1	4	1	0	2	2	1	1	2	0	0	0	0	0	0	0
290	00306	00289	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
291	00307	00290	4	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
292	00308	00291	10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
293	00309	00292	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
294	00310	00293	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
295	00311	00294	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
296	00312	00295	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
297	00313	00296	17	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
298	00314	00297	45	1	3	1	0	1	0	1	5	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
299	00315	00298	21	3	4	1	0	0	1	0	1	1	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
300	00316	00299	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
301	00317	00300	10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
302	00320	00301	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
303	00322	00302	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
304	00323	00303	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
305	00325	00304	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
306	00327	00305	20	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
307	00328	00306	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
308	00329	00307	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
309	00330	00308	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
																										</										

Table 9

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BGBH	BI	BK	
310	00331	00309	6	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
311	00332	00310	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
312	00333	00311	16	1	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
313	00334	00312	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
314	00335	00313	86	1	16	4	3	1	1	0	3	7	3	1	5	6	1	3	2	1	1	1	1	4	2	5	0	10	3	436072	100 165	1 727	891
315	00336	00314	47	1	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
316	00337	00315	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
317	00338	00316	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
318	00339	00317	13	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
319	00340	00318	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
320	00341	00319	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
321	00342	00320	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
322	00343	00321	12	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
323	00344	00322	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
324	00346	00323	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
325	00347	00324	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
326	00348	00325	10	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
327	00349	00326	29	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
328	00350	00327	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
329	00351	00328	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
330	00352	00329	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
331	00353	00330	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
332	00354	00331	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
333	00355	00332	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
334	00356	00333	43	1	17	0	0	2	2	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
335	00357	00334	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
336	00358	00335	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
337	00359	00336	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
338	00360	00337	19	2	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
339	00361	00338	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
340	00362	00339	19	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
341	00363	00340	29	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
342	00364	00341	632	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
343	00365	00342	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
344	00366	00343	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
345	00367	00344	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 10

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK		
346	00368	00345	11	1	0	0	0	2	0	0	2	0	0	0	0	0	0	0	0	3	0	0	1	0	0	0	0	1	M31627	98.6	141	1	1657	1818	
347	00369	00346	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	L10379	98.6	142	1	1581	1725	
348	00370	00347	7	1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	3	0	0							
349	00372	00348	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
350	00373	00349	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
351	00374	00350	10	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
352	00375	00351	36	2	3	0	0	3	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
353	00376	00352	21	2	0	0	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
354	00377	00353	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
355	00378	00354	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
356	00379	00355	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
357	00380	00356	47	1	12	0	1	0	1	0	0	2	5	2	0	1	3	1	1	1	1	1	1	1	2	0	0	0							
358	00381	00357	22	1	0	2	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
359	00382	00358	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
360	00383	00359	28	3	1	3	3	0	1	0	0	2	0	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0						
361	00384	00360	10	1	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
362	00385	00361	4	3	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
363	00386	00362	6	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
364	00387	00363	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
365	00388	00364	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
366	00389	00365	4	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
367	00390	00366	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
368	00391	00367	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
369	00392	00368	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
370	00393	00369	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
371	00394	00370	2	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
372	00395	00371	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
373	00396	00372	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
374	00397	00373	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
375	00398	00374	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
376	00399	00375	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
377	00400	00376	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
378	00401	00377	16	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
379	00402	00378	39	1	0	0	0	2	0	0	0	1	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
380	00403	00379	21	7	0	1	0	0	0	0	0	0	0	1	0	0	1	3	0	1	0	0	0	0	0	0	0	0	0	0					
381	00404	00380	2																																

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	A	A	C	A	I	A	K	A	M	A	C	A	S	A	U	A	V	A	B	C	BE	BF	BGBH	BI	BK
382	00405	00381	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
383	00406	00382	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
384	00407	00383	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
385	00408	00384	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
386	00409	00385	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
387	00410	00386	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
388	00411	00387	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
389	00412	00388	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
390	00413	00389	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
391	00414	00390	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
392	00415	00391	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
393	00416	00392	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
394	00417	00393	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
395	00418	00394	116	5	22	1	13	1	5	1	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
396	00419	00395	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
397	00420	00396	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
398	00421	00397	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
399	00422	00398	16	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
400	00423	00399	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
401	00424	00400	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
402	00425	00401	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
403	00426	00402	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
404	00427	00403	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
405	00428	00404	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
406	00429	00405	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
407	00430	00406	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
408	00431	00407	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
409	00433	00408	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
410	00434	00409	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
411	00435	00410	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
412	00436	00411	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												

Table 12

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BGBH	BI	BK		
418	00442	00417	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
419	00443	00418	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
420	00444	00419	71	6	10	1	4	2	4	1	1	0	3	1	0	5	0	0	1	4	0	5	0	1	0	0	M81757	98.9	90	1	410	510	
421	00445	00420	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
422	00446	00421	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
423	00447	00422	38	2	6	1	1	0	3	2	0	2	6	2	0	1	0	0	3	1	1	1	1	1	0	3	X69391	96.5	86	1	841	926	
424	00448	00423	17	1	0	0	1	1	0	0	0	1	2	0	1	0	0	0	1	1	0	2	0	1	0	1							
425	00450	00424	30	3	2	2	2	0	0	0	0	0	0	0	2	1	0	2	0	3	1	10	0	0	0	0							
426	00451	00425	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
427	00453	00426	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
428	00454	00427	7	1	0	0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
429	00455	00428	10	2	0	1	0	0	0	1	0	0	1	0	0	0	0	0	1	0	0	0	1	0	2	0	0						
430	00456	00429	18	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2	0	1	0	1	2	1	0	0						
431	00457	00430	3	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0						
432	00458	00431	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
433	00459	00432	8	1	0	0	0	0	0	0	1	0	1	0	0	0	0	0	1	0	0	2	0	0	1	0	0	0	97.5	79	1	395	692
434	00460	00433	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
435	00461	00434	3	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
436	00462	00435	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
437	00463	00436	26	2	2	0	1	1	0	0	0	0	0	1	0	0	2	0	2	2	3	1	1	2	4	0	X02152	94.7	76		1	1587	1661
438	00464	00437	18	1	1	2	0	0	1	0	0	1	3	0	1	1	0	0	0	2	2	1	0	1	1	0	0	98.6	74		1	2925	2998
439	00465	00438	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	1	0	0	96	75		1	2513	2587	
440	00466	00439	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
441	00467	00440	4	1	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
442	00468	00441	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
443	00469	00442	6	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
444	00470	00443	3	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0						
445	00471	00444	8	1	0	1	0	0	1	1	0	0	0	0	0	1	0	0	1	0	0	0	1	0	0	0	0						
446	00473	00445	10	1	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	1	5	0	0	0	0	0	0						
447	00474	00446	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X16154	100	71		1	3387	3464
448	00475	00447	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
449	00477	00448	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
450	00478	00449	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
451	00479	00450	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
452	00480	00451	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
453	00481	00452	24	1	1	0	0	0	1	0	3	0	0	2	0	0	1	3	0	0	3	0	1	3	2	0	1	0					

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AP	AR	AS	AT	AW	AY	BA	BB	BF	BG	BH	BI	BK
454	00482	00453	7	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
455	00483	00454	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
456	00484	00455	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
457	00485	00456	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
458	00486	00457	6	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
459	00487	00458	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
460	00488	00459	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
461	00489	00460	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
462	00491	00461	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
463	00493	00462	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
464	00494	00463	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
465	00495	00464	12	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
466	00496	00465	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
467	00497	00466	11	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
468	00498	00467	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
469	00500	00468	54	6	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
470	00503	00469	8	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
471	00504	00470	56	1	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
472	00505	00471	7	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
473	00506	00472	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
474	00507	00473	9	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
475	00510	00474	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
476	00511	00475	7	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
477	00532	00476	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
478	00533	00477	44	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
479	00534	00478	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
480	00535	00479	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
481	00536	00480	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
482	00537	00481	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
483	00538	00482	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
484	00539	00483	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
485	00540	00484	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0</																

Table 14

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	J	A	N	A	C	A	S	A	L	A	W	A	B	B	C	B	E	F	BG	BH	BI	BK
490	00545	00489	36							2	1	2	3	0	1	3	1	1	0	2	1	1	0	1	1	3	0	7	1	M94314	93.4	439	1	75	556	
491	00546	00490	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
492	00547	00491	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
493	00548	00492	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
494	00549	00493	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
495	00551	00494	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
496	00552	00495	4	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
497	00553	00496	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
498	00554	00497	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
499	00555	00498	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
500	00556	00499	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
501	00557	00500	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
502	00558	00501	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
503	00560	00502	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
504	00561	00503	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
505	00562	00504	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
506	00564	00505	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
507	00565	00506	70	4	2	5	0	0	1	1	1	1	4	5	1	1	0	4	6	2	1	1	2	0	0	0	0	0	0	0						
508	00567	00507	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
509	00568	00508	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
510	00569	00509	10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
511	00571	00510	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
512	00572	00511	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
513	00573	00512	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
514	00574	00513	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
515	00575	00514	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
516	00576	00515	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
517	00577	00516	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
518	00578	00517	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
519	00579	00518	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
520	00580	00519	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
521	00581	00520	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
522	00582	00521	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
523	00583	00522	34	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
524	00584	00523	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
525	00585	00524	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
526	00586	00525	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
527	00587	00526	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
528	00588	00527	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
529	00589	00528	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
530	00590	00529	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
531	00591	00530	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
532	00592	00531	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
533	00593	00532	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
534	00594	00533	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
535	00595	00534	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
536	00596	00535	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
537	00597	00536	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
538	00598	00537	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
539	00599	00538	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
540	00600	00539	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
541	00601	00540	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
542	00602	00541	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
543	00603	00542	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
544	00604	00543	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
545	00605	00544	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0										

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
562	00626	00561	4		2	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
563	00627	00562	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
564	00628	00563	4		1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
565	00629	00564	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
566	00630	00565	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
567	00631	00566	2		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
568	00632	00567	5		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
569	00633	00568	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
570	00634	00569	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
571	00635	00570	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
572	00636	00571	5		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
573	00637	00572	3		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
574	00638	00573	3		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
575	00639	00574	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
576	00640	00575	10		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
577	00641	00576	8		2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
578	00642	00577	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
579	00643	00578	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
580	00644	00579	24		5	0	2	0	1	1	0	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
581	00645	00580	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
582	00646	00581	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
583	00647	00582	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
584	00648	00583	8		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
585	00649	00584	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
586	00650	00585	52		14	2	6	0	2	0	1	1	2	1	6	3	2	0	0	0	0	0	0	0	0	0	0	0						
587	00651	00586	9		4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
588	00652	00587	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
589	00653	00588	13		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
590	00654	00589	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
591	00655	00590	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
592	00657	00591	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
593	00658	00592	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
594	00659	00593	6		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
595	00661	00594	9		2	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
596	00662	00595	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
597	00663	00596	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 17

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AU	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
598	00664	00597	3		1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
599	00665	00598	2		1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
600	00666	00599	5		1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
601	00667	00600	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
602	00668	00601	8		2	0	1	0	0	0	1	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
603	00669	00602	2		1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
604	00670	00603	12		2	0	0	0	2	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
605	00671	00604	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
606	00672	00605	7		3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
607	00673	00606	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
608	00674	00607	5		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
609	00675	00608	31		4	1	4	0	1	0	2	1	1	0	0	0	2	5	0	0	1	0	2	0	0	0	0								
610	00676	00609	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
611	00677	00610	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
612	00678	00611	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
613	00679	00612	15		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
614	00680	00613	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
615	00681	00614	7		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
616	00682	00615	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
617	00683	00616	20		1	2	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
618	00684	00617	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
619	00685	00618	18		2	5	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
620	00686	00619	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
621	00687	00620	16		1	3	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
622	00689	00621	40		1	1	2	0	1	3	0	4	0	3	2	2	1	2	2	1	2	1	1	1	1	0	2								
623	00690	00622	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
624	00691	00623	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
625	00692	00624	6		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
626	00693	00625	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
627	00694	00626	3		2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
628	00695	00627	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
629	00696	00628	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
630	00697	00629	7		2	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
631	00698	00630	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
632	00699	00631	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
633	00700	00632	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								

Table 18

[illegible]

Table 19

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK		
670	00739	00669	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
671	00740	00670	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
672	00741	00671	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
673	00742	00672	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
674	00743	00673	54	7	1	7	2	0	1	0	1	8	0	0	0	0	3	2	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0		
675	00745	00674	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
676	00746	00675	13	1	1	2	1	0	0	0	0	0	0	0	0	0	1	6	2	0	0	0	1	1	1	2	0	0	0	0	0	0	0		
677	00747	00676	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		562904	95.9	170	1	1389	2742		
678	00748	00677	5	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
679	00749	00678	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
680	00750	00679	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
681	00751	00680	5	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
682	00752	00681	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
683	00753	00682	6	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
684	00754	00683	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
685	00755	00684	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
686	00757	00685	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
687	00758	00686	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
688	00759	00687	25	4	1	1	0	0	1	1	0	0	2	1	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
689	00760	00688	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
690	00761	00689	10	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
691	00762	00690	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
692	00763	00691	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
693	00764	00692	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
694	00765	00693	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
695	00766	00694	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
696	00768	00695	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
697	00769	00696	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
698	00770	00697	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
699	00771	00698	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
700	00772	00699	6	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
701	00773	00700	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
702	00774	00701	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
703	00775	00702	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
704	00777	00703	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		
705	00778	00704	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0		

Table 20

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	BABC	BE	BF	BGBH	BI	BK				
706	00779	00705	3		3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X55668	92.6	149	1	824	965		
707	00780	00706	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X70944	100	152	1	2916	3071	
708	00781	00707	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
709	00782	00708	8		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
710	00783	00709	5		1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
711	00784	00710	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
712	00785	00711	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X37716	100	145	1	329	491	
713	00786	00712	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
714	00787	00713	8		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
715	00788	00714	4		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
716	00789	00715	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M15502	96.5	141	1	1310	1447
717	00790	00716	5		1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X59417	96.6	149	1	824	979
718	00791	00717	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
719	00792	00718	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
720	00793	00719	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
721	00794	00720	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
722	00795	00721	42		1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
723	00796	00722	2		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
724	00797	00723	36		4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
725	00798	00724	4		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
726	00799	00725	13		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
727	00800	00726	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
728	00801	00727	9		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
729	00802	00728	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
730	00803	00729	7		1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
731	00804	00730	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
732	00805	00731	6		2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
733	00806	00732	7		1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
734	00807	00733	23		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
735	00808	00734	8		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
736	00809	00735	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
737	00810	00736	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
738	00811	00737	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
739	00813	00738	7		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
740	00814	00739	8		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
741	00815	00740	1		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 21

Table 22

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
778	00853	00777	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
779	00854	00778	8		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
780	00855	00779	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
781	00856	00780	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
782	00857	00781	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
783	00858	00782	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
784	00859	00783	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
785	00860	00784	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
786	00861	00785	34		6	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
787	00862	00786	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
788	00863	00787	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
789	00864	00788	5		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
790	00865	00789	56		9	2	1	0	0	0	0	2	2	8	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
791	00866	00790	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
792	00867	00791	8		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
793	00868	00792	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
794	00869	00793	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
795	00870	00794	4		1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
796	00871	00795	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
797	00872	00796	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
798	00873	00797	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
799	00874	00798	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
800	00875	00799	21		2	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
801	00876	00800	9		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
802	00877	00801	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
803	00878	00802	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
804	00879	00803	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
805	00880	00804	5		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
806	00882	00805	20		1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
807	00883	00806	5		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
808	00884	00807	3		2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
809	00885	00808	2		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
810	00886	00809	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
811	00887	00810	14		2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
812	00889	00811	17		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
813	00890	00812	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 23

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	BAB	BC	BE	BF	BG	BH	BI	BK
814	00891	00813	5	1	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
815	00892	00814	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
816	00894	00815	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
817	00895	00816	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
818	00896	00817	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
819	00897	00818	10	2	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
820	00898	00819	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
821	00900	00820	27	1	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
822	00903	00821	3	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
823	00904	00822	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
824	00905	00823	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
825	00906	00824	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
826	00908	00825	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
827	00910	00826	9	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
828	00911	00827	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
829	00912	00828	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
830	00913	00829	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
831	00914	00830	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
832	00915	00831	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
833	00917	00832	43	3	1	3	0	3	3	3	0	2	1	5	6	3	0	0	0	0	0	0	0	0	0	0						
834	00918	00833	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
835	00919	00834	7	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
836	00920	00835	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
837	00922	00836	9	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
838	00924	00837	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
839	00925	00838	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
840	00926	00839	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
841	00929	00840	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
842	00930	00841	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
843	00931	00842	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
844	00932	00843	16	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
845	00934	00844	34	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
846	00935	00845	6	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
847	00936	00846	8	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
848	00937	00847	62	2	1	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
849	00938	00848	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
850	00939	00849	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
851	00940	00850	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
852	00941	00851	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
853	00942	00852	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
854	00943	00853	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
855	00944	00854	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
856	00945	00855	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
857	00946	00856	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
858	00947	00857	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
859	00948	00858	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
860	00949	00859	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
861	00950	00860	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
862	00951	00861	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
863	00952	00862	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
864	00953	00863	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
865	00954	00864	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
866	00955	00865	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
867	00956	00866	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
868	00957	00867	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
869	00958	00868	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
870	00959	00869	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
871	00960	00870	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
872	00961	00871	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
873	00962	00872	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
874	00963	00873	8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	BA	CA	IA	KA	MA	QA	AS	AL	AW	AY	BABC	BE	BF	BGBH	BI	BK
850	00955	00849	6		3	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
851	00972	00850	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
852	00973	00851	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
853	00974	00852	59		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
854	00976	00853	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
855	00977	00854	5		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
856	00978	00855	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
857	00979	00856	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
858	00980	00857	12		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
859	00981	00858	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
860	00982	00859	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
861	00983	00860	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
862	00984	00861	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
863	00985	00862	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
864	00986	00863	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
865	00987	00864	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
866	00988	00865	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
867	00989	00866	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
868	00990	00867	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
869	00991	00868	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
870	00992	00869	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
871	00993	00870	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
872	00994	00871	19		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
873	00995	00872	23		0	3	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
874	00996	00873	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
875	00997	00874	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
876	00998	00875	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
877	00999	00876	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
878	01000	00877	3		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
879	01001	00878	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
880	01002	00879	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
881	01003	00880	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
882	01004	00881	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
883	01005	00882	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
884	01006	00883	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								

Table 25

[illegible]

A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	GA	IA	KA	MA	QA	SA	TA	WA	YA	BA	BC	BE	BF	BG	BH	BI	BK		
922	01048	00921	5																									0M84694	96.9	382	1	708	1089		
923	01049	00922	2	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
924	01051	00923	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0								
925	01052	00924	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
926	01053	00925	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	M92423	90.3	380	24	3711	4221	
927	01054	00926	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
928	01055	00927	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
929	01057	00928	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
930	01061	00929	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M74782	98.3	347	1	1115	1460	
931	01062	00930	8	0	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	1	0	1	0	0	0	0	0	V00599	97.2	394	1	1011	1441
932	01063	00931	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
933	01064	00932	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
934	01065	00933	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
935	01066	00934	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
936	01067	00935	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
937	01068	00936	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
938	01069	00937	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
939	01070	00938	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
940	01071	00939	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
941	01072	00940	8	0	2	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0								
942	01073	00941	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
943	01074	00942	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	
944	01075	00943	10	0	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
945	01076	00944	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
946	01077	00945	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
947	01078	00946	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
948	01079	00947	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
949	01080	00948	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
950	01081	00949	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
951	01082	00950	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
952	01083	00951	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
953	01084	00952	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
954	01085	00953	6	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
955	01086	00954	8	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
956	01087	00955	18	0	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
957	01088	00956	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AI	AK	AM	AC	AS	AL	AV	AY	B	BC	BE	BF	BG	BH	BI	BK	
958	01089	00957	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	M16592	91.8	367	1	1410	1926	
959	01090	00958	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
960	01091	00959	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
961	01092	00960	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93	343	16	1	1391	
962	01093	00961	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
963	01094	00962	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
964	01095	00963	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
965	01096	00964	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X66099	96.9	193	1	1981	2371
966	01097	00965	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
967	01098	00966	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
968	01099	00967	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.4	64	1	477	540
969	01100	00968	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.9	354	3	1513	1894
970	01101	00969	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
971	01102	00970	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
972	01103	00971	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
973	01104	00972	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
974	01105	00973	8		0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
975	01106	00974	16		0	0	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.6	351	1	945	1295
976	01107	00975	11		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.3	348	1	1142	1487
977	01108	00976	5		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.7	347	1	2227	2572
978	01109	00977	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
979	01110	00978	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
980	01111	00979	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
981	01112	00980	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
982	01115	00981	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.4	308	1	17851	8240
983	01116	00982	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
984	01117	00983	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
985	01118	00984	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
986	01119	00985	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
987	01120	00986	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
988	01122	00987	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
989	01123	00988	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
990	01126	00989	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
991	01127	00990	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
992	01128	00991	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.2	332	1	837	1382
993	01129	00992	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 28

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AN	AO	AP	AQ	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
994	01130	00993	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
995	01131	00994	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
996	01132	00995	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
997	01133	00996	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
998	01134	00997	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
999	01135	00998	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1000	01136	00999	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1001	01137	01000	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1002	01138	01001	6		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1003	01139	01002	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1004	01140	01003	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1005	01141	01004	18		0	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1006	01142	01005	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1007	01143	01006	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1008	01144	01007	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1009	01145	01008	7		0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1010	01147	01009	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1011	01148	01010	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1012	01149	01011	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1013	01150	01012	6		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1014	01151	01013	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1015	01152	01014	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1016	01153	01015	3		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1017	01154	01016	17		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1018	01155	01017	3		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1019	01156	01018	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1020	01157	01019	9		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1021	01158	01020	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1022	01159	01021	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1023	01160	01022	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								

Table 29

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AF	AG	AI	AK	AM	AQ	AS	AV	AY	BABC	BE	BF	BG	BH	BI	BK	
1030	01168	01029	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1031	01169	01030	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1032	01170	01031	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1033	01171	01032	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1034	01172	01033	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1035	01173	01034	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1036	01174	01035	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1037	01175	01036	14		0	1	2	1	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.9	275	1	21	415
1038	01176	01037	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1039	01177	01038	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1040	01178	01039	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1041	01179	01040	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1042	01180	01041	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1043	01181	01042	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1044	01182	01043	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1045	01183	01044	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1046	01184	01045	7		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1047	01186	01046	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1048	01187	01047	8		0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1049	01188	01048	5		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.9	285	1	1055	1349
1050	01189	01049	13		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1051	01191	01050	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1052	01192	01051	8		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1053	01193	01052	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1054	01194	01053	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1055	01195	01054	6		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1056	01196	01055	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1057	01197	01056	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96	278	1	1374	1685
1058	01198	01057	10		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1059	01199	01058	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1060	01200	01059	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1061	01201	01060	4		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1062	01202	01061	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.8	290	1	1934	2397
1063	01203	01062	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1064	01204	01063	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.6	276	1	1931	2206
1065	01205	01064	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 30

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AV	AW	B	BC	BE	BF	BG	BH	BI	BK	
1066	01207	01065	5								1	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0							
1067	01208	01066	2								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1068	01209	01067	2								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1069	01210	01068	1								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1070	01211	01069	1								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1071	01212	01070	1								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1072	01213	01071	1								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1073	01214	01072	2								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1074	01215	01073	15								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1075	01216	01074	7								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1076	01217	01075	7								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1077	01218	01076	1								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1078	01219	01077	2								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1079	01220	01078	1								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1080	01221	01079	1								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1081	01222	01080	3								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1082	01223	01081	8								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1083	01224	01082	10								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1084	01225	01083	1								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1085	01226	01084	3								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1086	01227	01085	15								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1087	01228	01086	12								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1088	01229	01087	2								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1089	01230	01088	2								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1090	01231	01089	2								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1091	01232	01090	2								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1092	01233	01091	1								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1093	01235	01092	1								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1094	01236	01093	1								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1095	01237	01094	1								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1096	01238	01095	2								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1097	01239	01096	8								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1098	01240	01097	2								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1099	01241	01098	2								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1100	01242	01099	1								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1101	01243	01100	2								0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 31

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	BABC	BE	BF	BG	BH	BI	BK	
1138	01283	01137	9		0	2	1	0	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	1	0	1	0	430448	98 6 222	1	669	2527
1139	01284	01138	2		0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1140	01285	01139	6		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
1141	01286	01140	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1142	01287	01141	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1143	01288	01142	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1144	01289	01143	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1145	01290	01144	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1146	01291	01145	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1147	01292	01146	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1148	01293	01147	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1149	01294	01148	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1150	01295	01149	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1151	01296	01150	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1152	01297	01151	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1153	01298	01152	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1154	01299	01153	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1155	01300	01154	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1156	01301	01155	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1157	01302	01156	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1158	01303	01157	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1159	01304	01158	10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1160	01305	01159	28		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1161	01306	01160	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1162	01307	01161	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1163	01308	01162	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1164	01309	01163	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1165	01310	01164	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1166	01311	01165	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1167	01312	01166	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1168	01313	01167	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1169	01314	01168	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1170	01315	01169	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1171	01316	01170	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1172	01317	01171	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1173	01318	01172	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 33

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AT	AV	AW	B	BC	BE	BF	BG	BH	BI	BK
1174	01319	01173	1																															
1175	01320	01174	1																															
1176	01321	01175	19																															
1177	01322	01176	3																															
1178	01323	01177	1																															
1179	01324	01178	1																															
1180	01325	01179	17																															
1181	01326	01180	1																															
1182	01327	01181	4																															
1183	01328	01182	2																															
1184	01329	01183	2																															
1185	01330	01184	4																															
1186	01331	01185	3																															
1187	01332	01186	3																															
1188	01333	01187	1																															
1189	01334	01188	7																															
1190	01335	01189	1																															
1191	01336	01190	4																															
1192	01337	01191	1																															
1193	01338	01192	1																															
1194	01339	01193	1																															
1195	01340	01194	1																															
1196	01341	01195	1																															
1197	01342	01196	1																															
1198	01343	01197	1																															
1199	01344	01198	2																															
1200	01345	01199	4																															
1201	01346	01200	1																															
1202	01347	01201	5																															
1203	01348	01202	13																															
1204	01349	01203	1																															
1205	01350	01204	1																															
1206	01351	01205	7																															
1207	01352	01206	2																															
1208	01353	01207	2																															
1209	01354	01208	2																															

Table 34

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	ABC	BE	BF	BGBH	BI	BK		
1210	01355	01209	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
1211	01356	01210	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
1212	01357	01211	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1213	01358	01212	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1214	01359	01213	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.3	127	1	453	579
1215	01360	01214	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1216	01361	01215	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1217	01362	01216	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1218	01363	01217	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1219	01364	01218	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1220	01365	01219	4		0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1221	01366	01220	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1222	01367	01221	21		0	3	1	0	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1223	01368	01222	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.2	216	1	1324	1558
1224	01369	01223	5		0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1225	01370	01224	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1226	01371	01225	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1227	01372	01226	7		0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.4	58	1	495	462
1228	01373	01227	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1229	01374	01228	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1230	01375	01229	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1231	01377	01230	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1232	01378	01231	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1233	01379	01232	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1234	01380	01233	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1235	01381	01234	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1236	01382	01235	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1237	01383	01236	3		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1238	01384	01237	16		0	1	1	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1239	01385	01238	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1240	01386	01239	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1241	01387	01240	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1242	01388	01241	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1243	01389	01242	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1244	01390	01243	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1245	01391	01244	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 35

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AK	AM	AO	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1246	01392	01245	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1247	01393	01246	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1248	01394	01247	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1249	01395	01248	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1250	01396	01249	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1251	01397	01250	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1252	01398	01251	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1253	01400	01252	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1254	01401	01253	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1255	01402	01254	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1256	01403	01255	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1257	01404	01256	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1258	01405	01257	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1259	01406	01258	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1260	01407	01259	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1261	01408	01260	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1262	01409	01261	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1263	01410	01262	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1264	01411	01263	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1265	01412	01264	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1266	01413	01265	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1267	01414	01266	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1268	01415	01267	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1269	01416	01268	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1270	01417	01269	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1271	01418	01270	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1272	01419	01271	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1273	01420	01272	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1274	01421	01273	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1275	01422	01274	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1276	01423	01275	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1277	01424	01276	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1278	01426	01277	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1279	01427	01278	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1280	01428	01279	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1281	01429	01280	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 36

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
1318	01467	01317	4		0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
1319	01468	01318	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1320	01469	01319	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1321	01470	01320	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1322	01471	01321	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1323	01472	01322	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1324	01473	01323	9		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1325	01474	01324	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1326	01475	01325	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1327	01476	01326	19		0	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1328	01477	01327	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1329	01478	01328	5		0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1330	01479	01329	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1331	01481	01330	3		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1332	01482	01331	2		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1333	01483	01332	9		0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1334	01484	01333	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1335	01485	01334	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1336	01486	01335	3		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1337	01487	01336	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1338	01488	01337	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1339	01489	01338	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1340	01490	01339	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1341	01491	01340	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1342	01492	01341	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1343	01493	01342	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1344	01494	01343	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1345	01495	01344	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1346	01496	01345	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1347	01497	01346	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1348	01498	01347	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1349	01499	01348	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1350	01500	01349	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1351	01501	01350	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1352	01502	01351	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1353	01503	01352	9		0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 38

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1282	01430	01281	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1283	01431	01282	6		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1284	01432	01283	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1285	01433	01284	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1286	01434	01285	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1287	01435	01286	7		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1288	01436	01287	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1289	01437	01288	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1290	01438	01289	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1291	01439	01290	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1292	01440	01291	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1293	01441	01292	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1294	01442	01293	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1295	01443	01294	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1296	01444	01295	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1297	01445	01296	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1298	01446	01297	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1299	01447	01298	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1300	01448	01299	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1301	01449	01300	10		0	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1302	01450	01301	4		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1303	01451	01302	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1304	01452	01303	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1305	01453	01304	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1306	01454	01305	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1307	01455	01306	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1308	01456	01307	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1309	01457	01308	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1310	01458	01309	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1311	01459	01310	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1312	01460	01311	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1313	01461	01312	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1314	01462	01313	6		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1315	01463	01314	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1316	01464	01315	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1317	01466	01316	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 37

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	EA	GA	KA	MA	QA	SA	TA	VA	WA	YA	BA	BC	BE	BF	BGBH	BI	BK
1354	01505	01353	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.3	406	1	1923	2327
1355	01506	01354	1	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.1	112	1	1617	1760
1356	01507	01355	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1357	01508	01356	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1358	01509	01357	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1359	01510	01358	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1360	01511	01359	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1361	01512	01360	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1362	01513	01361	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1363	01514	01362	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1364	01515	01363	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1365	01516	01364	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1366	01517	01365	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1367	01518	01366	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1368	01519	01367	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1369	01520	01368	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1370	01521	01369	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1371	01522	01370	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1372	01523	01371	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1373	01524	01372	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1374	01525	01373	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1375	01526	01374	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1376	01527	01375	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1377	01528	01376	16	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1378	01529	01377	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1379	01530	01378	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1380	01531	01379	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1381	01532	01380	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1382	01533	01381	19	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1383	01534	01382	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1384	01535	01383	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1385	01536	01384	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1386	01537	01385	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1387	01538	01386	12	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1388	01539	01387	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1389	01540	01388	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1390	01541	01389	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 39

Table 40

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK	
1426	01579	01425	1				1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1427	01580	01426	4				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1428	01581	01427	1				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1429	01582	01428	3				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1430	01583	01429	5				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1431	01584	01430	1				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1432	01585	01431	8				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1433	01586	01432	2				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1434	01587	01433	2				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1435	01588	01434	1				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1436	01589	01435	10				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1437	01590	01436	1				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1438	01591	01437	1				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1439	01592	01438	4				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1440	01593	01439	1				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1441	01594	01440	4				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1442	01595	01441	7				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1443	01596	01442	1				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1444	01597	01443	2				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1445	01598	01444	1				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1446	01599	01445	1				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1447	01600	01446	2				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1448	01601	01447	1				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1449	01602	01448	4				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1450	01603	01449	5				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1451	01604	01450	1				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1452	01605	01451	2				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1453	01606	01452	1				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1454	01607	01453	4				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1455	01608	01454	23				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1456	01609	01455	16				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1457	01610	01456	5				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1458	01611	01457	3				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1459	01612	01458	5				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1460	01614	01459	4				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1461	01615	01460	1				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 41

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AG	AS	AS	AL	AW	AY	B	BC	DE	DF	BG	BH	BI	BK	
1462	01616	01461	32	0	1	3	1	0	0	0	0	0	0	3	0	0	0	1	0	5	11	0	2	1	0	0	1	0	3	103558	98.2	55	1	588	642
1463	01617	01462	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1464	01618	01463	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1465	01619	01464	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1466	01620	01465	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1467	01621	01466	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1468	01622	01467	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1469	01623	01468	5	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1470	01624	01469	8	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1471	01625	01470	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1472	01626	01471	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1473	01627	01472	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1474	01628	01473	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1475	01629	01474	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1476	01630	01475	9	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1477	01632	01476	11	0	3	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1478	01633	01477	7	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1479	01642	01478	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1480	01671	01479	35	0	2	0	0	0	0	0	5	7	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1481	01673	01480	6	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1482	01686	01481	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1483	01687	01482	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1484	01688	01483	6	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1485	01689	01484	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1486	01691	01485	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1487	01692	01486	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1488	01693	01487	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1489	01694	01488	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1490	01695	01489	11	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1491	01696	01490	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1492	01697	01491	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1493	01698	01492	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1494	01699	01493	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1495	01700	01494	9	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1496	01701	01495	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1497	01702	01496	4	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 42

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
1498	01703	01497	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1499	01704	01498	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1500	01705	01499	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1501	01706	01500	12		0	0	4	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.1 421	1	120	580
1502	01707	01501	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.3 471	1	1652	2113
1503	01708	01502	5		0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1504	01709	01503	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1505	01710	01504	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1506	01711	01505	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1507	01713	01506	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1508	01714	01507	3		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1509	01715	01508	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1510	01718	01509	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1511	01719	01510	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1512	01720	01511	43		0	0	1	0	0	4	2	4	3	1	1	0	0	5	7	9	4	0	0	0	0	0	0	96.4 448	1	1052	1497
1513	01721	01512	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1514	01722	01513	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1515	01724	01514	9		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1516	01726	01515	5		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1517	01727	01516	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1518	01728	01517	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1519	01729	01518	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1520	01730	01519	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1521	01731	01520	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1522	01732	01521	4		0	0	1	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	96.7 276	127	521	1009
1523	01733	01522	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1524	01734	01523	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1525	01735	01524	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1526	01736	01525	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1527	01737	01526	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1528	01738	01527	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1529	01739	01528	8		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1530	01740	01529	8		0	0	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1531	01741	01530	5		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1532	01742	01531	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1533	01745	01532	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 43

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK		
1534	01746	01533	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1535	01747	01534	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1536	01748	01535	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1537	01749	01536	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0X73685	92.7	358	1	850	2177	
1538	01750	01537	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0X16166	99.2	358	1	278	637	
1539	01751	01538	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1540	01752	01539	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1541	01753	01540	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1542	01754	01541	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1543	01755	01542	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1544	01756	01543	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1545	01758	01544	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1546	01759	01545	7		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1547	01760	01546	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1548	01761	01547	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1549	01763	01548	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1550	01764	01549	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1551	01765	01550	7		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1552	01766	01551	63		0	0	0	15	2	4	2	0	4	0	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1553	01767	01552	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1554	01768	01553	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1555	01769	01554	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1556	01770	01555	5		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1557	01771	01556	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1558	01772	01557	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1559	01773	01558	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1560	01774	01559	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1561	01775	01560	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1562	01776	01561	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1563	01777	01562	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1564	01778	01563	2		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1565	01779	01564	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1566	01780	01565	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1567	01781	01566	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1568	01782	01567	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1569	01783	01568	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 44

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
1570	01784	01569	2		0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99 301	1	1101	1401
1571	01785	01570	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1572	01786	01571	8		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1573	01787	01572	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1574	01788	01573	3		0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1575	01789	01574	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1576	01790	01575	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1577	01791	01576	34		0	0	1	0	0	2	3	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95 9 295	1	1011	1301
1578	01792	01577	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1579	01793	01578	6		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1580	01794	01579	6		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1581	01795	01580	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1582	01796	01581	7		0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1583	01797	01582	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99 3 285	1	2974	3220
1584	01798	01583	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1585	01799	01584	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1586	01800	01585	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1587	01801	01586	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1588	01802	01587	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1589	01803	01588	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1590	01804	01589	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1591	01805	01590	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1592	01806	01591	26		0	0	7	0	0	0	0	0	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	95 8 262	1	1142	1399
1593	01807	01592	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1594	01808	01593	47		0	0	6	0	0	2	1	1	3	7	4	2	4	0	0	0	0	0	0	0	0	0	0	98 253	1	201	453
1595	01809	01594	19		0	0	3	0	0	0	0	0	0	1	2	6	0	0	0	0	0	0	0	0	0	0	0	96 1 256	1	610	875
1596	01810	01595	2		0	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0				
1597	01811	01596	39		0	0	1	0	0	0	0	0	0	0	0	2	2	1	0	0	0	0	0	0	0	0	0				
1598	01812	01597	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98 204	1	618	1305
1599	01813	01598	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1600	01814	01599	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1601	01815	01600	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96 8 219	1	2394	2616
1602	01816	01601	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1603	01817	01602	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1604	01818	01603	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97 233	1	280	512
1605	01819	01604	6		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96 9 322	1	741	1107

Table 45

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1606	01820	01605	9		0	0	1	1	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1607	01821	01606	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1608	01822	01607	7		0	0	2	0	0	0	0	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1609	01823	01608	24		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1610	01824	01609	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1611	01825	01610	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1612	01826	01611	6		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1613	01827	01612	-1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1614	01828	01613	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1615	01829	01614	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1616	01830	01615	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1617	01831	01616	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1618	01832	01617	8		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1619	01833	01618	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1620	01834	01619	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1621	01835	01620	5		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1622	01836	01621	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1623	01837	01622	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1624	01838	01623	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1625	01839	01624	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1626	01840	01625	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1627	01841	01626	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1628	01842	01627	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1629	01843	01628	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1630	01844	01629	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1631	01845	01630	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1632	01846	01631	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1633	01847	01632	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1634	01848	01633	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1635	01849	01634	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1636	01850	01635	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1637	01851	01636	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1638	01852	01637	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1639	01853	01638	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1640	01854	01639	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1641	01855	01640	7		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 46

Table 47

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AS	AT	AV	AW	AX	AY	BA	BC	BE	BF	BG	BH	BI	BK			
1678	01893	01677	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1679	01895	01678	7		0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1680	01896	01679	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1681	01897	01680	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1682	01898	01681	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1683	01899	01682	14		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1684	01900	01683	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1685	01901	01684	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1686	01902	01685	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1687	01903	01686	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1688	01904	01687	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1689	01905	01688	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1690	01906	01689	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1691	01907	01690	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1692	01908	01691	21		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1693	01909	01692	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1694	01910	01693	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1695	01911	01694	10		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1696	01912	01695	5		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1697	01913	01696	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1698	01914	01697	3		0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1699	01915	01698	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1700	01916	01699	3		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1701	01917	01700	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1702	01918	01701	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1703	01919	01702	11		0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1704	01920	01703	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1705	01921	01704	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1706	01922	01705	3		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1707	01923	01706	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1708	01924	01707	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1709	01925	01708	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1710	01926	01709	24		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1711	01927	01710	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1712	01928	01711	10		0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1713	01929	01712	19		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 48

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	A	A	C	A	F	A	G	A	I	A	K	A	M	A	C	A	S	A	L	A	M	A	B	C	BE	BF	BG	BH	BI	BK					
1714	01930	01713	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1715	01931	01714	4	0	0	0	2	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1716	01932	01715	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1717	01933	01716	10	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1718	01934	01717	5	0	0	0	1	1	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1719	01935	01718	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1720	01936	01719	2	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1721	01937	01720	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1722	01938	01721	3	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1723	01939	01722	3	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1724	01940	01723	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1725	01941	01724	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1726	01943	01725	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1727	01944	01726	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1728	01945	01727	7	0	0	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1729	01946	01728	3	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1730	01947	01729	6	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1731	01948	01730	4	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1732	01949	01731	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1733	01950	01732	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1734	01951	01733	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1735	01952	01734	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1736	01953	01735	17	0	0	0	2	2	0	0	0	1	0	1	0	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1737	01954	01736	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1738	01955	01737	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1739	01956	01738	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1740	01957	01739	4	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1741	01958	01740	6	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1742	01959	01741	5	0	0	0	1	0	1	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1743	01960	01742	6	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1744	01961	01743	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1745	01962	01744	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1746	01963	01745	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1747	01964	01746	6	0	0	0	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1748	01965	01747	4	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1749	01966	01748	8	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	BA	BC	BE	BF	BG	BI	BI	DK		
1750	01967	01749	13	0	0	1	1	0	0	1	0	0	0	1	2	1	0	0	2	1	2	0	0	1	0	0	0	0	0	X14986	100	57	36	1	57
1751	01968	01750	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1752	01969	01751	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1753	01970	01752	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1754	01972	01753	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1755	01973	01754	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1756	01974	01755	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1757	01975	01756	6	0	0	0	0	0	0	0	2	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1758	01976	01757	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1759	01977	01758	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1760	01978	01759	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1761	01979	01760	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1762	01981	01761	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1763	01982	01762	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1764	01983	01763	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1765	01984	01764	3	0	0	0	0	0	0	0	3	2	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1766	01985	01765	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1767	01986	01766	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1768	01987	01767	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1769	01988	01768	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1770	01989	01769	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1771	01990	01770	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1772	01991	01771	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1773	01992	01772	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1774	01994	01773	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1775	01995	01774	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1776	01996	01775	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1777	01997	01776	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1778	01998	01777	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1779	01999	01778	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1780	02000	01779	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1781	02001	01780	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1782	02002	01781	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1783	02003	01782	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1784	02005	01783	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1785	02006	01784	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK	
1822	02070	01821	2		0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
1823	02071	01822	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1824	02072	01823	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1825	02073	01824	16		0	0	0	1	0	0	1	2	0	0	0	3	0	3	0	1	0	0	2	1	0	0	1	1	0					
1826	02074	01825	7		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	3	0	0	0	X07173	96.4308	1.2762	3089	
1827	02075	01826	7		0	0	0	1	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1828	02076	01827	4		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1829	02077	01828	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	
1830	02078	01829	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1831	02079	01830	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1832	02080	01831	11		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1833	02081	01832	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1834	02082	01833	7		0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1835	02084	01834	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1836	02085	01835	83		0	0	0	16	26	40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1837	02086	01836	4		0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1838	02087	01837	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1839	02088	01838	2		0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1840	02089	01839	2		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1841	02090	01840	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1842	02091	01841	9		0	0	0	1	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1843	02092	01842	11		0	0	0	2	1	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	M14936	97.6210	1.878	1088	
1844	02093	01843	11		0	0	0	2	3	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	X00129	98.254	1.629	882	
1845	02094	01844	6		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X02747	100.241	1.1412	1652	
1846	02095	01845	2		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1847	02096	01846	2		0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X17544	99.2237	1.1308	1545	
1848	02097	01847	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1849	02098	01848	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X04481	99.6229	1.2381	2609	
1850	02099	01849	3		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1851	02100	01850	5		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
1852	02101	01851	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1853	02102	01852	5		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1854	02103	01853	5		0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1855	02104	01854	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1856	02105	01855	109		0	0	0	6	4	3	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M25097	97.8223	1.187	439
1857	02106	01856	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X02761	99.1219	1.7462	7680

Table 52

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1858	02107	01857	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X55551	98.2	218	1	8718	11435
1859	02108	01858	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X16609	98.2	219	1	5919	7252
1860	02110	01859	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1861	02111	01860	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1862	02112	01861	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1863	02113	01862	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1864	02115	01863	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1865	02116	01864	12		0	0	0	3	2	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M12272	100	208	1	1262	1486
1866	02117	01865	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M14057	98.6	70	1	1884	2171
1867	02118	01866	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M64982	96.8	188	11	5234	5943
1868	02119	01867	8		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1869	02120	01868	19		0	0	0	3	12	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1870	02121	01869	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M64983	99.5	197	1	8075	8878
1871	02122	01870	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	J02770	95.3	191	1	1773	1963
1872	02123	01871	28		0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1873	02124	01872	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1874	02126	01873	7		0	0	0	6	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1875	02127	01874	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1876	02128	01875	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1877	02129	01876	4		0	0	0	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1878	02130	01877	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M11723	98.9	175	1	1785	1959
1879	02131	01878	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1880	02132	01879	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	J03810	100	169	1	3000	3168
1881	02133	01881	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1882	02134	01881	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1883	02135	01882	6		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1884	02136	01883	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1885	02137	01884	4		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1886	02138	01885	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1887	02139	01886	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1888	02140	01887	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1889	02141	01888	8		0	0	0	5	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M12654	100	148	1	1506	1653
1890	02142	01889	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1891	02143	01890	3		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1892	02144	01891	2		0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1893	02145	01892	8		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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	A	B	C	E	F	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
1894	02146	01893	1																																
1895	02147	01894	4																																
1896	02148	01895	21																																
1897	02149	01896	4																																
1898	02150	01897	2																																
1899	02151	01898	14																																
1900	02152	01899	7																																
1901	02153	01900	6																																
1902	02154	01901	1																																
1903	02155	01902	28																																
1904	02156	01903	8																																
1905	02157	01904	35																																
1906	02158	01905	3																																
1907	02159	01906	1																																
1908	02160	01907	1																																
1909	02161	01908	9																																
1910	02162	01909	1																																
1911	02163	01910	4																																
1912	02164	01911	5																																
1913	02165	01912	1																																
1914	02166	01913	4																																
1915	02167	01914	1																																
1916	02168	01915	1																																
1917	02169	01916	9																																
1918	02170	01917	3																																
1919	02171	01918	6																																
1920	02172	01919	4																																
1921	02173	01920	2																																
1922	02174	01921	25																																
1923	02175	01922	4																																
1924	02176	01923	13																																
1925	02177	01924	7																																
1926	02178	01925	1																																
1927	02179	01926	2																																
1928	02180	01927	1																																
1929	02181	01928	14																																

Table 54

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AP	AR	AS	AT	AW	AY	BA	BB	BC	BE	BF	BG	BH	BI	BK		
1930	02182	01929	3		0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1931	02183	01930	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1932	02184	01931	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1933	02185	01932	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1934	02186	01933	68		0	0	0	1	1	2	0	0	2	1	0	0	2	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	X14723	96	99	1	1551	1676	
1935	02187	01934	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1936	02188	01935	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1937	02189	01936	11		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1938	02191	01937	6		0	0	0	4	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X04608	98	8	83	1	842	923	
1939	02192	01938	2		0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1940	02193	01939	3		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1941	02194	01940	2		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	U02493	97	8	91	1	1606	2593	
1942	02195	01941	8		0	0	0	4	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M6752	97	3	73	11	2040	2113	
1943	02196	01942	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1944	02197	01943	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1945	02198	01944	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1946	02199	01945	5		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1947	02200	01946	6		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1948	02202	01947	32		0	0	0	15	12	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L19501	100	76	1	2451	2544	
1949	02203	01948	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1950	02204	01949	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1951	02205	01950	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1952	02206	01951	4		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1953	02207	01952	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1954	02208	01953	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1955	02209	01954	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1956	02210	01955	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1957	02211	01956	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1958	02212	01957	2		0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M35433	98	2	57	1	143	282
1959	02213	01958	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1960	02214	01959	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1961	02215	01960	4		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1962	02216	01961	2		0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1963	02217	01962	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1964	02238	01963	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	D90282	93	1	101	1	5116	5215
1965	02239	01964	6		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X51745	97	3	447	1	964	1418

Table 55

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
1966	02240	01965	5		0	0	0	0	0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1967	02241	01966	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1968	02242	01967	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1969	02243	01968	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1970	02244	01969	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1971	02245	01970	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1972	02246	01971	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1973	02247	01972	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1974	02248	01973	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1975	02249	01974	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1976	02250	01975	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1977	02252	01976	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1978	02254	01977	3		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1979	02255	01978	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1980	02256	01979	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1981	02257	01980	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1982	02258	01981	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1983	02259	01982	10		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1984	02260	01983	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1985	02261	01984	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1986	02262	01985	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1987	02263	01986	4		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1988	02264	01987	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1989	02266	01988	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1990	02268	01989	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1991	02269	01990	4		0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1992	02270	01991	3		0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1993	02271	01992	12		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1994	02272	01993	9		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1995	02274	01994	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1996	02275	01995	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1997	02276	01996	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1998	02277	01997	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1999	02278	01998	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2000	02279	01999	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2001	02280	02000	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 56

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
2002	02281	02001	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2003	02282	02002	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2004	02283	02003	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2005	02285	02004	10		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2006	02287	02005	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2007	02288	02006	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2008	02289	02007	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2009	02290	02008	16		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2010	02291	02009	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2011	02292	02010	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2012	02293	02011	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2013	02294	02012	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2014	02295	02013	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2015	02296	02014	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2016	02297	02015	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2017	02298	02016	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2018	02299	02017	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2019	02300	02018	3		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2020	02301	02019	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2021	02302	02020	5		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2022	02303	02021	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2023	02304	02022	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2024	02305	02023	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2025	02306	02024	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2026	02307	02025	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2027	02308	02026	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2028	02309	02027	18		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2029	02310	02028	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2030	02311	02029	6		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2031	02312	02030	5		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2032	02313	02031	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2033	02314	02032	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2034	02315	02033	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2035	02316	02034	12		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2036	02317	02035	5		0	0	0	0	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2037	02318	02036	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 57

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	QA	QA	CA	SA	LA	WA	YB	ABC	BE	BF	BG	BI	BK
2038	02319	02037	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2039	02321	02038	7		0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2040	02322	02039	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2041	02323	02040	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2042	02324	02041	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2043	02325	02042	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2044	02326	02043	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2045	02327	02044	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2046	02328	02045	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2047	02329	02046	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2048	02330	02047	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2049	02331	02048	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2050	02332	02049	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2051	02333	02050	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2052	02334	02051	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2053	02336	02052	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2054	02337	02053	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2055	02338	02054	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2056	02339	02055	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2057	02340	02056	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2058	02341	02057	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2059	02342	02058	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2060	02343	02059	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2061	02345	02060	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2062	02346	02061	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2063	02347	02062	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2064	02348	02063	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2065	02349	02064	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2066	02350	02065	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2067	02351	02066	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2068	02352	02067	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2069	02353	02068	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2070	02354	02069	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2071	02355	02070	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2072	02356	02071	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2073	02357	02072	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 58

Table 59

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AJ	AK	AM	AN	AO	AP	AS	AT	AW	AY	BA	BB	BF	BG	BH	BI	BK	
2110	02414	02109	2		0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2111	02415	02110	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2112	02416	02111	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2113	02417	02112	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2114	02418	02113	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2115	02419	02114	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2116	02420	02115	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2117	02421	02116	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2118	02422	02117	7		0	0	0	0	0	0	1	0	0	5	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
2119	02423	02118	3		0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2120	02424	02119	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2121	02425	02120	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2122	02426	02121	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2123	02427	02122	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2124	02428	02123	4		0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
2125	02429	02124	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2126	02430	02125	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2127	02431	02126	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2128	02432	02127	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2129	02433	02128	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2130	02434	02129	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2131	02435	02130	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2132	02436	02131	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2133	02437	02132	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2134	02438	02133	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2135	02439	02134	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2136	02441	02135	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2137	02442	02136	3		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2138	02443	02137	8		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2139	02444	02138	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2140	02445	02139	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2141	02446	02140	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2142	02447	02141	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2143	02448	02142	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2144	02449	02143	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2145	02450	02144	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	ACA	BAC	AI	AK	AM	ACA	QAS	AS	AL	AW	AY	B	ABC	BE	BF	BGBH	BI	BK		
2146	02452	02145	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2147	02453	02146	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
2148	02454	02147	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2149	02455	02148	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2150	02456	02149	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2151	02457	02150	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2152	02458	02151	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2153	02459	02152	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2154	02461	02153	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		97.9	236	1	1746	1981
2155	02462	02154	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2156	02463	02155	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		98.8	245	1	913	1157
2157	02464	02156	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2158	02465	02157	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		98.7	231	1	969	1199
2159	02466	02158	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2160	02467	02159	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2161	02468	02160	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2162	02469	02161	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2163	02471	02162	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2164	02472	02163	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2165	02473	02164	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2166	02474	02165	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2167	02475	02166	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2168	02476	02167	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2169	02477	02168	4		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2170	02478	02169	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2171	02479	02170	6		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2172	02480	02171	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2173	02481	02172	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		94.4	197	1	1355	1560
2174	02482	02173	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2175	02483	02174	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		98.5	197	1	3184	3394
2176	02484	02175	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		100	192	1	1856	2051
2177	02486	02176	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2178	02487	02177	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		91.3	173	15	5142	5417
2179	02488	02178	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2180	02489	02179	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		98.9	180	1	2513	2694
2181	02490	02180	16		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		97.7	177	1	988	1166

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
2182	02491	02181	1		0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
2183	02493	02182	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2184	02494	02183	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2185	02495	02184	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2186	02496	02185	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2187	02497	02186	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2188	02498	02187	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2189	02499	02188	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2190	02500	02189	3		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2191	02501	02190	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2192	02502	02191	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2193	02503	02192	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2194	02504	02193	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2195	02505	02194	5		0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2196	02506	02195	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2197	02507	02196	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2198	02508	02197	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2199	02509	02198	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2200	02510	02199	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2201	02511	02200	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2202	02512	02201	13		0	0	0	0	0	0	0	1	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2203	02513	02202	3		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2204	02514	02203	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2205	02515	02204	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2206	02516	02205	5		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2207	02517	02206	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2208	02518	02207	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2209	02519	02208	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2210	02520	02209	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2211	02521	02210	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2212	02522	02211	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2213	02523	02212	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2214	02524	02213	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2215	02525	02214	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2216	02526	02215	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2217	02527	02216	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 62

[illegible]

[illegible]

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2290	02645	02289	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2291	02646	02290	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2292	02648	02291	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2293	02650	02292	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2294	02651	02293	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2295	02652	02294	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2296	02653	02295	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2297	02654	02296	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2298	02656	02297	20		0	0	0	0	0	0	3	0	0	1	2	2	2	3	2	0	0	0	0	3	1	0	0						
2299	02657	02298	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2300	02658	02299	6		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2301	02659	02300	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2302	02660	02301	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2303	02661	02302	3		0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2304	02662	02303	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2305	02663	02304	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2306	02664	02305	5		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2307	02665	02306	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2308	02666	02307	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2309	02667	02308	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2310	02668	02309	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2311	02669	02310	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2312	02670	02311	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2313	02672	02312	5		0	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0						
2314	02673	02313	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2315	02675	02314	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2316	02676	02315	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2317	02677	02316	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2318	02678	02317	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2319	02679	02318	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2320	02680	02319	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2321	02681	02320	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2322	02682	02321	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2323	02684	02322	13		0	0	0	0	0	0	1	0	5	3	0	0	0	0	0	0	0	0	0	0	0	0	0						
2324	02685	02323	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2325	02686	02324	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 65

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AG	AI	AK	AM	AO	AS	AV	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2326	02687	02325	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2327	02688	02326	2		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2328	02689	02327	4		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2329	02690	02328	4		0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2330	02691	02329	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2331	02692	02330	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2332	02693	02331	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2333	02694	02332	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2334	02695	02333	5		0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
2335	02696	02334	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2336	02697	02335	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2337	02698	02336	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2338	02699	02337	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2339	02700	02338	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2340	02701	02339	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2341	02702	02340	5		0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2342	02703	02341	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2343	02704	02342	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2344	02705	02343	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2345	02706	02344	13		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2346	02707	02345	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2347	02708	02346	8		0	0	0	0	0	0	2	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
2348	02709	02347	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2349	02710	02348	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2350	02711	02349	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2351	02712	02350	8		0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2352	02713	02351	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2353	02714	02352	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2354	02715	02353	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2355	02716	02354	18		0	0	0	0	0	0	2	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0							
2356	02717	02355	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2357	02718	02356	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2358	02719	02357	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2359	02721	02358	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2360	02722	02359	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2361	02723	02360	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 66

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	B	BC	BE	BF	BH	BI	BK
2398	02765	02397	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2399	02767	02398	9		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2400	02768	02399	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2401	02769	02400	7		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2402	02770	02401	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2403	02771	02402	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2404	02772	02403	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2405	02773	02404	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2406	02774	02405	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2407	02775	02406	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2408	02776	02407	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2409	02777	02408	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2410	02778	02409	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2411	02779	02410	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2412	02780	02411	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2413	02781	02412	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2414	02782	02413	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2415	02783	02414	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2416	02785	02415	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2417	02786	02416	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2418	02787	02417	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2419	02788	02418	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2420	02789	02419	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2421	02790	02420	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2422	02791	02421	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2423	02792	02422	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2424	02793	02423	9		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2425	02794	02424	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2426	02795	02425	7		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2427	02796	02426	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2428	02797	02427	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2429	02798	02428	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2430	02799	02429	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2431	02800	02430	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2432	02801	02431	9		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2433	02802	02432	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AG	AI	AK	AM	AN	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK	
2434	02803	02433	2								1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2435	02804	02434	5							0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2436	02805	02435	4							0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
2437	02806	02436	1							0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
2438	02807	02437	2							0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
2439	02808	02438	1							0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
2440	02809	02439	1							0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2441	02810	02440	2							0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2442	02811	02441	4							0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2443	02812	02442	12							0	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2444	02813	02443	5							0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2445	02814	02444	15							0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2446	02815	02445	4							0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2447	02816	02446	2							0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2448	02817	02447	2							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2449	02818	02448	5							0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2450	02819	02449	1							0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2451	02820	02450	29							0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2452	02821	02451	22							0	0	0	0	0	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2453	02822	02452	1							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2454	02823	02453	5							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2455	02824	02454	2							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2456	02825	02455	1							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2457	02826	02456	1							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2458	02827	02457	1							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2459	02828	02458	1							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2460	02829	02459	1							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2461	02830	02460	1							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2462	02831	02461	3							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2463	02832	02462	2							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2464	02833	02463	7							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2465	02834	02464	1							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2466	02835	02465	4							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2467	02836	02466	3							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2468	02837	02467	1							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2469	02838	02468	1							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
2470	02839	02469	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2471	02840	02470	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2472	02843	02471	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2473	02844	02472	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2474	02845	02473	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2475	02846	02474	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2476	02847	02475	11		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2477	02848	02476	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2478	02849	02477	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2479	02850	02478	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2480	02851	02479	9		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2481	02852	02480	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2482	02853	02481	8		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2483	02854	02482	4		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2484	02855	02483	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2485	02856	02484	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2486	02857	02485	3		0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2487	02858	02486	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2488	02859	02487	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2489	02860	02488	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2490	02861	02489	10		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2491	02862	02490	7		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2492	02863	02491	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2493	02864	02492	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2494	02865	02493	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2495	02866	02494	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2496	02867	02495	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2497	02868	02496	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2498	02869	02497	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2499	02870	02498	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2500	02872	02499	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2501	02873	02500	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2502	02874	02501	6		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2503	02875	02502	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2504	02876	02503	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2505	02877	02504	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 70

[illegible]

[illegible]

Table 72

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A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AA	AK	AM	AA	CA	AS	AA	AW	AB	ABC	DE	BF	RG	BI	BI	BK
2578	02959	02577	9	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	93.8	80	6	1	2436
2579	02960	02578	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2580	02962	02579	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2581	02963	02580	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2582	02964	02581	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2583	02965	02582	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2584	02966	02583	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2585	02967	02584	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2586	02968	02585	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2587	02969	02586	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2588	02970	02587	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2589	02971	02588	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2590	02972	02589	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2591	02973	02590	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2592	02974	02591	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2593	02975	02592	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2594	02976	02593	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2595	02978	02594	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2596	02980	02595	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2597	02981	02596	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2598	02982	02597	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2599	02983	02598	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2600	02984	02599	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2601	02985	02600	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2602	02986	02601	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2603	02987	02602	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2604	02988	02603	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2605	02989	02604	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2606	02990	02605	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2607	02991	02606	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2608	02992	02607	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2609	02993	02608	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2610	02994	02609	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2611	02995	02610	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2612	02996	02611	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2613	02997	02612	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 73

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2614	02999	02613	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2615	03002	02614	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2616	03005	02615	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2617	03028	02616	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2618	03030	02617	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2619	03031	02618	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2620	03053	02619	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2621	03055	02620	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							634
2622	03056	02621	3		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2623	03058	02622	3		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2624	03059	02623	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2625	03060	02624	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2626	03061	02625	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2627	03062	02626	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2628	03063	02627	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2629	03064	02628	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2630	03065	02629	4		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2631	03066	02630	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2632	03067	02631	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2633	03068	02632	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2634	03069	02633	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2635	03070	02634	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2636	03071	02635	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2637	03072	02636	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2638	03073	02637	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2639	03074	02638	44		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2640	03075	02639	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2641	03077	02640	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2642	03078	02641	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2643	03079	02642	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2644	03080	02643	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2645	03081	02644	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2646	03082	02645	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2647	03083	02646	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2648	03084	02647	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227
2649	03085	02648	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							1227

Table 74

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2650	03086	02649	5		0	0	0	0	0	0	0	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2651	03087	02650	8		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2652	03088	02651	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2653	03089	02652	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2654	03090	02653	8		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2655	03091	02654	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2656	03092	02655	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2657	03094	02656	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2658	03095	02657	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2659	03096	02658	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2660	03097	02659	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2661	03098	02660	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2662	03099	02661	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2663	03100	02662	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2664	03101	02663	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2665	03102	02664	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2666	03103	02665	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2667	03104	02666	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2668	03105	02667	15		0	0	0	0	0	0	0	2	3	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2669	03106	02668	9		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2670	03108	02669	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2671	03109	02670	13		0	0	0	0	0	0	0	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2672	03110	02671	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2673	03111	02672	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2674	03112	02673	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2675	03115	02674	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2676	03116	02675	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2677	03117	02676	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2678	03118	02677	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2679	03119	02678	5		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2680	03120	02679	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2681	03121	02680	6		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2682	03122	02681	5		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2683	03123	02682	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2684	03124	02683	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2685	03125	02684	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 75

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2686	03126	02685	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2687	03127	02686	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2688	03128	02687	19		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2689	03129	02688	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2690	03131	02689	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2691	03132	02690	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2692	03133	02691	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2693	03134	02692	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2694	03135	02693	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2695	03136	02694	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2696	03138	02695	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2697	03139	02696	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2698	03140	02697	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2699	03141	02698	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2700	03142	02699	9		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2701	03145	02700	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2702	03146	02701	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2703	03147	02702	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2704	03148	02703	12		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2705	03149	02704	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2706	03150	02705	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2707	03151	02706	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2708	03152	02707	8		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2709	03153	02708	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2710	03154	02709	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2711	03155	02710	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2712	03156	02711	15		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2713	03157	02712	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2714	03159	02713	3		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2715	03160	02714	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2716	03162	02715	4		0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2717	03163	02716	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2718	03164	02717	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2719	03166	02718	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2720	03167	02719	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2721	03168	02720	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 76

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2758	03213	02757	3	3	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
2759	03214	02758	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2760	03215	02759	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2761	03216	02760	4	4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2762	03217	02761	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2763	03218	02762	2	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2764	03219	02763	3	3	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2765	03220	02764	2	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2766	03221	02765	2	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2767	03222	02766	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2768	03223	02767	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2769	03224	02768	4	4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2770	03225	02769	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2771	03227	02770	2	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2772	03229	02771	2	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2773	03230	02772	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2774	03231	02773	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2775	03233	02774	2	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2776	03234	02775	2	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2777	03235	02776	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2778	03236	02777	2	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2779	03237	02778	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2780	03239	02779	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2781	03240	02780	4	4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2782	03241	02781	2	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2783	03242	02782	2	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2784	03243	02783	2	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2785	03244	02784	3	3	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2786	03245	02785	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2787	03247	02786	2	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2788	03248	02787	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2789	03249	02788	6	6	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2790	03251	02789	2	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2791	03252	02790	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2792	03253	02791	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2793	03255	02792	5	5	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 78

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2794	03257	02793	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2795	03258	02794	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2796	03259	02795	10		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2797	03261	02796	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2798	03263	02797	5		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2799	03264	02798	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2800	03267	02799	3		0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2801	03268	02800	5		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2802	03271	02801	3		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2803	03274	02802	7		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2804	03279	02803	8		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2805	03281	02804	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2806	03282	02805	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2807	03283	02806	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2808	03284	02807	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2809	03286	02808	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2810	03289	02809	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2811	03294	02810	5		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2812	03296	02811	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2813	03297	02812	4		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2814	03299	02813	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2815	03300	02814	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2816	03304	02815	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2817	03305	02816	15		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2818	03306	02817	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2819	03307	02818	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2820	03308	02819	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2821	03310	02820	7		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2822	03311	02821	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2823	03312	02822	4		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2824	03313	02823	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2825	03315	02824	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2826	03318	02825	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2827	03319	02826	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2828	03324	02827	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2829	03325	02828	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 79

Table: 81

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
2902	03443	02901	14		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	3	4	1	0	0	0	5	0	0					
2903	03444	02902	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2904	03445	02903	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2905	03446	02904	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2906	03447	02905	5		0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	1	0	0	1	0	0	0	554769	96.2 264	1	161 429
2907	03448	02906	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2908	03449	02907	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2909	03450	02908	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2910	03451	02909	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2911	03452	02910	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2912	03453	02911	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2913	03454	02912	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2914	03455	02913	5		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2915	03456	02914	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2916	03457	02915	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2917	03458	02916	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2918	03459	02917	7		0	0	0	0	0	0	0	0	2	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.1 247	1	1311	1557	
2919	03460	02918	8		0	0	0	0	0	0	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.5 242	1	2363	2620
2920	03461	02919	5		0	0	0	0	0	0	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2921	03462	02920	1		0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0						
2922	03463	02921	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2923	03464	02922	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2924	03465	02923	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2925	03466	02924	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2926	03467	02925	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2927	03468	02926	5		0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2928	03469	02927	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2929	03470	02928	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2930	03471	02929	6		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2931	03472	02930	2		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2932	03473	02931	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2933	03474	02932	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2934	03476	02933	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2935	03477	02934	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2936	03478	02935	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2937	03479	02936	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
2938	03480	02937	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2939	03481	02938	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2940	03482	02939	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2941	03483	02940	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2942	03484	02941	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2943	03485	02942	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2944	03486	02943	7		0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	M29063	98 6 212	1 1175	1398	
2945	03487	02944	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2946	03488	02945	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2947	03489	02946	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2948	03490	02947	3		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
2949	03491	02948	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2950	03492	02949	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2951	03493	02950	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2952	03494	02951	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2953	03495	02952	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2954	03496	02953	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2955	03497	02954	3		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	M34671	100 191	1 917	1671	
2956	03498	02955	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2957	03499	02956	5		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2958	03500	02957	4		0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0					
2959	03501	02958	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2960	03502	02959	6		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2961	03503	02960	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2962	03504	02961	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2963	03505	02962	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2964	03506	02963	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2965	03507	02964	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2966	03508	02965	3		0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0					
2967	03509	02966	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2968	03510	02967	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2969	03511	02968	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2970	03512	02969	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2971	03513	02970	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2972	03514	02971	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2973	03515	02972	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 83

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK		
2974	03516	02973	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
2975	03517	02974	10		0	0	0	0	0	0	0	0	4	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2976	03518	02975	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100 96	1 1335	1433		
2977	03519	02976	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2978	03520	02977	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2979	03521	02978	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97 6 166	1 2428	3727	
2980	03522	02979	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2981	03523	02980	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2982	03524	02981	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2983	03525	02982	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2984	03526	02983	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2985	03527	02984	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2986	03528	02985	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2987	03529	02986	6		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2988	03530	02987	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2989	03531	02988	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2990	03532	02989	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2991	03533	02990	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2992	03534	02991	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2993	03535	02992	9		0	0	0	0	0	0	0	0	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2994	03536	02993	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2995	03537	02994	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2996	03538	02995	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2997	03539	02996	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2998	03540	02997	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2999	03541	02998	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3000	03542	02999	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3001	03543	03000	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3002	03544	03001	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3003	03545	03002	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3004	03546	03003	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3005	03547	03004	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3006	03548	03005	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3007	03549	03006	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3008	03550	03007	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3009	03551	03008	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 84

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
3010	03552	03009	4		0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0					
3011	03553	03010	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3012	03554	03011	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3013	03555	03012	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3014	03556	03013	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3015	03557	03014	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3016	03558	03015	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3017	03559	03016	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3018	03560	03017	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3019	03561	03018	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3020	03562	03019	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3021	03563	03020	11		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3022	03564	03021	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3023	03565	03022	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3024	03566	03023	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3025	03567	03024	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3026	03568	03025	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3027	03569	03026	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3028	03570	03027	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3029	03571	03028	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3030	03572	03029	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3031	03573	03030	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3032	03574	03031	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3033	03575	03032	17		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3034	03576	03033	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3035	03577	03034	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3036	03578	03035	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3037	03579	03036	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3038	03580	03037	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3039	03581	03038	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3040	03582	03039	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3041	03583	03040	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3042	03584	03041	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3043	03585	03042	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3044	03586	03043	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3045	03587	03044	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 85

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AV	AW	AY	B	BC	BE	BF	BG	BH	BI	BK																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
3046	03588	03045	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
3047	03589	03046	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
3048	03590	03047	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
3049	03591	03048	9		0	0	0	0	0	0	2	0	0	0	0	0	1	1	0	2	0	0	0	0	0	0	1	0	0	06328	97.8	179	1	1061	1404																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
3050	03592	03049	2		0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0</

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	FA	GA	IA	KA	MA	QA	SA	TA	WA	YA	BA	CA	BE	BF	BG	BH	BI	BK		
3082	03625	03081	2		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
3083	03626	03082	2		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3084	03627	03083	5		0	0	0		0	0	0	1	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	86	1	6647	6732
3085	03628	03084	2		0	0	0		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3086	03629	03085	9		0	0	0		0	0	0	0	1	1	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3087	03631	03086	3		0	0	0		0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3088	03632	03087	1		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3089	03633	03088	2		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3090	03634	03089	8		0	0	0		0	0	0	1	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3091	03635	03090	3		0	0	0		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3092	03636	03091	1		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3093	03637	03092	1		0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3094	03638	03093	1		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3095	03639	03094	2		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3096	03640	03095	2		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3097	03641	03096	2		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3098	03642	03097	2		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3099	03643	03098	2		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3100	03644	03099	1		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3101	03645	03100	2		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3102	03646	03101	1		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3103	03647	03102	1		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3104	03648	03103	1		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3105	03649	03104	8		0	0	0		0	0	0	2	0	2	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3106	03650	03105	1		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3107	03651	03106	3		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3108	03652	03107	1		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3109	03653	03108	1		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3110	03654	03109	3		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3111	03655	03110	3		0	0	0		0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3112	03659	03111	6		0	0	0		0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3113	03661	03112	2		0	0	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3114	03679	03113	1		0	0	0		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3115	03680	03114	1		0	0	0		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3116	03681	03115	3		0	0	0		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3117	03682	03116	1		0	0	0		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AK	AM	AN	AO	AP	AR	AS	AT	AW	AY	BABC	BE	BF	BG	BH	BI	BK
3118	03683	03117	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3119	03684	03118	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3120	03685	03119	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3121	03686	03120	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3122	03688	03121	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3123	03689	03122	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3124	03690	03123	4		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3125	03691	03124	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3126	03693	03125	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3127	03694	03126	10		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3128	03695	03127	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3129	03696	03128	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3130	03697	03129	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3131	03698	03130	13		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3132	03699	03131	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3133	03701	03132	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3134	03702	03133	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3135	03703	03134	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3136	03704	03135	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3137	03705	03136	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3138	03707	03137	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3139	03708	03138	4		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3140	03709	03139	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3141	03710	03140	4		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3142	03711	03141	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3143	03712	03142	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3144	03713	03143	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3145	03714	03144	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3146	03715	03145	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3147	03716	03146	4		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3148	03717	03147	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3149	03718	03148	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3150	03719	03149	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3151	03720	03150	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3152	03721	03151	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3153	03722	03152	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 88

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	AG	AI	AK	AM	AN	AO	AS	AW	AY	B	BE	BF	BG	BH	BI	BK
3190	03760	03189	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3191	03761	03190	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3192	03762	03191	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3193	03763	03192	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3194	03764	03193	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3195	03765	03194	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3196	03766	03195	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3197	03767	03196	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3198	03768	03197	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3199	03769	03198	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3200	03770	03199	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3201	03771	03200	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3202	03772	03201	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3203	03773	03202	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3204	03774	03203	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3205	03775	03204	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3206	03776	03205	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3207	03777	03206	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3208	03778	03207	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3209	03779	03208	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3210	03780	03209	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3211	03781	03210	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3212	03782	03211	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3213	03783	03212	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3214	03784	03213	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3215	03785	03214	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3216	03786	03215	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3217	03787	03216	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3218	03788	03217	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3219	03789	03218	6		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3220	03790	03219	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3221	03791	03220	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3222	03792	03221	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3223	03793	03222	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3224	03794	03223	5		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3225	03795	03224	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 90

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AJ	AK	AM	AN	AS	AV	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3226	03796	03225	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3227	03797	03226	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3228	03798	03227	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3229	03799	03228	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3230	03800	03229	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3231	03801	03230	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3232	03802	03231	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3233	03803	03232	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3234	03804	03233	7		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3235	03805	03234	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3236	03806	03235	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3237	03807	03236	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3238	03808	03237	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3239	03809	03238	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3240	03810	03239	1		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3241	03811	03240	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3242	03812	03241	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3243	03813	03242	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3244	03814	03243	6		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3245	03815	03244	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3246	03816	03245	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3247	03817	03246	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3248	03818	03247	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3249	03819	03248	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3250	03820	03249	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3251	03821	03250	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3252	03822	03251	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3253	03823	03252	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3254	03824	03253	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3255	03825	03254	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3256	03826	03255	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3257	03827	03256	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3258	03828	03257	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3259	03829	03258	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3260	03830	03259	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3261	03831	03260	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 91

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3262	03832	03261	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3263	03833	03262	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3264	03835	03263	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3265	03836	03264	1		0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0						
3266	03837	03265	13		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3267	03838	03266	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3268	03839	03267	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3269	03840	03268	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3270	03841	03269	3		0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0						
3271	03842	03270	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3272	03843	03271	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3273	03844	03272	50		0	0	0	0	0	0	0	0	0	35	0	0	0	0	0	0	0	0	0	0	0	0	0						
3274	03845	03273	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3275	03846	03274	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3276	03847	03275	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3277	03848	03276	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3278	03849	03277	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3279	03850	03278	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3280	03851	03279	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3281	03852	03280	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3282	03853	03281	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3283	03854	03282	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3284	03855	03283	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3285	03856	03284	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3286	03857	03285	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3287	03859	03286	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3288	03860	03287	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3289	03861	03288	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3290	03862	03289	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3291	03863	03290	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3292	03864	03291	6		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3293	03865	03292	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3294	03866	03293	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3295	03867	03294	20		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
3296	03868	03295	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3297	03869	03296	7		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						

Table 92

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3298	03870	03297	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3299	03871	03298	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3300	03872	03299	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3301	03873	03300	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3302	03874	03301	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3303	03875	03302	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3304	03876	03303	5		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3305	03877	03304	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3306	03878	03305	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3307	03879	03306	7		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3308	03880	03307	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3309	03881	03308	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0						
3310	03882	03309	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3311	03883	03310	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3312	03884	03311	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0						
3313	03885	03312	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3314	03886	03313	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3315	03887	03314	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3316	03888	03315	5		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3317	03889	03316	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3318	03890	03317	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3319	03891	03318	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3320	03892	03319	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3321	03893	03320	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3322	03894	03321	5		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0						
3323	03895	03322	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3324	03896	03323	7		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3325	03897	03324	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3326	03898	03325	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3327	03899	03326	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3328	03900	03327	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0						
3329	03901	03328	5		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3330	03902	03329	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3331	03903	03330	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3332	03904	03331	5		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3333	03905	03332	5		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0						

Table 93

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3334	03906	03333	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3335	03907	03334	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3336	03908	03335	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3337	03909	03336	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3338	03910	03337	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3339	03911	03338	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3340	03912	03339	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3341	03913	03340	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3342	03914	03341	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3343	03915	03342	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3344	03916	03343	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3345	03917	03344	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3346	03918	03345	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3347	03919	03346	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3348	03920	03347	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3349	03921	03348	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3350	03922	03349	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3351	03923	03350	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3352	03924	03351	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3353	03925	03352	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3354	03926	03353	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3355	03927	03354	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3356	03928	03355	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3357	03929	03356	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3358	03930	03357	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3359	03931	03358	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3360	03932	03359	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3361	03933	03360	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3362	03934	03361	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3363	03935	03362	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3364	03936	03363	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3365	03937	03364	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3366	03938	03365	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3367	03939	03366	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3368	03940	03367	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3369	03941	03368	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 94

[illegible]

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3442	04051	03441	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3443	04052	03442	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3444	04053	03443	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3445	04054	03444	9		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3446	04055	03445	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3447	04056	03446	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3448	04057	03447	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3449	04058	03448	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3450	04059	03449	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3451	04060	03450	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3452	04061	03451	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3453	04062	03452	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3454	04063	03453	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3455	04064	03454	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3456	04065	03455	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3457	04066	03456	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3458	04067	03457	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3459	04068	03458	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3460	04069	03459	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3461	04070	03460	3		0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3462	04071	03461	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3463	04072	03462	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3464	04073	03463	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3465	04074	03464	5		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3466	04075	03465	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3467	04076	03466	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3468	04077	03467	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3469	04078	03468	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3470	04079	03469	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3471	04080	03470	10		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3472	04081	03471	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3473	04082	03472	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3474	04083	03473	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3475	04084	03474	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3476	04086	03475	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3477	04087	03476	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AI	AK	AM	AO	AS	AT	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
3478	04088	03477	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3479	04089	03478	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3480	04090	03479	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3481	04091	03480	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3482	04092	03481	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3483	04093	03482	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3484	04094	03483	13		0	0	0	0	0	0	0	0	0	0	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3485	04095	03484	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3486	04096	03485	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3487	04097	03486	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3488	04098	03487	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3489	04099	03488	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3490	04100	03489	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3491	04101	03490	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3492	04102	03491	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3493	04103	03492	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3494	04104	03493	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3495	04105	03494	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3496	04106	03495	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3497	04107	03496	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3498	04108	03497	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3499	04109	03498	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3500	04110	03499	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3501	04111	03500	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3502	04112	03501	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3503	04113	03502	4		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3504	04114	03503	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3505	04115	03504	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3506	04116	03505	12		0	0	0	0	0	0	0	0	0	0	19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3507	04117	03506	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3508	04118	03507	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3509	04119	03508	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3510	04120	03509	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3511	04121	03510	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3512	04122	03511	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3513	04123	03512	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
3514	04125	03513	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3515	04126	03514	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3516	04127	03515	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3517	04128	03516	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3518	04129	03517	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3519	04130	03518	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3520	04131	03519	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0					
3521	04132	03520	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3522	04133	03521	7		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3523	04134	03522	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3524	04135	03523	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3525	04136	03524	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3526	04137	03525	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3527	04139	03526	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0					
3528	04140	03527	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3529	04141	03528	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3530	04142	03529	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3531	04143	03530	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3532	04144	03531	11		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0					
3533	04145	03532	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3534	04146	03533	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3535	04147	03534	6		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3536	04148	03535	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3537	04149	03536	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0					
3538	04150	03537	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3539	04151	03538	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3540	04152	03539	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3541	04153	03540	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3542	04154	03541	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3543	04155	03542	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3544	04156	03543	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3545	04157	03544	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3546	04158	03545	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3547	04159	03546	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3548	04160	03547	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3549	04161	03548	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
3550	04162	03549	3		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0					
3551	04163	03550	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3552	04164	03551	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3553	04165	03552	6		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	96.1 127	1	990	1116
3554	04166	03553	3		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.2 132	1	533	1452
3555	04167	03554	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3556	04169	03555	1		0	0	0	0	0	0	0	0	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0					
3557	04170	03556	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3558	04171	03557	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3559	04172	03558	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3560	04173	03559	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3561	04174	03560	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3562	04175	03561	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3563	04176	03562	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3564	04177	03563	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3565	04179	03564	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3566	04180	03565	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3567	04181	03566	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3568	04182	03567	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3569	04183	03568	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3570	04184	03569	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3571	04186	03570	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3572	04187	03571	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3573	04188	03572	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3574	04189	03573	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3575	04190	03574	10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3576	04191	03575	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3577	04192	03576	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3578	04193	03577	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3579	04194	03578	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3580	04195	03579	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3581	04196	03580	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3582	04197	03581	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3583	04198	03582	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3584	04199	03583	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3585	04200	03584	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 100

A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	CA	IA	KA	MA	QA	SA	TA	WA	YA	BA	BC	BE	BF	BG	BH	BI	BK
3586	04201	03585	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3587	04202	03586	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3588	04203	03587	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3589	04204	03588	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3590	04205	03589	2	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3591	04206	03590	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3592	04207	03591	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3593	04210	03592	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3594	04211	03593	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3595	04213	03594	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3596	04214	03595	3	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3597	04215	03596	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3598	04216	03597	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3599	04218	03598	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3600	04219	03599	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3601	04220	03600	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3602	04247	03601	3	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3603	04248	03602	1	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3604	04249	03603	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3605	04250	03604	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3606	04252	03605	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3607	04253	03606	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3608	04256	03607	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3609	04257	03608	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3610	04258	03609	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3611	04259	03610	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3612	04261	03611	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3613	04264	03612	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3614	04265	03613	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3615	04266	03614	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3616	04267	03615	2	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3617	04268	03616	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3618	04269	03617	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3619	04270	03618	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3620	04271	03619	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3621	04272	03620	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 101

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	EA	GA	IA	KA	MA	QA	SA	TA	VA	WA	XA	YA	Z	BC	BE	BF	BG	BH	BI	BK	
3622	04273	03621	1																																		
3623	04274	03622	1																																		
3624	04275	03623	2																																		
3625	04276	03624	1																																		
3626	04278	03625	4																																		
3627	04279	03626	1																																		
3628	04280	03627	1																																		
3629	04281	03628	1																																		
3630	04282	03629	1																																		
3631	04284	03630	1																																		
3632	04285	03631	1																																		
3633	04286	03632	1																																		
3634	04287	03633	2																																		
3635	04288	03634	3																																		
3636	04289	03635	2																																		
3637	04290	03636	8																																		
3638	04291	03637	1																																		
3639	04292	03638	1																																		
3640	04293	03639	2																																		
3641	04294	03640	6																																		
3642	04295	03641	2																																		
3643	04296	03642	2																																		
3644	04297	03643	1																																		
3645	04298	03644	1																																		
3646	04299	03645	1																																		
3647	04300	03646	1																																		
3648	04302	03647	2																																		
3649	04303	03648	1																																		
3650	04304	03649	1																																		
3651	04305	03650	3																																		
3652	04306	03651	1																																		
3653	04307	03652	2																																		
3654	04308	03653	1																																		
3655	04309	03654	2																																		
3656	04310	03655	1																																		
3657	04311	03656	3																																		

Table 102

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3658	04312	03657	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3659	04313	03658	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3660	04314	03659	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3661	04315	03660	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3662	04316	03661	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3663	04317	03662	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3664	04318	03663	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3665	04319	03664	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3666	04320	03665	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3667	04321	03666	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3668	04322	03667	12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3669	04323	03668	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3670	04324	03669	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3671	04325	03670	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3672	04326	03671	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3673	04327	03672	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3674	04328	03673	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3675	04329	03674	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3676	04330	03675	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3677	04331	03676	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3678	04332	03677	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3679	04333	03678	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3680	04334	03679	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3681	04335	03680	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3682	04336	03681	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3683	04337	03682	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3684	04338	03683	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3685	04339	03684	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3686	04340	03685	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3687	04341	03686	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3688	04342	03687	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3689	04343	03688	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3690	04344	03689	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3691	04345	03690	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3692	04346	03691	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3693	04347	03692	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3694	04348	03693	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3695	04349	03694	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3696	04350	03695	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3697	04351	03696	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3698	04352	03697	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3699	04353	03698	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3700	04354	03699	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3701	04355	03700	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3702	04356	03701	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3703	04357	03702	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3704	04358	03703	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3705	04359	03704	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3706	04360	03705	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3707	04361	03706	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3708	04362	03707	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3709	04363	03708	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3710	04364	03709	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3711	04365	03710	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3712	04366	03711	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0														

Table 103

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BI	BK
3730	04388	03729	1																													
3731	04389	03730	3																													
3732	04390	03731	2																													
3733	04391	03732	3																													
3734	04392	03733	1																													
3735	04393	03734	3																													
3736	04394	03735	1																													
3737	04395	03736	2																													
3738	04396	03737	1																													
3739	04397	03738	1																													
3740	04398	03739	1																													
3741	04399	03740	1																													
3742	04400	03741	1																													
3743	04401	03742	1																													
3744	04402	03743	7																													
3745	04403	03744	1																													
3746	04404	03745	1																													
3747	04405	03746	2																													
3748	04406	03747	1																													
3749	04407	03748	3																													
3750	04408	03749	1																													
3751	04409	03750	1																													
3752	04410	03751	1																													
3753	04411	03752	2																													
3754	04412	03753	2																													
3755	04414	03754	5																													
3756	04415	03755	3																													
3757	04416	03756	1																													
3758	04417	03757	2																													
3759	04418	03758	2																													
3760	04419	03759	1																													
3761	04420	03760	1																													
3762	04421	03761	2																													
3763	04422	03762	1																													
3764	04423	03763	1																													
3765	04424	03764	1																													

Table 105

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	CA	CC	CA	AS	AA	AA	AY	BA	BC	BE	BF	BG	BI	BK
3766	04425	03765	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3767	04426	03766	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3768	04427	03767	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3769	04428	03768	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3770	04429	03769	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3771	04430	03770	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3772	04431	03771	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3773	04432	03772	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3774	04433	03773	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3775	04434	03774	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3776	04435	03775	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3777	04436	03776	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3778	04437	03777	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3779	04439	03778	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3780	04440	03779	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3781	04441	03780	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3782	04442	03781	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3783	04443	03782	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3784	04445	03783	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3785	04446	03784	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3786	04447	03785	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3787	04448	03786	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3788	04449	03787	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3789	04450	03788	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3790	04452	03789	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3791	04453	03790	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3792	04454	03791	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3793	04455	03792	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3794	04456	03793	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3795	04457	03794	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3796	04460	03795	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3797	04462	03796	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3798	04463	03797	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3799	04464	03798	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3800	04465	03799	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3801	04466	03800	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 106

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	TA	GA	IA	KA	MA	QA	SA	LA	WA	YA	BA	BC	BE	BF	BG	BH	BI	BK
3802	04467	03801	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3803	04468	03802	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3804	04469	03803	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3805	04470	03804	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3806	04471	03805	2		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
3807	04472	03806	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3808	04473	03807	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3809	04474	03808	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3810	04476	03809	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3811	04478	03810	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3812	04482	03811	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3813	04483	03812	6		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3814	04484	03813	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3815	04485	03814	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3816	04486	03815	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3817	04487	03816	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3818	04488	03817	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3819	04489	03818	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3820	04491	03819	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3821	04492	03820	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3822	04493	03821	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3823	04494	03822	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3824	04495	03823	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3825	04496	03824	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3826	04497	03825	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3827	04498	03826	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3828	04499	03827	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3829	04500	03828	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3830	04501	03829	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3831	04502	03830	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3832	04503	03831	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3833	04504	03832	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3834	04506	03833	5		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3835	04507	03834	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3836	04509	03835	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3837	04510	03836	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 107

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	DK
3838	04511	03837	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0					
3839	04512	03838	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3840	04513	03839	2		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0					
3841	04514	03840	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3842	04515	03841	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3843	04516	03842	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3844	04517	03843	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3845	04518	03844	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3846	04519	03845	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3847	04520	03846	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3848	04521	03847	2		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0					
3849	04522	03848	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3850	04523	03849	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3851	04525	03850	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3852	04527	03851	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3853	04528	03852	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3854	04529	03853	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3855	04530	03854	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3856	04531	03855	2		0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0					
3857	04532	03856	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3858	04533	03857	4		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3859	04534	03858	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3860	04535	03859	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3861	04536	03860	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3862	04537	03861	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3863	04538	03862	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3864	04539	03863	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3865	04541	03864	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3866	04542	03865	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3867	04543	03866	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3868	04546	03867	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3869	04547	03868	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3870	04548	03869	2		0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0					
3871	04552	03870	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3872	04556	03871	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3873	04557	03872	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					

Table 108

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	A	A	C	A	I	A	K	A	M	A	C	A	S	A	L	A	V	W	A	B	C	BE	BF	BG	BH	BI	BK			
3910	04634	03909	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
3911	04635	03910	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3912	04636	03911	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3913	04637	03912	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3914	04638	03913	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		408
3915	04639	03914	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3916	04640	03915	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3917	04641	03916	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3918	04642	03917	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3919	04643	03918	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3920	04644	03919	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3921	04645	03920	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3922	04646	03921	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3923	04647	03922	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3924	04648	03923	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3925	04649	03924	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3926	04650	03925	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3927	04651	03926	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3928	04652	03927	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3929	04653	03928	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3930	04654	03929	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3931	04655	03930	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		2273
3932	04656	03931	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3933	04657	03932	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3934	04658	03933	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3935	04659	03934	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3936	04660	03935	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3937	04661	03936	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3938	04662	03937	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3939	04663	03938	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3940	04664	03939	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3941	04665	03940	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3942	04666	03941	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3943	04667	03942	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3944	04668	03943	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
3945	04669	03944	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		4545

Table 110

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
3946	04670	03945	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3947	04671	03946	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3948	04672	03947	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3949	04673	03948	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3950	04674	03949	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3951	04675	03950	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3952	04676	03951	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3953	04677	03952	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3954	04678	03953	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3955	04679	03954	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3956	04680	03955	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3957	04681	03956	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3958	04682	03957	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3959	04683	03958	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3960	04684	03959	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3961	04685	03960	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3962	04686	03961	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3963	04687	03962	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3964	04688	03963	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3965	04689	03964	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3966	04690	03965	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3967	04691	03966	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3968	04692	03967	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3969	04693	03968	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3970	04694	03969	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3971	04695	03970	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3972	04696	03971	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3973	04697	03972	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3974	04698	03973	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3975	04699	03974	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3976	04700	03975	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3977	04701	03976	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3978	04702	03977	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3979	04703	03978	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3980	04704	03979	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3981	04705	03980	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 111

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AV	AW	BA	BC	BE	BF	BG	BH	BI	BK
3982	04706	03981	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3983	04707	03982	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3984	04708	03983	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3985	04709	03984	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3986	04710	03985	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3987	04711	03986	7		0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3988	04712	03987	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3989	04713	03988	1		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3990	04714	03989	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3991	04715	03990	5		0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3992	04716	03991	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3993	04717	03992	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3994	04718	03993	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3995	04719	03994	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3996	04720	03995	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3997	04721	03996	4		0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3998	04722	03997	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3999	04723	03998	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4000	04724	03999	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4001	04725	04000	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4002	04728	04001	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4003	04729	04002	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4004	04730	04003	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4005	04732	04004	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4006	04733	04005	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4007	04734	04006	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4008	04735	04007	3		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4009	04736	04008	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4010	04737	04009	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4011	04738	04010	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4012	04739	04011	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4013	04740	04012	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4014	04741	04013	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4015	04742	04014	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4016	04743	04015	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4017	04744	04016	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 112

[illegible]

[illegible]

A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CC	EE	AG	AK	AM	AO	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4090	04819	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
4091	04820	3	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0						
4092	04821	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4093	04822	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0						
4094	04823	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	MS217	100	101	1	2311	2411
4095	04824	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4096	04826	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4097	04827	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4098	04828	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4099	04829	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
4100	04830	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4101	04831	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4102	04832	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4103	04833	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4104	04834	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4105	04835	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4106	04836	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
4107	04837	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4108	04838	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4109	04839	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4110	04840	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4111	04841	3	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
4112	04842	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4113	04843	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4114	04844	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4115	04845	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4116	04846	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4117	04847	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4118	04848	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
4119	04850	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
4120	04851	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4121	04852	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4122	04853	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4123	04854	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4124	04855	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4125	04856	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						

Table 115

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
4126	04859	04125	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4127	04860	04126	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4128	04861	04127	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4129	04862	04128	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4130	04863	04129	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4131	04864	04130	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4132	04865	04131	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4133	04866	04132	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4134	04867	04133	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4135	04868	04134	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4136	04869	04135	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4137	04870	04136	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4138	04872	04137	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4139	04873	04138	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4140	04874	04139	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4141	04875	04140	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4142	04877	04141	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4143	04878	04142	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4144	04879	04143	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4145	04881	04144	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4146	04882	04145	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4147	04883	04146	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4148	04884	04147	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4149	04885	04148	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4150	04886	04149	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4151	04887	04150	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4152	04888	04151	25		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4153	04889	04152	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4154	04890	04153	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4155	04891	04154	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4156	04892	04155	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4157	04893	04156	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4158	04894	04157	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4159	04895	04158	14		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4160	04897	04159	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0										

Table 116

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4198	04987	04197	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4199	04988	04198	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4200	04989	04199	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4201	04990	04200	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4202	04991	04201	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4203	04992	04202	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4204	04993	04203	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4205	04994	04204	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4206	04997	04205	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4207	04998	04206	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4208	04999	04207	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4209	05001	04208	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4210	05002	04209	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4211	05003	04210	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4212	05004	04211	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4213	05005	04212	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4214	05006	04213	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4215	05007	04214	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4216	05008	04215	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4217	05009	04216	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4218	05010	04217	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4219	05011	04218	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4220	05013	04219	14		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4221	05014	04220	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4222	05016	04221	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4223	05018	04222	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4224	05019	04223	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4225	05021	04224	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4226	05023	04225	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4227	05024	04226	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4228	05025	04227	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4229	05026	04228	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4230	05027	04229	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4231	05028	04230	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4232	05029	04231	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4233	05030	04232	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 118

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK	
4270	05076	04269	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4271	05077	04270	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4272	05079	04271	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4273	05080	04272	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4274	05081	04273	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
4275	05082	04274	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4276	05083	04275	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4277	05085	04276	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4278	05086	04277	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4279	05087	04278	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4280	05088	04279	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4281	05089	04280	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4282	05090	04281	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4283	05092	04282	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4284	05094	04283	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4285	05095	04284	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4286	05096	04285	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4287	05099	04286	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4288	05100	04287	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4289	05102	04288	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4290	05103	04289	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4291	05104	04290	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4292	05105	04291	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4293	05106	04292	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4294	05107	04293	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4295	05108	04294	12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4296	05109	04295	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4297	05110	04296	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4298	05111	04297	16		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4299	05112	04298	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4300	05113	04299	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4301	05114	04300	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4302	05115	04301	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4303	05116	04302	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4304	05117	04303	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4305	05118	04304	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AT	AV	AW	AY	B	BC	BE	BF	BGBH	BI	BK
4306	05119	04305	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4307	05120	04306	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4308	05121	04307	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4309	05122	04308	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4310	05123	04309	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4311	05124	04310	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4312	05127	04311	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4313	05128	04312	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4314	05129	04313	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4315	05130	04314	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4316	05132	04315	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4317	05133	04316	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4318	05134	04317	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4319	05135	04318	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4320	05136	04319	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4321	05137	04320	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4322	05138	04321	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4323	05139	04322	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4324	05140	04323	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4325	05141	04324	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4326	05142	04325	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4327	05143	04326	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4328	05144	04327	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4329	05145	04328	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4330	05147	04329	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4331	05148	04330	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4332	05149	04331	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4333	05150	04332	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4334	05151	04333	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4335	05152	04334	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4336	05153	04335	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4337	05155	04336	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4338	05157	04337	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4339	05158	04338	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4340	05159	04339	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4341	05160	04340	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 121

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4378	05204	04377	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4379	05205	04378	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4380	05206	04379	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4381	05207	04380	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4382	05208	04381	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4383	05209	04382	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4384	05210	04383	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4385	05211	04384	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4386	05212	04385	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4387	05213	04386	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4388	05214	04387	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4389	05215	04388	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4390	05216	04389	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4391	05217	04390	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4392	05218	04391	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4393	05219	04392	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4394	05220	04393	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4395	05221	04394	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4396	05223	04395	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4397	05224	04396	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4398	05227	04397	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4399	05228	04398	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4400	05229	04399	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4401	05230	04400	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4402	05231	04401	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4403	05232	04402	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4404	05233	04403	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4405	05234	04404	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4406	05235	04405	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4407	05236	04406	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4408	05237	04407	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4409	05238	04408	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4410	05239	04409	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4411	05240	04410	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4412	05241	04411	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4413	05242	04412	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 123

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A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4414	05243	04413	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4415	05244	04414	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4416	05245	04415	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4417	05246	04416	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4418	05247	04417	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4419	05248	04418	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4420	05249	04419	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4421	05251	04420	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4422	05252	04421	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4423	05253	04422	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4424	05254	04423	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4425	05255	04424	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4426	05259	04425	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4427	05260	04426	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4428	05262	04427	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4429	05263	04428	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4430	05264	04429	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4431	05266	04430	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4432	05267	04431	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4433	05269	04432	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4434	05270	04433	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4435	05271	04434	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4436	05272	04435	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4437	05273	04436	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4438	05274	04437	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4439	05275	04438	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4440	05276	04439	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4441	05278	04440	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4442	05279	04441	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4443	05280	04442	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4444	05281	04443	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4445	05282	04444	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4446	05283	04445	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4447	05284	04446	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4448	05285	04447	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4449	05286	04448	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 124

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AL	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4450	05287	04449	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4451	05288	04450	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4452	05289	04451	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4453	05290	04452	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4454	05291	04453	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4455	05292	04454	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4456	05293	04455	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4457	05294	04456	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4458	05295	04457	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4459	05296	04458	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4460	05297	04459	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4461	05298	04460	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4462	05300	04461	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4463	05301	04462	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4464	05302	04463	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4465	05303	04464	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4466	05304	04465	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4467	05305	04466	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4468	05306	04467	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4469	05307	04468	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4470	05308	04469	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4471	05309	04470	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4472	05310	04471	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4473	05311	04472	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4474	05312	04473	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4475	05313	04474	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4476	05314	04475	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4477	05315	04476	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4478	05316	04477	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4479	05318	04478	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4480	05319	04479	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4481	05320	04480	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4482	05321	04481	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4483	05322	04482	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4484	05323	04483	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4485	05325	04484	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 125

[illegible]

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	BC	BE	BF	BG	BH	BI	BK
4558	05409	04557	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4559	05410	04558	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4560	05411	04559	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4561	05412	04560	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4562	05413	04561	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4563	05414	04562	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4564	05415	04563	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4565	05416	04564	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4566	05417	04565	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4567	05418	04566	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4568	05419	04567	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4569	05420	04568	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4570	05421	04569	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4571	05422	04570	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4572	05423	04571	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4573	05424	04572	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4574	05425	04573	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4575	05427	04574	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4576	05428	04575	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4577	05429	04576	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4578	05430	04577	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4579	05431	04578	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4580	05432	04579	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4581	05433	04580	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4582	05434	04581	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4583	05435	04582	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4584	05436	04583	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4585	05437	04584	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4586	05438	04585	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4587	05439	04586	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4588	05440	04587	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4589	05441	04588	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4590	05442	04589	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4591	05443	04590	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4592	05444	04591	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
4593	05445	04592	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						

Table 128

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4594	05446	04593	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4595	05447	04594	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
4596	05448	04595	3		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	1	0	0	0					
4597	05451	04596	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4598	05452	04597	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4599	05453	04598	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4600	05454	04599	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4601	05455	04600	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4602	05456	04601	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
4603	05458	04602	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4604	05459	04603	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4605	05460	04604	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4606	05461	04605	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4607	05462	04606	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4608	05464	04607	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4609	05465	04608	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4610	05466	04609	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4611	05467	04610	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
4612	05468	04611	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4613	05469	04612	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4614	05470	04613	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4615	05471	04614	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4616	05472	04615	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4617	05474	04616	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4618	05475	04617	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4619	05476	04618	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4620	05477	04619	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4621	05478	04620	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4622	05479	04621	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4623	05480	04622	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4624	05481	04623	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4625	05482	04624	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4626	05483	04625	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4627	05484	04626	1		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
4628	05485	04627	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4629	05486	04628	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 129

	A	B	C	E	G	I	K	M	Q	S	U	W	Y	AA	CA	EA	GA	IA	KA	MA	QA	SA	TU	VW	X	BA	BC	BE	BF	BG	BH	BI	BK	
4630	05488	04629	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4631	05490	04630	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4632	05491	04631	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4633	05492	04632	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4634	05493	04633	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4635	05494	04634	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4636	05495	04635	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4637	05496	04636	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4638	05497	04637	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4639	05498	04638	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4640	05502	04639	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4641	05503	04640	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4642	05504	04641	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4643	05505	04642	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4644	05506	04643	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4645	05507	04644	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4646	05508	04645	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4647	05509	04646	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4648	05510	04647	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4649	05511	04648	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4650	05513	04649	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4651	05514	04650	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4652	05515	04651	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4653	05516	04652	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4654	05518	04653	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4655	05519	04654	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4656	05520	04655	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4657	05521	04656	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4658	05522	04657	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4659	05523	04658	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4660	05524	04659	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4661	05525	04660	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4662	05526	04661	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4663	05528	04662	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4664	05529	04663	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
4665	05531	04664	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4702	05577	04701	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4703	05578	04702	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4704	05579	04703	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4705	05580	04704	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4706	05581	04705	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4707	05582	04706	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4708	05583	04707	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4709	05585	04708	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4710	05586	04709	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4711	05587	04710	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4712	05588	04711	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4713	05589	04712	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4714	05590	04713	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4715	05591	04714	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4716	05593	04715	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4717	05595	04716	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4718	05598	04717	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4719	05599	04718	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4720	05600	04719	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4721	05601	04720	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4722	05602	04721	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4723	05603	04722	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4724	05604	04723	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4725	05606	04724	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4726	05607	04725	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4727	05608	04726	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4728	05610	04727	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4729	05612	04728	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4730	05613	04729	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4731	05614	04730	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4732	05615	04731	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4733	05616	04732	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4734	05618	04733	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4735	05619	04734	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4736	05621	04735	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4737	05622	04736	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 132

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AV	AY	B	BC	DE	BF	BG	BH	BI	IK
4738	05623	04737	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4739	05624	04738	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4740	05625	04739	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4741	05627	04740	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4742	05628	04741	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4743	05629	04742	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4744	05630	04743	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4745	05631	04744	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4746	05632	04745	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4747	05634	04746	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4748	05635	04747	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4749	05636	04748	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4750	05637	04749	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4751	05639	04750	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4752	05640	04751	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4753	05642	04752	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4754	05643	04753	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4755	05644	04754	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4756	05645	04755	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4757	05646	04756	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4758	05647	04757	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4759	05648	04758	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4760	05649	04759	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4761	05650	04760	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4762	05651	04761	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4763	05652	04762	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4764	05653	04763	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4765	05654	04764	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4766	05655	04765	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4767	05656	04766	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4768	05657	04767	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4769	05658	04768	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4770	05659	04769	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4771	05660	04770	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4772	05661	04771	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4773	05662	04772	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 133

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	BI	BK
4810	05718	04809	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4811	05719	04810	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4812	05720	04811	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4813	05721	04812	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4814	05722	04813	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4815	05723	04814	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4816	05724	04815	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4817	05725	04816	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4818	05726	04817	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4819	05727	04818	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4820	05729	04819	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4821	05730	04820	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4822	05731	04821	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4823	05732	04822	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4824	05733	04823	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4825	05734	04824	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4826	05735	04825	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4827	05736	04826	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4828	05738	04827	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4829	05741	04828	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4830	05742	04829	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4831	05743	04830	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4832	05747	04831	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4833	05748	04832	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4834	05749	04833	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4835	05751	04834	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4836	05752	04835	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4837	05754	04836	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4838	05755	04837	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4839	05756	04838	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4840	05757	04839	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4841	05758	04840	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4842	05759	04841	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4843	05763	04842	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4844	05765	04843	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4845	05767	04844	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 135

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A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4846	05768	04845	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4847	05769	04846	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4848	05770	04847	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4849	05771	04848	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4850	05772	04849	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4851	05773	04850	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4852	05774	04851	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4853	05775	04852	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4854	05776	04853	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4855	05777	04854	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4856	05778	04855	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4857	05779	04856	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4858	05780	04857	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4859	05781	04858	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4860	05782	04859	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4861	05783	04860	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4862	05784	04861	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4863	05785	04862	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4864	05787	04863	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4865	05789	04864	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4866	05790	04865	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4867	05792	04866	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4868	05793	04867	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4869	05794	04868	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4870	05795	04869	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4871	05796	04870	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4872	05797	04871	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4873	05798	04872	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4874	05799	04873	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4875	05800	04874	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4876	05801	04875	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4877	05802	04876	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4878	05803	04877	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4879	05804	04878	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4880	05805	04879	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4881	05806	04880	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 136

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4918	05856	04917	4		0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4919	05857	04918	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
4920	05858	04919	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4921	05859	04920	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4922	05860	04921	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4923	05862	04922	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4924	05863	04923	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4925	05864	04924	10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4926	05865	04925	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4927	05866	04926	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4928	05867	04927	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4929	05868	04928	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4930	05869	04929	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4931	05870	04930	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4932	05871	04931	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4933	05872	04932	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4934	05874	04933	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4935	05875	04934	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4936	05876	04935	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4937	05877	04936	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4938	05879	04937	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4939	05880	04938	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4940	05882	04939	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4941	05885	04940	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4942	05886	04941	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4943	05887	04942	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4944	05888	04943	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4945	05889	04944	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4946	05890	04945	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4947	05892	04946	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4948	05893	04947	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4949	05894	04948	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4950	05895	04949	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4951	05896	04950	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4952	05897	04951	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4953	05898	04952	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 138

[illegible]

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	EA	GA	IA	KA	MA	QA	SA	TA	WA	YA	BA	BC	BE	BF	BG	BH	BI	BK
5026	06000	05025	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5027	06001	05026	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5028	06004	05027	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5029	06005	05028	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5030	06008	05029	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5031	06010	05030	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5032	06011	05031	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5033	06013	05032	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5034	06014	05033	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5035	06015	05034	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5036	06016	05035	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5037	06017	05036	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5038	06018	05037	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5039	06020	05038	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5040	06021	05039	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5041	06022	05040	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5042	06023	05041	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5043	06024	05042	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5044	06025	05043	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5045	06026	05044	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5046	06027	05045	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5047	06028	05046	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5048	06030	05047	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5049	06031	05048	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5050	06032	05049	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5051	06034	05050	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5052	06035	05051	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5053	06036	05052	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5054	06038	05053	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5055	06039	05054	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5056	06040	05055	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5057	06041	05056	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5058	06042	05057	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5059	06043	05058	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5060	06044	05059	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
5061	06045	05060	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				

Table 141

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5062	06046	05061	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5063	06047	05062	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5064	06048	05063	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5065	06049	05064	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5066	06050	05065	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5067	06051	05066	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5068	06052	05067	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5069	06053	05068	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5070	06054	05069	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5071	06055	05070	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5072	06056	05071	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5073	06057	05072	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5074	06059	05073	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5075	06060	05074	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5076	06061	05075	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5077	06062	05076	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5078	06064	05077	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5079	06065	05078	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5080	06066	05079	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5081	06067	05080	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5082	06068	05081	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5083	06069	05082	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5084	06070	05083	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5085	06071	05084	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5086	06072	05085	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5087	06074	05086	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5088	06075	05087	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5089	06076	05088	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5090	06077	05089	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5091	06078	05090	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5092	06079	05091	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5093	06080	05092	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5094	06081	05093	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5095	06083	05094	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5096	06084	05095	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5097	06085	05096	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 142

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	EA	GA	IA	KA	MA	QA	SA	TA	WA	YA	BAC	BE	BF	BGBH	BI	BK	
5098	06086	05097	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5099	06087	05098	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5100	06089	05099	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5101	06090	05100	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5102	06091	05101	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5103	06092	05102	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5104	06093	05103	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5105	06094	05104	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5106	06095	05105	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5107	06097	05106	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5108	06098	05107	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5109	06100	05108	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5110	06101	05109	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5111	06102	05110	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5112	06103	05111	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5113	06104	05112	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5114	06105	05113	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5115	06107	05114	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5116	06108	05115	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5117	06109	05116	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5118	06110	05117	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5119	06111	05118	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5120	06112	05119	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5121	06113	05120	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5122	06114	05121	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5123	06115	05122	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5124	06116	05123	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5125	06117	05124	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5126	06118	05125	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5127	06119	05126	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5128	06122	05127	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5129	06123	05128	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5130	06125	05129	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5131	06126	05130	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5132	06127	05131	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5133	06128	05132	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	CA	IA	KA	MA	QA	SA	TA	WA	YA	B	BC	BE	BF	BG	BH	BI	BK
5170	06173	05169	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5171	06174	05170	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5172	06175	05171	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5173	06176	05172	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5174	06177	05173	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5175	06179	05174	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5176	06180	05175	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5177	06181	05176	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5178	06182	05177	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5179	06183	05178	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5180	06184	05179	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5181	06185	05180	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5182	06186	05181	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5183	06187	05182	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5184	06188	05183	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5185	06189	05184	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5186	06190	05185	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5187	06191	05186	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5188	06192	05187	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5189	06195	05188	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5190	06196	05189	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5191	06197	05190	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5192	06198	05191	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5193	06199	05192	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5194	06200	05193	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5195	06201	05194	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5196	06202	05195	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5197	06203	05196	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5198	06204	05197	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5199	06205	05198	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5200	06206	05199	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5201	06207	05200	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5202	06208	05201	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5203	06209	05202	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5204	06210	05203	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5205	06211	05204	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 145

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK
5206	06213	05205	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5207	06215	05206	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5208	06216	05207	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5209	06217	05208	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5210	06218	05209	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5211	06219	05210	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5212	06220	05211	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5213	06221	05212	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5214	06222	05213	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5215	06224	05214	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5216	06225	05215	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5217	06226	05216	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5218	06227	05217	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5219	06228	05218	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5220	06229	05219	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5221	06230	05220	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5222	06232	05221	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5223	06233	05222	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5224	06234	05223	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5225	06235	05224	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5226	06236	05225	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5227	06237	05226	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5228	06238	05227	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5229	06240	05228	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5230	06241	05229	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5231	06243	05230	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5232	06244	05231	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5233	06246	05232	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5234	06247	05233	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5235	06248	05234	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5236	06249	05235	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5237	06250	05236	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5238	06251	05237	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5239	06253	05238	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5240	06254	05239	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				
5241	06255	05240	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0				

Table 146

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AO	AS	AW	AY	BAB	BE	BF	BG	BH	BI	BK
5242	06256	05241	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5243	06257	05242	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2	0						
5244	06258	05243	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5245	06259	05244	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2	0	X52056	98.5	68	1	1297	1364
5246	06260	05245	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5247	06261	05246	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5248	06262	05247	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5249	06264	05248	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5250	06267	05249	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5251	06268	05250	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5252	06269	05251	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5253	06270	05252	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5254	06271	05253	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5255	06272	05254	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5256	06273	05255	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	M80359	93.9	181	1	2062	2914
5257	06274	05256	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5258	06275	05257	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2	0	M90104	94.2	173	1	1700	1879
5259	06277	05258	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5260	06278	05259	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5261	06279	05260	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5262	06280	05261	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5263	06281	05262	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	M64784	95.6	338	1	638	1138
5264	06282	05263	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5265	06283	05264	11		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	9X52426	100	102	1	1574	1677
5266	06284	05265	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5267	06286	05266	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5268	06288	05267	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5269	06289	05268	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5270	06290	05269	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5271	06291	05270	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5272	06292	05271	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5273	06293	05272	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5274	06294	05273	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5275	06295	05274	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5276	06296	05275	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5277	06297	05276	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	M86400	92.4	197	1	1196	2834

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5278	06299	05277	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5279	06300	05278	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5280	06301	05279	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5281	06302	05280	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5282	06303	05281	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5283	06304	05282	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5284	06305	05283	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5285	06306	05284	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5286	06307	05285	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5287	06308	05286	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5288	06309	05287	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5289	06310	05288	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5290	06311	05289	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5291	06313	05290	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5292	06314	05291	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5293	06315	05292	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5294	06316	05293	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5295	06317	05294	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5296	06318	05295	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5297	06319	05296	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5298	06320	05297	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5299	06321	05298	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5300	06322	05299	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5301	06323	05300	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5302	06324	05301	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5303	06325	05302	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5304	06326	05303	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5305	06327	05304	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5306	06329	05305	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5307	06330	05306	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5308	06331	05307	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5309	06332	05308	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5310	06333	05309	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5311	06334	05310	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5312	06335	05311	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5313	06337	05312	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 148

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BI	RI	BK
5314	06338	05313	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5315	06339	05314	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5316	06341	05315	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5317	06343	05316	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5318	06344	05317	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5319	06345	05318	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5320	06346	05319	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5321	06347	05320	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5322	06348	05321	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5323	06350	05322	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5324	06351	05323	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5325	06353	05324	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5326	06354	05325	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5327	06355	05326	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5328	06356	05327	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5329	06357	05328	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5330	06358	05329	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5331	06359	05330	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5332	06360	05331	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5333	06361	05332	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5334	06362	05333	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5335	06363	05334	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5336	06364	05335	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5337	06365	05336	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5338	06366	05337	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5339	06367	05338	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5340	06369	05339	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5341	06370	05340	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5342	06371	05341	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5343	06372	05342	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5344	06373	05343	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5345	06374	05344	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5346	06376	05345	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5347	06377	05346	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5348	06378	05347	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5349	06379	05348	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AJ	AK	AM	AO	AS	AV	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5350	06380	05349	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5351	06381	05350	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5352	06382	05351	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5353	06383	05352	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5354	06384	05353	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5355	06385	05354	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5356	06386	05355	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5357	06387	05356	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5358	06388	05357	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5359	06389	05358	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5360	06390	05359	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5361	06392	05360	26		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	26	0	0	0	0	0	0	0	0						
5362	06393	05361	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5363	06394	05362	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5364	06395	05363	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5365	06396	05364	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5366	06397	05365	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5367	06398	05366	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5368	06399	05367	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5369	06400	05368	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5370	06401	05369	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5371	06402	05370	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5372	06403	05371	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5373	06404	05372	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5374	06405	05373	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5375	06407	05374	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
5376	06408	05375	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5377	06409	05376	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5378	06410	05377	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5379	06411	05378	15		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	15	0	0	0	0	0	0	0	0						
5380	06412	05379	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5381	06413	05380	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5382	06414	05381	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5383	06415	05382	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5384	06416	05383	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
5385	06417	05384	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						

Table 150

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BB	BC	BE	BF	BG	BH	BI	BK
5422	06454	05421	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5423	06455	05422	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5424	06456	05423	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5425	06457	05424	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5426	06458	05425	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5427	06459	05426	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5428	06460	05427	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5429	06461	05428	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5430	06462	05429	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5431	06463	05430	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5432	06464	05431	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5433	06465	05432	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5434	06466	05433	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5435	06468	05434	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5436	06469	05435	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5437	06470	05436	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5438	06471	05437	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5439	06472	05438	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5440	06473	05439	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5441	06474	05440	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5442	06475	05441	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5443	06476	05442	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5444	06477	05443	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5445	06478	05444	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5446	06481	05445	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5447	06482	05446	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5448	06483	05447	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5449	06484	05448	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5450	06485	05449	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5451	06486	05450	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5452	06487	05451	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5453	06488	05452	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5454	06489	05453	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5455	06490	05454	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5456	06491	05455	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5457	06492	05456	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AT	AW	AY	B	BC	DE	DF	BG	BH	BI	BK
5494	06532	05493	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5495	06533	05494	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5496	06536	05495	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5497	06537	05496	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5498	06538	05497	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5499	06539	05498	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5500	06540	05499	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5501	06541	05500	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5502	06542	05501	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5503	06544	05502	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5504	06545	05503	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5505	06546	05504	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5506	06547	05505	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5507	06548	05506	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5508	06549	05507	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5509	06550	05508	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5510	06551	05509	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5511	06552	05510	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5512	06553	05511	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5513	06555	05512	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5514	06556	05513	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5515	06557	05514	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5516	06558	05515	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5517	06559	05516	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5518	06560	05517	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5519	06561	05518	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5520	06563	05519	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5521	06564	05520	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5522	06565	05521	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5523	06566	05522	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5524	06567	05523	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5525	06569	05524	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5526	06571	05525	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5527	06572	05526	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5528	06573	05527	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5529	06574	05528	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 154

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BI	BK	
5530	06576	05529	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5531	06577	05530	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5532	06578	05531	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5533	06579	05532	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98 203			1 1410	1970
5534	06580	05533	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5535	06581	05534	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5536	06582	05535	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5537	06583	05536	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5538	06584	05537	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5539	06585	05538	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5540	06586	05539	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5541	06587	05540	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5542	06588	05541	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5543	06590	05542	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5544	06592	05543	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5545	06593	05544	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5546	06594	05545	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5547	06595	05546	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5548	06596	05547	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5549	06597	05548	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5550	06599	05549	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5551	06600	05550	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5552	06601	05551	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5553	06602	05552	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5554	06603	05553	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5555	06604	05554	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5556	06605	05555	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5557	06606	05556	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5558	06607	05557	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5559	06608	05558	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5560	06609	05559	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5561	06610	05560	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5562	06611	05561	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5563	06612	05562	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
5564	06613	05563	2		0	0	0	0	0	0	0	0	0	0	0																	

Table 155

[illegible]

Table 156

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	IA	KA	MA	QA	SA	TA	VA	WA	YA	BA	BC	BE	BF	BG	BH	BI	BK
5602	06656	05601	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5603	06659	05602	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5604	06660	05603	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5605	06661	05604	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5606	06662	05605	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5607	06664	05606	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5608	06666	05607	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5609	06667	05608	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5610	06668	05609	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5611	06669	05610	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5612	06670	05611	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5613	06672	05612	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5614	06673	05613	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5615	06674	05614	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5616	06675	05615	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5617	06676	05616	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5618	06677	05617	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5619	06678	05618	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5620	06679	05619	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5621	06680	05620	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5622	06681	05621	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5623	06682	05622	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5624	06683	05623	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5625	06684	05624	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5626	06685	05625	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5627	06686	05626	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5628	06687	05627	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5629	06688	05628	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5630	06689	05629	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5631	06690	05630	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5632	06691	05631	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5633	06692	05632	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5634	06693	05633	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5635	06694	05634	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5636	06696	05635	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5637	06697	05636	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 157

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AG	AI	AK	AM	AC	AC	AS	AL	AW	AY	B	ABC	BE	BF	BGBH	BI	BK
5638	06098	05637	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5639	06699	05638	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5640	06700	05639	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5641	06701	05640	5	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5642	06702	05641	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5643	06703	05642	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5644	06704	05643	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5645	06705	05644	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5646	06706	05645	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5647	06707	05646	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5648	06709	05647	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5649	06710	05648	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5650	06711	05649	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5651	06712	05650	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5652	06713	05651	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5653	06714	05652	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5654	06715	05653	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5655	06716	05654	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5656	06717	05655	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5657	06718	05656	2	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5658	06719	05657	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5659	06720	05658	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5660	06721	05659	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5661	06724	05660	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5662	06725	05661	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5663	06726	05662	3	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5664	06727	05663	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5665	06728	05664	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5666	06730	05665	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5667	06731	05666	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5668	06732	05667	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5669	06733	05668	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5670	06734	05669	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5671	06735	05670	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5672	06736	05671	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5673	06737	05672	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 158

[illegible]

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	A	B	C	E	G	I	K	M	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5782	06859	05781	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5783	06863	05782	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5784	06864	05783	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5785	06865	05784	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5786	06866	05785	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5787	06869	05786	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5788	06870	05787	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5789	06871	05788	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5790	06872	05789	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5791	06873	05790	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5792	06874	05791	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5793	06875	05792	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5794	06876	05793	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5795	06878	05794	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5796	06879	05795	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5797	06880	05796	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5798	06882	05797	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5799	06883	05798	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5800	06884	05799	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5801	06885	05800	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5802	06886	05801	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5803	06888	05802	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5804	06889	05803	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5805	06890	05804	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5806	06891	05805	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5807	06893	05806	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5808	06894	05807	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5809	06895	05808	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5810	06896	05809	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5811	06897	05810	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5812	06898	05811	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5813	06899	05812	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5814	06900	05813	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5815	06901	05814	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5816	06902	05815	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5817	06903	05816	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 162

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AN	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5818	06904	05817	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5819	06906	05818	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5820	06909	05819	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5821	06910	05820	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5822	06911	05821	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5823	06912	05822	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5824	06913	05823	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5825	06915	05824	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5826	06916	05825	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5827	06917	05826	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5828	06919	05827	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5829	06920	05828	27		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5830	06922	05829	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5831	06923	05830	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5832	06927	05831	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5833	06928	05832	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5834	06929	05833	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5835	06930	05834	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5836	06931	05835	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5837	06932	05836	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5838	06933	05837	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5839	06934	05838	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5840	06935	05839	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5841	06936	05840	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5842	06937	05841	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5843	06938	05842	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5844	06939	05843	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5845	06941	05844	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5846	06942	05845	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5847	06943	05846	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5848	06945	05847	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5849	06946	05848	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5850	06947	05849	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5851	06948	05850	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5852	06949	05851	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5853	06951	05852	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 163

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AG	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5854	06952	05853	1																													
5855	06953	05854	1																													
5856	06954	05855	2																													
5857	06955	05856	1																													
5858	06956	05857	1																													
5859	06957	05858	2																													
5860	06958	05859	1																													
5861	06959	05860	1																													
5862	06961	05861	1																													
5863	06963	05862	1																													
5864	06964	05863	1																													
5865	06965	05864	2																													
5866	06966	05865	1																													
5867	06967	05866	2																													
5868	06969	05867	1																													
5869	06971	05868	3																													
5870	06972	05869	2																													
5871	06973	05870	1																													
5872	06975	05871	1																													
5873	06977	05872	1																													
5874	06978	05873	2																													
5875	06979	05874	1																													
5876	06981	05875	1																													
5877	06982	05876	2																													
5878	06983	05877	1																													
5879	06984	05878	1																													
5880	06985	05879	2																													
5881	06986	05880	1																													
5882	06987	05881	1																													
5883	06988	05882	1																													
5884	06989	05883	1																													
5885	06990	05884	1																													
5886	06991	05885	1																													
5887	06992	05886	1																													
5888	06993	05887	1																													
5889	06994	05888	5																													

Table 164

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	B	BE	BF	BG	BH	BI	BK
5926	07034	05925	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5927	07035	05926	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5928	07036	05927	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5929	07037	05928	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5930	07038	05929	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5931	07039	05930	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5932	07040	05931	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5933	07041	05932	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5934	07043	05933	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5935	07044	05934	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5936	07046	05935	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5937	07047	05936	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5938	07048	05937	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5939	07049	05938	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5940	07050	05939	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5941	07053	05940	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5942	07054	05941	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5943	07055	05942	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5944	07056	05943	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5945	07057	05944	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5946	07058	05945	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5947	07059	05946	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5948	07060	05947	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5949	07061	05948	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5950	07062	05949	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0					
5951	07063	05950	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5952	07065	05951	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5953	07066	05952	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5954	07067	05953	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5955	07068	05954	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5956	07069	05955	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5957	07071	05956	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5958	07072	05957	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5959	07074	05958	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5960	07075	05959	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5961	07076	05960	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					

Table 166

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BI	BK
5962	07079	05961	1																												
5963	07080	05962	2																												
5964	07081	05963	1																												
5965	07082	05964	1																												
5966	07083	05965	3																												
5967	07084	05966	1																												
5968	07085	05967	1																												
5969	07086	05968	1																												
5970	07087	05969	1																												
5971	07088	05970	1																												
5972	07089	05971	1																												
5973	07091	05972	1																												
5974	07093	05973	1																												
5975	07094	05974	1																												
5976	07095	05975	2																												
5977	07096	05976	1																												
5978	07097	05977	1																												
5979	07098	05978	1																												
5980	07099	05979	1																												
5981	07100	05980	1																												
5982	07101	05981	1																												
5983	07102	05982	1																												
5984	07103	05983	1																												
5985	07104	05984	1																												
5986	07105	05985	2																												
5987	07106	05986	3																												
5988	07108	05987	1																												
5989	07110	05988	1																												
5990	07111	05989	1																												
5991	07112	05990	1																												
5992	07113	05991	1																												
5993	07114	05992	2																												
5994	07115	05993	1																												
5995	07116	05994	1																												
5996	07117	05995	1																												
5997	07118	05996	4																												

Table 167

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5998	07119	05997	1																														
5999	07120	05998	1																														
6000	07121	05999	1																														
6001	07122	06000	1																														
6002	07123	06001	1																														
6003	07124	06002	1																														
6004	07125	06003	1																														
6005	07126	06004	1																														
6006	07127	06005	1																														
6007	07128	06006	1																														
6008	07129	06007	1																														
6009	07130	06008	1																														
6010	07131	06009	1																														
6011	07132	06010	1																														
6012	07133	06011	1																														
6013	07134	06012	1																														
6014	07135	06013	2																														
6015	07136	06014	2																														
6016	07137	06015	1																														
6017	07138	06016	1																														
6018	07139	06017	2																														
6019	07140	06018	3																														
6020	07141	06019	1																														
6021	07142	06020	1																														
6022	07143	06021	1																														
6023	07144	06022	2																														
6024	07145	06023	1																														
6025	07146	06024	1																														
6026	07147	06025	1																														
6027	07150	06026	1																														
6028	07151	06027	1																														
6029	07152	06028	1																														
6030	07153	06029	1																														
6031	07154	06030	1																														
6032	07156	06031	1																														
6033	07157	06032	1																														

Table 168

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	GA	IA	KA	MA	QA	SA	WA	YA	B	BE	BF	BG	BH	BI	BK
6034	07158	06033	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6035	07160	06034	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6036	07161	06035	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6037	07162	06036	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6038	07163	06037	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6039	07164	06038	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6040	07165	06039	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6041	07166	06040	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6042	07167	06041	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6043	07169	06042	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6044	07170	06043	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6045	07171	06044	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6046	07173	06045	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6047	07174	06046	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6048	07175	06047	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6049	07178	06048	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6050	07179	06049	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6051	07180	06050	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6052	07181	06051	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6053	07182	06052	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6054	07183	06053	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6055	07185	06054	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6056	07186	06055	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6057	07187	06056	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6058	07188	06057	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6059	07192	06058	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6060	07193	06059	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6061	07194	06060	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6062	07195	06061	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6063	07196	06062	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6064	07199	06063	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6065	07200	06064	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6066	07201	06065	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6067	07202	06066	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6068	07204	06067	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6069	07206	06068	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 169

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AQ	AS	AT	AV	BA	BC	BE	BF	BG	BH	BI	BK
6070	07209	06069	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6071	07210	06070	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
6072	07211	06071	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6073	07212	06072	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6074	07213	06073	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6075	07214	06074	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6076	07215	06075	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6077	07216	06076	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
6078	07217	06077	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6079	07218	06078	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
6080	07219	06079	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
6081	07220	06080	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6082	07221	06081	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6083	07222	06082	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6084	07223	06083	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6085	07224	06084	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6086	07225	06085	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6087	07226	06086	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6088	07227	06087	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6089	07228	06088	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6090	07229	06089	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6091	07230	06090	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6092	07231	06091	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6093	07232	06092	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6094	07233	06093	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6095	07238	06094	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6096	07241	06095	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6097	07243	06096	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6098	07244	06097	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6099	07245	06098	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6100	07246	06099	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
6101	07249	06100	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6102	07250	06101	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6103	07251	06102	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6104	07253	06103	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6105	07257	06104	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 170

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
6106	07259	06105	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
6107	07261	06106	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6108	07263	06107	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6109	07264	06108	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6110	07265	06109	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6111	07266	06110	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6112	07267	06111	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6113	07268	06112	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6114	07269	06113	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6115	07270	06114	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6116	07272	06115	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6117	07274	06116	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6118	07275	06117	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6119	07276	06118	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6120	07277	06119	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0				
6121	07278	06120	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0				
6122	07279	06121	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6123	07280	06122	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6124	07281	06123	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6125	07282	06124	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6126	07283	06125	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6127	07284	06126	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6128	07285	06127	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6129	07286	06128	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6130	07287	06129	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6131	07288	06130	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6132	07289	06131	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0				
6133	07290	06132	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6134	07291	06133	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6135	07292	06134	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6136	07293	06135	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6137	07294	06136	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0				
6138	07295	06137	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0				
6139	07296	06138	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6140	07297	06139	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				
6141	07298	06140	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				

Table 171

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	CA	CI	AK	AM	AA	CA	AS	AL	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
6178	07337	06177	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6179	07338	06178	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6180	07339	06179	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6181	07340	06180	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6182	07341	06181	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6183	07342	06182	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6184	07343	06183	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6185	07344	06184	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6186	07345	06185	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6187	07346	06186	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6188	07348	06187	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6189	07349	06188	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6190	07350	06189	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6191	07351	06190	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6192	07352	06191	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6193	07353	06192	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6194	07354	06193	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6195	07355	06194	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6196	07356	06195	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6197	07357	06196	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6198	07358	06197	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6199	07359	06198	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6200	07360	06199	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6201	07361	06200	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6202	07362	06201	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6203	07363	06202	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6204	07364	06203	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6205	07365	06204	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6206	07366	06205	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6207	07367	06206	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6208	07368	06207	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6209	07369	06208	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6210	07370	06209	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6211	07371	06210	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6212	07372	06211	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6213	07373	06212	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 173

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A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	AG	AI	AK	AM	AN	AO	AP	AR	AS	AW	AY	B	BE	BF	BG	BH	BI	BK
6214	07374	06213	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6215	07375	06214	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6216	07376	06215	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6217	07377	06216	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6218	07378	06217	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6219	07379	06218	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6220	07380	06219	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6221	07381	06220	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6222	07382	06221	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6223	07383	06222	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6224	07384	06223	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6225	07385	06224	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6226	07386	06225	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6227	07387	06226	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6228	07388	06227	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6229	07389	06228	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6230	07390	06229	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6231	07391	06230	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6232	07392	06231	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6233	07393	06232	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6234	07394	06233	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6235	07395	06234	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6236	07396	06235	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6237	07397	06236	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6238	07398	06237	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6239	07399	06238	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6240	07400	06239	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6241	07401	06240	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6242	07402	06241	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6243	07403	06242	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6244	07404	06243	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6245	07405	06244	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6246	07406	06245	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6247	07407	06246	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6248	07408	06247	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6249	07409	06248	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 174

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AV	AW	AY	B	BC	BE	BF	BGBH	BI	BK
6250	07410	06249	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6251	07411	06250	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6252	07412	06251	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6253	07413	06252	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6254	07414	06253	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6255	07415	06254	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6256	07416	06255	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6257	07417	06256	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6258	07418	06257	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6259	07419	06258	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6260	07420	06259	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6261	07421	06260	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6262	07422	06261	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6263	07423	06262	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6264	07424	06263	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6265	07425	06264	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6266	07426	06265	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6267	07427	06266	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6268	07429	06267	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6269	07430	06268	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6270	07431	06269	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6271	07432	06270	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6272	07433	06271	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6273	07434	06272	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6274	07435	06273	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6275	07436	06274	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6276	07437	06275	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6277	07438	06276	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6278	07439	06277	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6279	07440	06278	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6280	07441	06279	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6281	07442	06280	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6282	07443	06281	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6283	07444	06282	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6284	07445	06283	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6285	07446	06284	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 175

[illegible]

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A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AX	AY	BA	BC	BE	BF	BG	BI	BK
6394	07558	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	97.5	1	674	834
6395	07559	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6396	07560	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6397	07561	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6398	07562	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6399	07563	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6400	07564	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6401	07565	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6402	07567	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6403	07568	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6404	07569	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6405	07570	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6406	07571	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6407	07572	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6408	07573	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6409	07574	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6410	07575	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6411	07576	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
6412	07577	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6413	07578	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6414	07579	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6415	07580	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6416	07581	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6417	07582	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6418	07583	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
6419	07584	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6420	07585	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6421	07586	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6422	07587	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6423	07588	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6424	07589	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6425	07590	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6426	07591	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6427	07592	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6428	07593	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
6429	07594	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
	07594			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0

Table 179

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A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AV	AY	BA	BC	BE	BF	BG	BH	BI	BK
6466	06165	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6467	06166	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6468	06467	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6469	06468	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6470	06469	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6471	06470	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6472	06471	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6473	06472	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6474	06473	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6475	06474	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6476	06475	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6477	06476	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6478	06477	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6479	06478	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6480	06479	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6481	06480	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6482	06481	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6483	06482	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6484	06483	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6485	06484	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6486	06485	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6487	06486	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6488	06487	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6489	06488	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6490	06489	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6491	06490	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6492	06491	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6493	06492	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6494	06493	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6495	06494	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6496	06495	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6497	06496	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6498	06497	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6499	06498	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6500	06499	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0										

Table 181

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
6574	07751	06573	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6575	07752	06574	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6576	07753	06575	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6577	07754	06576	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6578	07755	06577	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0					
6579	07756	06578	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0					
6580	07757	06579	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6581	07758	06580	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6582	07759	06581	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6583	07760	06582	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6584	07761	06583	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6585	07762	06584	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6586	07763	06585	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6587	07764	06586	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6588	07765	06587	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6589	07766	06588	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6590	07768	06589	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6591	07769	06590	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6592	07770	06591	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6593	07771	06592	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6594	07773	06593	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6595	07774	06594	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6596	07775	06595	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6597	07776	06596	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6598	07777	06597	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6599	07778	06598	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6600	07779	06599	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0					
6601	07780	06600	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6602	07781	06601	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6603	07782	06602	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6604	07783	06603	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6605	07785	06604	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6606	07786	06605	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6607	07787	06606	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6608	07788	06607	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
6609	07789	06608	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					

Table 184

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AD	AE	AF	AG	AH	AI	AJ	AK	AM	AN	AO	AP	AQ	AR	AS	AT	AW	AX	AY	BA	BB	BC	BE	BF	BG	BH	BI	BK			
6610	07790	06609	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6611	07792	06610	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6612	07793	06611	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6613	07794	06612	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6614	07795	06613	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6615	07796	06614	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6616	07797	06615	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6617	07798	06616	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6618	07800	06617	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6619	07801	06618	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6620	07802	06619	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6621	07804	06620	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6622	07805	06621	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6623	07807	06622	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6624	07808	06623	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6625	07810	06624	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6626	07811	06625	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6627	07812	06626	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6628	07813	06627	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6629	07814	06628	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6630	07815	06629	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6631	07816	06630	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6632	07817	06631	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6633	07818	06632	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																		

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AT	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
6682	07880	06681	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	98.6294	1	1700	2360
6683	07881	06682	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6684	07882	06683	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6685	07883	06684	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6686	07884	06685	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6687	07885	06686	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6688	07886	06687	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6689	07887	06688	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6690	07889	06689	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6691	07890	06690	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6692	07891	06691	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6693	07892	06692	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6694	07893	06693	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6695	07894	06694	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6696	07895	06695	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6697	07896	06696	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6698	07897	06697	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6699	07898	06698	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6700	07900	06699	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6701	07901	06700	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6702	07902	06701	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6703	07903	06702	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6704	07904	06703	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6705	07905	06704	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6706	07909	06705	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6707	07911	06706	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6708	07912	06707	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6709	07913	06708	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6710	07915	06709	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6711	07916	06710	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6712	07917	06711	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6713	07918	06712	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6714	07919	06713	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6715	07920	06714	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6716	07921	06715	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6717	07922	06716	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 187

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AP	AQ	AS	AT	AV	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
6718	07923	06717	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6719	07925	06718	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6720	07927	06719	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6721	07928	06720	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6722	07932	06721	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6723	07933	06722	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6724	07934	06723	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6725	07935	06724	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6726	07936	06725	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6727	07937	06726	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6728	07938	06727	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6729	07939	06728	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6730	07941	06729	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6731	07942	06730	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6732	07944	06731	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6733	07945	06732	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6734	07946	06733	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6735	07948	06734	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6736	07949	06735	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6737	07951	06736	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6738	07952	06737	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6739	07953	06738	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6740	07954	06739	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6741	07955	06740	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6742	07956	06741	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6743	07957	06742	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6744	07958	06743	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6745	07959	06744	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6746	07960	06745	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6747	07961	06746	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6748	07963	06747	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6749	07964	06748	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6750	07965	06749	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6751	07966	06750	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6752	07967	06751	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6753	07969	06752	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 188

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AT	AW	AY	BA	BC	BE	BF	BGBH	BI	BK
6754	07971	06753	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6755	07973	06754	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6756	07974	06755	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6757	07975	06756	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6758	07976	06757	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6759	07977	06758	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6760	07981	06759	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6761	07986	06760	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6762	07987	06761	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6763	07988	06762	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6764	07989	06763	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6765	07990	06764	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6766	07991	06765	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6767	07992	06766	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6768	07994	06767	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6769	07995	06768	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6770	07997	06769	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6771	07998	06770	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6772	07999	06771	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6773	08000	06772	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6774	08001	06773	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6775	08002	06774	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6776	08003	06775	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6777	08004	06776	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6778	08005	06777	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6779	08006	06778	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6780	08007	06779	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6781	08008	06780	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6782	08009	06781	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6783	08010	06782	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6784	08011	06783	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6785	08012	06784	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6786	08013	06785	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6787	08014	06786	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6788	08015	06787	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6789	08016	06788	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				

Table 189

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
6790	08017	06789	3																								0 228407	92.7	300	1	236	852	
6791	08018	06790	1																														
6792	08019	06791	1																														
6793	08020	06792	1																														
6794	08021	06793	1																														
6795	08022	06794	1																														
6796	08023	06795	1																														
6797	08024	06796	1																														
6798	08025	06797	27																														
6799	08026	06798	1																														
6800	08027	06799	2																								X65024	98.2	112	1	3344	3455	
6801	08028	06800	1																														
6802	08029	06801	1																														
6803	08030	06802	2																														
6804	08031	06803	1																														
6805	08032	06804	1																														
6806	08033	06805	1																														
6807	08034	06806	1																														
6808	08036	06807	1																														
6809	08037	06808	1																								M14199	98.8	240	32	236	475	
6810	08038	06809	1																														
6811	08039	06810	1																														
6812	08040	06811	2																								M16453	94.4	143	1	172	369	
6813	08041	06812	1																														
6814	08042	06813	1																														
6815	08043	06814	1																														
6816	08044	06815	3																								M63625	91.433	1	1019	1684		
6817	08045	06816	1																								M92439	96.5	229	1	3739	4782	
6818	08046	06817	2																														
6819	08047	06818	1																														
6820	08048	06819	1																														
6821	08049	06820	1																														
6822	08050	06821	1																														
6823	08051	06822	2																														
6824	08052	06823	1																														
6825	08053	06824	1																														

Table 190

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
6826	08054	06825	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6827	08055	06826	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6828	08056	06827	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6829	08057	06828	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6830	08058	06829	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6831	08059	06830	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6832	08060	06831	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6833	08061	06832	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6834	08062	06833	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6835	08063	06834	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6836	08064	06835	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6837	08065	06836	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6838	08066	06837	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6839	08067	06838	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6840	08068	06839	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6841	08069	06840	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6842	08070	06841	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6843	08071	06842	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6844	08073	06843	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6845	08074	06844	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6846	08075	06845	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6847	08076	06846	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6848	08077	06847	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6849	08078	06848	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6850	08079	06849	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6851	08080	06850	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6852	08081	06851	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6853	08082	06852	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6854	08083	06853	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6855	08084	06854	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6856	08085	06855	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6857	08086	06856	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6858	08087	06857	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6859	08088	06858	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6860	08089	06859	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6861	08090	06860	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6862	08091	06861	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6863	08092	06862	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6864	08093	06863	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6865	08094	06864	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6866	08095	06865	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6867	08096	06866	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6868	08097	06867	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6869	08098	06868	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6870	08099	06869	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6871	08100	06870	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6872	08101	06871	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6873	08102	06872	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6874	08103	06873	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6875	08104	06874	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6876	08105	06875	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6877	08107	06876	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6878	08108	06877	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6879	08109	06878	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6880	08110	06879	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6881	08111	06880	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6882	08112	06881	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6883	08113	06882	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6884	08114	06883	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6885	08115	06884	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6886	08116	06885	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6887	08117	06886	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6888	08118	06887	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6889	08119	06888	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6890	08120	06889	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6891	08121	06890	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6892	08122	06891	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6893	08123	06892	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6894	08124	06893	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6895	08125	06894	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6896	08126	06895	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6897	08127	06896	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 192

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AN	AO	AS	AT	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
6898	08128	06897	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6899	08129	06898	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6900	08130	06899	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6901	08131	06900	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6902	08132	06901	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6903	08133	06902	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6904	08134	06903	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6905	08135	06904	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6906	08136	06905	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6907	08137	06906	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6908	08138	06907	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6909	08139	06908	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6910	08140	06909	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6911	08141	06910	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6912	08142	06911	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6913	08143	06912	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6914	08144	06913	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6915	08145	06914	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6916	08146	06915	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6917	08147	06916	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6918	08148	06917	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6919	08149	06918	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6920	08150	06919	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6921	08151	06920	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6922	08152	06921	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6923	08153	06922	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6924	08154	06923	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6925	08155	06924	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6926	08156	06925	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6927	08157	06926	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6928	08158	06927	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6929	08159	06928	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6930	08160	06929	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6931	08161	06930	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6932	08162	06931	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6933	08163	06932	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6934	08164	06933	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 193

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AJ	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BGBH	BI	BK	
6934	08165	06933	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.2	103	7	2589	2691
6935	08166	06934	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6936	08167	06935	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6937	08168	06936	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6938	08169	06937	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6939	08170	06938	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6940	08172	06939	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6941	08173	06940	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6942	08174	06941	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6943	08175	06942	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6944	08176	06943	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6945	08177	06944	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6946	08178	06945	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6947	08179	06946	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6948	08180	06947	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6949	08181	06948	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6950	08182	06949	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6951	08184	06950	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6952	08185	06951	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6953	08186	06952	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6954	08188	06953	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6955	08189	06954	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6956	08190	06955	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6957	08191	06956	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6958	08192	06957	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6959	08193	06958	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6960	08194	06959	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6961	08195	06960	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6962	08196	06961	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6963	08197	06962	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6964	08198	06963	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6965	08199	06964	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6966	08200	06965	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6967	08201	06966	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6968	08202	06967	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6969	08203	06968	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 194

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AT	AV	AW	BA	BB	BE	BF	BG	BI	BK
7006	08241	07005	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7007	08242	07006	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7008	08243	07007	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7009	08244	07008	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7010	08245	07009	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7011	08246	07010	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7012	08247	07011	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7013	08248	07012	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7014	08249	07013	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7015	08250	07014	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7016	08251	07015	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7017	08252	07016	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7018	08253	07017	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7019	08254	07018	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7020	08255	07019	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7021	08256	07020	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7022	08257	07021	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7023	08258	07022	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7024	08259	07023	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7025	08260	07024	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7026	08261	07025	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7027	08262	07026	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7028	08263	07027	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7029	08264	07028	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7030	08265	07029	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7031	08266	07030	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7032	08267	07031	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7033	08268	07032	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7034	08269	07033	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7035	08270	07034	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7036	08271	07035	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7037	08272	07036	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7038	08273	07037	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7039	08274	07038	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7040	08275	07039	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7041	08276	07040	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 196

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7042	08277	07041	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7043	08278	07042	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7044	08279	07043	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7045	08280	07044	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7046	08281	07045	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7047	08282	07046	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7048	08283	07047	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7049	08284	07048	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7050	08285	07049	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7051	08286	07050	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7052	08287	07051	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7053	08288	07052	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7054	08289	07053	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7055	08290	07054	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7056	08291	07055	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7057	08292	07056	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7058	08293	07057	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7059	08294	07058	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7060	08295	07059	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7061	08296	07060	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7062	08297	07061	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7063	08298	07062	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7064	08299	07063	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7065	08300	07064	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7066	08301	07065	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7067	08302	07066	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7068	08303	07067	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7069	08304	07068	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7070	08305	07069	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7071	08306	07070	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7072	08307	07071	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7073	08308	07072	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7074	08309	07073	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7075	08310	07074	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7076	08311	07075	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7077	08312	07076	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 197

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7078	08313	07077	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7079	08314	07078	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7080	08315	07079	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7081	08316	07080	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7082	08317	07081	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7083	08318	07082	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7084	08319	07083	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7085	08320	07084	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7086	08321	07085	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7087	08322	07086	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7088	08323	07087	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7089	08324	07088	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7090	08325	07089	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7091	08326	07090	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7092	08327	07091	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7093	08328	07092	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7094	08329	07093	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7095	08330	07094	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7096	08331	07095	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7097	08332	07096	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7098	08333	07097	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7099	08334	07098	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7100	08335	07099	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7101	08336	07100	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7102	08337	07101	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7103	08338	07102	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7104	08339	07103	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7105	08340	07104	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7106	08341	07105	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7107	08342	07106	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7108	08343	07107	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7109	08344	07108	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7110	08345	07109	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7111	08346	07110	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7112	08347	07111	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7113	08348	07112	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 198

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AF	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BI	DI	DK
7114	08349	07113	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0X17519	98.4	306	1	1624	2323
7115	08350	07114	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7116	08351	07115	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0						
7117	08352	07116	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7118	08353	07117	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7119	08354	07118	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7120	08355	07119	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0M62505	97.1	204	1	2110	2328
7121	08356	07120	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7122	08357	07121	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7123	08358	07122	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7124	08359	07123	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7125	08360	07124	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7126	08361	07125	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7127	08362	07126	16		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	16	0	0	0X55720	100	85	1	2450	2546
7128	08363	07127	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7129	08364	07128	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7130	08365	07129	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7131	08366	07130	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7132	08367	07131	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7133	08368	07132	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7134	08369	07133	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7135	08371	07134	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7136	08372	07135	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7137	08373	07136	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7138	08374	07137	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7139	08375	07138	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0M69043	99.3	301	1	1250	1550
7140	08376	07139	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7141	08377	07140	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7142	08378	07141	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7143	08379	07142	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7144	08380	07143	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0						
7145	08381	07144	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7146	08382	07145	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7147	08383	07146	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	000115	97.2	180	1	3034	3536
7148	08384	07147	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7149	08385	07148	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						

Table 199

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AT	AW	AY	BAB	BC	BE	BF	BG	BI	BK
7186	08423	07185	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7187	08424	07186	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7188	08425	07187	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7189	08426	07188	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7190	08427	07189	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7191	08428	07190	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7192	08429	07191	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7193	08430	07192	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7194	08431	07193	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7195	08432	07194	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7196	08434	07195	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7197	08435	07196	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7198	08436	07197	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7199	08437	07198	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7200	08438	07199	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7201	08439	07200	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7202	08440	07201	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7203	08441	07202	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7204	08442	07203	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7205	08443	07204	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7206	08444	07205	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7207	08445	07206	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7208	08446	07207	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7209	08447	07208	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7210	08448	07209	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7211	08449	07210	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7212	08450	07211	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7213	08451	07212	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7214	08452	07213	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7215	08453	07214	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7216	08454	07215	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7217	08455	07216	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7218	08456	07217	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7219	08457	07218	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7220	08458	07219	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
7221	08459	07220	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				

Table 201

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7222	08460	07221	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7223	08461	07222	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7224	08462	07223	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7225	08463	07224	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7226	08464	07225	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7227	08465	07226	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7228	08466	07227	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7229	08467	07228	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7230	08468	07229	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7231	08469	07230	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7232	08470	07231	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7233	08471	07232	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7234	08472	07233	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7235	08473	07234	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7236	08474	07235	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7237	08475	07236	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7238	08476	07237	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7239	08477	07238	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7240	08478	07239	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7241	08479	07240	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7242	08480	07241	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7243	08481	07242	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7244	08482	07243	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7245	08483	07244	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7246	08484	07245	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7247	08485	07246	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7248	08486	07247	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7249	08487	07248	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7250	08488	07249	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7251	08489	07250	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7252	08490	07251	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7253	08491	07252	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7254	08492	07253	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7255	08493	07254	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7256	08494	07255	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7257	08495	07256	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 202

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7258	08496	07257	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7259	08497	07258	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7260	08498	07259	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7261	08499	07260	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0						
7262	08500	07261	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7263	08501	07262	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7264	08502	07263	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7265	08503	07264	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7266	08504	07265	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7267	08505	07266	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7268	08506	07267	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7269	08507	07268	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7270	08508	07269	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7271	08509	07270	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7272	08510	07271	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7273	08511	07272	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7274	08512	07273	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7275	08513	07274	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7276	08514	07275	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7277	08515	07276	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7278	08516	07277	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7279	08517	07278	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7280	08518	07279	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7281	08519	07280	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7282	08520	07281	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7283	08521	07282	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7284	08522	07283	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7285	08523	07284	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7286	08524	07285	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7287	08525	07286	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7288	08526	07287	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7289	08527	07288	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7290	08528	07289	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7291	08529	07290	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7292	08530	07291	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0											

Table 203

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7294	08532	07293	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7295	08533	07294	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7296	08534	07295	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7297	08535	07296	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7298	08536	07297	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7299	08537	07298	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7300	08538	07299	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7301	08539	07300	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7302	08540	07301	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7303	08541	07302	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7304	08542	07303	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7305	08543	07304	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7306	08544	07305	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7307	08545	07306	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7308	08546	07307	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7309	08547	07308	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7310	08548	07309	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7311	08549	07310	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7312	08550	07311	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7313	08551	07312	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7314	08552	07313	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7315	08553	07314	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7316	08554	07315	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7317	08555	07316	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7318	08556	07317	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7319	08557	07318	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7320	08558	07319	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7321	08559	07320	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7322	08560	07321	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7323	08561	07322	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7324	08563	07323	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7325	08564	07324	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7326	08565	07325	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7327	08566	07326	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7328	08567	07327	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0											

Table 204

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7330	08569	07329	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7331	08570	07330	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7332	08571	07331	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7333	08572	07332	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7334	08573	07333	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7335	08574	07334	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7336	08575	07335	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7337	08576	07336	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7338	08577	07337	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7339	08578	07338	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7340	08579	07339	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7341	08580	07340	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7342	08581	07341	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7343	08582	07342	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7344	08583	07343	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7345	08584	07344	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7346	08585	07345	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7347	08586	07346	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7348	08587	07347	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7349	08588	07348	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7350	08589	07349	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7351	08591	07350	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7352	08592	07351	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7353	08593	07352	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7354	08594	07353	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7355	08595	07354	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7356	08596	07355	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7357	08597	07356	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7358	08598	07357	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7359	08599	07358	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7360	08600	07359	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7361	08601	07360	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7362	08602	07361	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7363	08603	07362	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7364	08604	07363	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7365	08605	07364	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 205

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7366	08606	07365	1																												
7367	08607	07366	1																												
7368	08608	07367	1																												
7369	08609	07368	1																												
7370	08610	07369	1																												
7371	08611	07370	1																												
7372	08612	07371	1																												
7373	08613	07372	1																												
7374	08614	07373	1																												
7375	08615	07374	1																												
7376	08616	07375	1																												
7377	08617	07376	1																												
7378	08618	07377	1																												
7379	08619	07378	1																												
7380	08620	07379	1																												
7381	08621	07380	1																												
7382	08622	07381	1																												
7383	08623	07382	1																												
7384	08624	07383	1																												
7385	08625	07384	1																												
7386	08626	07385	1																												
7387	08627	07386	1																												
7388	08628	07387	1																												
7389	08629	07388	1																												
7390	08630	07389	1																												
7391	08631	07390	1																												
7392	08632	07391	1																												
7393	08633	07392	1																												
7394	08634	07393	1																												
7395	08635	07394	1																												
7396	08636	07395	1																												
7397	08637	07396	1																												
7398	08638	07397	2																												
7399	08639	07398	1																												
7400	08640	07399	1																												
7401	08641	07400	1																												

Table 206

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AI	AG	AJ	AK	AM	AN	AO	AS	AT	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7402	08642	07401	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7403	08643	07402	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7404	08644	07403	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7405	08645	07404	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7406	08646	07405	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7407	08647	07406	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7408	08648	07407	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7409	08649	07408	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7410	08650	07409	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7411	08651	07410	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7412	08652	07411	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7413	08653	07412	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7414	08654	07413	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7415	08655	07414	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7416	08656	07415	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7417	08657	07416	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7418	08658	07417	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7419	08659	07418	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7420	08660	07419	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7421	08661	07420	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7422	08662	07421	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7423	08663	07422	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7424	08664	07423	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7425	08665	07424	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7426	08666	07425	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7427	08667	07426	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7428	08668	07427	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7429	08669	07428	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7430	08670	07429	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7431	08671	07430	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7432	08673	07431	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7433	08674	07432	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7434	08675	07433	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7435	08676	07434	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7436	08677	07435	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7437	08678	07436	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AN	AC	AT	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7438	08679	07437	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7439	08680	07438	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7440	08681	07439	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7441	08682	07440	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7442	08683	07441	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7443	08684	07442	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7444	08685	07443	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7445	08686	07444	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7446	08687	07445	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7447	08688	07446	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7448	08689	07447	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7449	08690	07448	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7450	08691	07449	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7451	08692	07450	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7452	08693	07451	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7453	08694	07452	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7454	08695	07453	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7455	08696	07454	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7456	08697	07455	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7457	08698	07456	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7458	08699	07457	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7459	08700	07458	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7460	08701	07459	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7461	08702	07460	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7462	08703	07461	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7463	08704	07462	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7464	08705	07463	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7465	08706	07464	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7466	08707	07465	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7467	08708	07466	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7468	08709	07467	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7469	08710	07468	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7470	08711	07469	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7471	08712	07470	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7472	08713	07471	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
7473	08714	07472	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AN	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7474	08715	07473	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7475	08716	07474	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7476	08717	07475	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7477	08718	07476	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7478	08719	07477	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7479	08720	07478	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7480	08721	07479	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7481	08722	07480	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7482	08723	07481	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7483	08724	07482	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7484	08725	07483	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7485	08726	07484	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7486	08727	07485	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7487	08728	07486	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7488	08729	07487	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7489	08730	07488	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7490	08731	07489	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7491	08732	07490	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7492	08733	07491	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7493	08734	07492	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7494	08735	07493	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7495	08736	07494	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7496	08737	07495	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7497	08738	07496	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7498	08739	07497	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7499	08740	07498	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7500	08741	07499	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7501	08742	07500	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7502	08743	07501	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7503	08744	07502	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7504	08745	07503	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7505	08746	07504	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7506	08747	07505	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7507	08748	07506	2		0	0	0	0	0	0	0	0	0	0	0																		

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7510	08751	07509	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7511	08752	07510	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7512	08753	07511	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7513	08754	07512	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7514	08755	07513	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7515	08756	07514	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7516	08757	07515	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7517	08758	07516	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7518	08759	07517	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7519	08760	07518	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7520	08761	07519	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	000760	97.5	326	1	541	866
7521	08762	07520	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7522	08763	07521	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7523	08764	07522	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7524	08765	07523	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7525	08766	07524	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7526	08768	07525	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7527	08769	07526	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7528	08770	07527	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	M7836	99	303	1	1491	1792
7529	08771	07528	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7530	08772	07529	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7531	08773	07530	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7532	08774	07531	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	M27937	98.7	311	1	326	832
7533	08775	07532	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7534	08777	07533	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7535	08778	07534	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7536	08779	07535	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7537	08780	07536	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7538	08781	07537	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7539	08782	07538	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7540	08783	07539	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7541	08785	07540	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7542	08786	07541	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7543	08787	07542	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	M87339	90.3	298	1	1051	1446
7544	08788	07543	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7545	08789	07544	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						

Table 210

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5	7546	08790 07545	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7547	08791 07546	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7548	08792 07547	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7549	08793 07548	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7550	08794 07549	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7551	08795 07550	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7552	08796 07551	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7553	08797 07552	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7554	08798 07553	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7555	08799 07554	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7556	08800 07555	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7557	08801 07556	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7558	08802 07557	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7559	08803 07558	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7560	08804 07559	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7561	08805 07560	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7562	08807 07561	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7563	08808 07562	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7564	08809 07563	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7565	08810 07564	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7566	08811 07565	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7567	08812 07566	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7568	08813 07567	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7569	08814 07568	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7570	08815 07569	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7571	08816 07570	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7572	08817 07571	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7573	08818 07572	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7574	08819 07573	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7575	08820 07574	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7576	08821 07575	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7577	08822 07576	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7578	08823 07577	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7579	08824 07578	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7580	08825 07579	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
	7581	08826 07580	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
15																																			
20																																			
25																																			
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35																																			
40																																			
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Table 211

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	EA	GA	IA	KA	MA	QA	SA	TA	VA	WA	YA	BA	BC	BE	BF	BG	BH	BI	BK
7582	08827	07581	1																																
7583	08828	07582	1																																
7584	08829	07583	1																																
7585	08830	07584	1																																
7586	08831	07585	4																																
7587	08832	07586	1																																
7588	08833	07587	1																																
7589	08834	07588	1																																
7590	08835	07589	1																																
7591	08836	07590	1																																
7592	08837	07591	1																																
7593	08838	07592	1																																
7594	08839	07593	1																																
7595	08840	07594	1																																
7596	08841	07595	1																																
7597	08842	07596	1																																
7598	08843	07597	1																																
7599	08844	07598	1																																
7600	08845	07599	1																																
7601	08846	07600	1																																
7602	08848	07601	1																																
7603	08849	07602	1																																
7604	08850	07603	1																																
7605	08851	07604	1																																
7606	08852	07605	1																																
7607	08853	07606	1																																
7608	08854	07607	1																																
7609	08855	07608	2																																
7610	08856	07609	1																																
7611	08857	07610	1																																
7612	08858	07611	2																																
7613	08859	07612	1																																
7614	08860	07613	1																																
7615	08861	07614	1																																
7616	08862	07615	1																																
7617	08863	07616	1																																

Table 212

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7618	08864	07617	1																							1	0	X68742	94.1	101	1	263	3453
7619	08865	07618	1																							1	0						
7620	08866	07619	1																							1	0						
7621	08867	07620	1																							1	0						
7622	08868	07621	1																							1	0						
7623	08869	07622	1																							1	0						
7624	08870	07623	2																							1	0						
7625	08871	07624	1																							1	0	M23613	94.8	290	83	966	1296
7626	08872	07625	1																							1	0						
7627	08873	07626	1																							1	0						
7628	08874	07627	1																							1	0						
7629	08875	07628	1																							1	0						
7630	08876	07629	1																							1	0						
7631	08877	07630	1																							1	0						
7632	08878	07631	1																							1	0						
7633	08879	07632	1																							1	0						
7634	08880	07633	1																							1	0						
7635	08881	07634	1																							1	0						
7636	08882	07635	1																							1	0						
7637	08883	07636	1																							1	0						
7638	08884	07637	1																							1	0						
7639	08885	07638	3																							3	0						
7640	08886	07639	3																							3	0						
7641	08887	07640	2																							2	0						
7642	08888	07641	1																							1	0						
7643	08889	07642	2																							2	0						
7644	08890	07643	1																							1	0						
7645	08891	07644	1																							1	0						
7646	08892	07645	1																							1	0						
7647	08893	07646	1																							1	0						
7648	08894	07647	1																							1	0						
7649	08895	07648	1																							1	0						
7650	08896	07649	1																							1	0						
7651	08897	07650	1																							1	0						
7652	08898	07651	1																							1	0						
7653	08899	07652	1																							1	0	011466	97.1	275	1	3253	3589

Table 213

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7654	08900	07653	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7655	08901	07654	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7656	08902	07655	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7657	08903	07656	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7658	08904	07657	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7659	08905	07658	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7660	08906	07659	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7661	08908	07660	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7662	08909	07661	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7663	08910	07662	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7664	08912	07663	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7665	08913	07664	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7666	08914	07665	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7667	08915	07666	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7668	08916	07667	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7669	08917	07668	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7670	08919	07669	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7671	08920	07670	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7672	08921	07671	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7673	08922	07672	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7674	08923	07673	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7675	08924	07674	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7676	08925	07675	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7677	08926	07676	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7678	08927	07677	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7679	08928	07678	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7680	08929	07679	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7681	08930	07680	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7682	08931	07681	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7683	08932	07682	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7684	08933	07683	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7685	08934	07684	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7686	08935	07685	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7687	08936	07686	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7688	08937	07687	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7689	08938	07688	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	CA	GA	IA	KA	MA	QA	CA	SA	IA	WA	YA	BA	BC	BE	BF	BG	BH	BI	BK
7690	08939	07689	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7691	08940	07690	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7692	08941	07691	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7693	08942	07692	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7694	08943	07693	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7695	08944	07694	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7696	08945	07695	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7697	08946	07696	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7698	08947	07697	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7699	08948	07698	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7700	08949	07699	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7701	08950	07700	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7702	08951	07701	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7703	08952	07702	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7704	08953	07703	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7705	08954	07704	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7706	08955	07705	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7707	08956	07706	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7708	08957	07707	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7709	08958	07708	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7710	08959	07709	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7711	08960	07710	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7712	08961	07711	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7713	08962	07712	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7714	08963	07713	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7715	08964	07714	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7716	08965	07715	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7717	08966	07716	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7718	08967	07717	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7719	08968	07718	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7720	08969	07719	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7721	08970	07720	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7722	08971	07721	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7723	08972	07722	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7724	08973	07723	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7725	08974	07724	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 215

[illegible]

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7762	09011	07761	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7763	09012	07762	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7764	09013	07763	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7765	09014	07764	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7766	09015	07765	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7767	09016	07766	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7768	09017	07767	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7769	09018	07768	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7770	09019	07769	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7771	09020	07770	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7772	09021	07771	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7773	09022	07772	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7774	09023	07773	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7775	09024	07774	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7776	09025	07775	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7777	09026	07776	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7778	09027	07777	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7779	09028	07778	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7780	09029	07779	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7781	09030	07780	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7782	09031	07781	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7783	09032	07782	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7784	09033	07783	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7785	09034	07784	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7786	09035	07785	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7787	09036	07786	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7788	09037	07787	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7789	09038	07788	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7790	09039	07789	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7791	09040	07790	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7792	09041	07791	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7793	09042	07792	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7794	09043	07793	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7795	09044	07794	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7796	09045	07795	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7797	09046	07796	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 217

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AP	AR	AS	AT	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7798	09047	07797	1																																		
7799	09048	07798	1																																		
7800	09049	07799	1																																		
7801	09050	07800	3																																		
7802	09051	07801	8																																		
7803	09052	07802	1																																		
7804	09053	07803	1																																		
7805	09054	07804	1																																		
7806	09055	07805	1																																		
7807	09056	07806	1																																		
7808	09057	07807	1																																		
7809	09058	07808	1																																		
7810	09059	07809	1																																		
7811	09060	07810	1																																		
7812	09061	07811	1																																		
7813	09062	07812	1																																		
7814	09063	07813	1																																		
7815	09064	07814	1																																		
7816	09065	07815	1																																		
7817	09066	07816	1																																		
7818	09067	07817	1																																		
7819	09068	07818	1																																		
7820	09069	07819	1																																		
7821	09070	07820	1																																		
7822	09071	07821	1																																		
7823	09072	07822	1																																		
7824	09073	07823	3																																		
7825	09074	07824	1																																		
7826	09075	07825	2																																		
7827	09076	07826	1																																		
7828	09077	07827	1																																		
7829	09078	07828	1																																		
7830	09079	07829	1																																		
7831	09080	07830	2																																		
7832	09081	07831	1																																		
7833	09082	07832	1																																		

Table 218

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AP	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7834	09083	07833		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
7835	09084	07834		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
7836	09085	07835		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	X56976	92 287	1	3066	3419
7837	09086	07836		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
7838	09087	07837		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					

Table 219

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT:

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(A) NAME: CHUGAI PHARMACEUTICAL CO., LTD.
(B) STREET: 41-8, Takada 3-chrome, Toshima-ku
(C) CITY: Tokyo
(E) COUNTRY: JAPAN
(F) ZIP: 171

(ii) TITLE OF INVENTION: GENE SIGNATURE

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(iii) NUMBER OF SEQUENCES: 7848

(iv) COMPUTER READABLE FORM:

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(A) MEDIUM TYPE: Diskette, 3.5 in., DS, 1.44 MB
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/ MS-DOS
(D) SOFTWARE: MS-DOS

(v) CURRENT APPLICATION DATA

(A) APPLICATION NUMBER: EP 95900295.7

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(vi) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER: PCT/JP94/01916
(B) FILING DATE: 11. November 1994

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EP 0 679 716 A1

SEQ ID NO:1

SEQUENCE LENGTH:704

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00001

SEQUENCE DESCRIPTION:

GATCTTCAAA CAAGCATCAG CGTTTTCCAG GGCTTCCCAG AGGTCTGTGC GACTAGCCCG 60
TGTCTATCAA AAGTTATTAG AGAGGATGAA GCATTAGCTT GAAGCACTAC AGGAGGAATG 120
CACCACGGCA GCTCTCCGCC AATTTCTCTC AGATTTCAC AGAGACTGTT TGAATGTTTT 180
CAAAACCAAG TATCACACTT TAATGTACAT GGGCCGCACC ATAATGAGAT GTGAGCCTTG 240
TGCATGTGGG GGAGGAGGGA GAGAGATGTA CTTTTTAAAT CATGTTCCCC CTAAACATGG 300
CTGTTAACCC ACTTGCATGC AGAACTTGG GATGTCACTT GCCTGACATT CACTTCCAG 360
GAGAGGACCC TATCCCCAAA TGTGGAATTG ACTTGCCTAT GGCCAAGGTC CCTTGGNAAA 420
GGGAGCTTCA GTATTGTGG GGGCNTCATA AAACCATGGN TTCAAGNCAA TCCAGCCTCA 480
TNGGGNNGGT CCTGGGNACA GTTTTTTGGT AAAGGCCCTT GGGCCAGNTG GGGGGAATGG 540
GCCTCCTTTT TAAGNTTTGG GNTGGAATNG TCTNGCAAAT TGGGGCTCCC ATTCNCGGG 600
GGTTTGGGGG TTTTNGGG CCTTNCNGG NNGGAAGGN TGGGTTTGGG GGNTNGGTTN 660
CCNTTGGGNG GGCCTGGGNG TTTGATTNA CCCGGGNCTT NNGN 704

SEQ ID NO:2

SEQUENCE LENGTH:659

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00002

SEQUENCE DESCRIPTION:

GATCTTTAAA ATACACACTC AAATCAAGAA ACTTAAGGTT ACCTTTNTTC CCAAATTCA 60
TACCTATCAT CTTAAGTAGG GACTTCTGTC TTCACAACAN ATTATNACCT TACAGAAGTT 120
TGAATTATCC GGTGCGGTTT TATTGTTTAA AATCATTCT GCATCAGCTG CTGAAACAAC 180
AAATAGGAAT TGTTTTTATG GAGGCTTTGC ATAGATTCCC TGAGCAGGAT TTTAATCTTT 240
TNCTAACTGG ACTGGTTCAA ATGTTGTNCT CTTCTTTAAA GGGATGGCAA GATGTGGGCA 300
GTGATGTAC TTAGGGCAGG GACAGGATAA GAGGGNTTAG GGAGAGAAGA TAGCAGGGCA 360
TGGCTGGGAA CCAAGTCCA AGCATACCAA CACGGAGCAG GCTACTGTCA AGCTCCCTC 420
GGAGGCGGNG CTGGTTCACA GCCAGCTGGC ACCAGNTTT NTNGNGGAAG NCTTTTCAA 480
ACAGTCTCAG GNAATCCAAT NTGCAAAGAC TTGCTTNAG NAAAACCCAG NAGTTGAAAG 540
GCTCCCAAGN ATTTAAGGG NACTTNCCAA AACGGGGCCC CNGGNCCCTT TTGGGTTTNG 600
GGGNTCAAAA CCCCGGAGGG GTTTGGGAAG NTTTTAATTG GNTTTAAAN ATNNNTNTN 659

SEQ ID NO:3

SEQUENCE LENGTH:625

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00003

SEQUENCE DESCRIPTION:

GATCTAACTG GGTACCTGAG ATATTNACA GCTGGACCTA GTTTCACAAT CTGTTGTCTC 60

CAGCTCTGCA TATGTCTGGC CAGGGGGCTT CTAGGAAGTA GGTTCATCT ATCAAATGTC 120
 TCCTCTGACT TCCTTTTGAA ACTTACTGCT CTTCTGTTTT ATTTGTTTT GTTTGAAGCT 180
 CAGAGGGAGA TGGGCAATTG ACAGGGATGC AATCCAGGGT GGGATTTCTT GAGGAAGTTA 240
 CAAATAAGCT TGTTACAACA TCAAGATAGA TGGAAATTGGA AGGATGCTAC CAGGAGAGTA 300
 CTTACATAGT GCTCAGGAGT TTCTCTTCTT AAAATGTTTA CTGCTGAAAG ATGAGCAGGA 360
 CCAGGGCGTT ATAGGCAGAG CCCTAGCCGA GAAACCTGCT GGCCTCTGCC TGTTCATT 420
 TCCCACTTTT GGTGTTGTG GCATTACTTT CAGAATTGTC ACTTCCTGC TTGTCATGAC 480
 TTTTTGGCA CACTTGCCAT GACGGGTGTT TCTGNGAACC ATGGAAGTTT TCGGCTAGTG 540
 CCTCCAGGGG CAGGGGGNAA GGAGGNGGTG TANTGTCATT TNGTNCAAAT AAATCCNGCC 600
 TATTGTTAAT NAACCAGTCT TTTGN 625

SEQ ID NO:4

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00004

SEQUENCE DESCRIPTION:

GATCTGCCAG GCTGGGGTGT TTTCGGTATC TGCTGTTTAC AGGTCTCCAC TGTAATCCGA 60
 AATACTTTGCC AGTGCACTAA TCTCTTTGGA GATAAAATTC ATTAGTGTGT TACTAAATGT 120
 NAATTTTNTT TTGCGGAAAA TACAGTACCG TGCTGANTT AATTATTAAT ATTNAAAAATA 180
 CTTCAATCCT TAACTCTCCC TCATTTGCTT TGCCACAGC CTATTCAGTT CCTTTGTTT 240
 GCAGGNTTCT GCAAAA 256

SEQ ID NO:5

SEQUENCE LENGTH:616

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00005

SEQUENCE DESCRIPTION:

GATCAAGCTC AAGAATAAGC TGAAATATGG CCAGACTATC AGGCCCATTT NTCTCCCCTG 60
 CACCGAGGGA ACAACTCGAG CTTTGAGGCT TCCTCCAACT ACCACTTGCC AGCAACAAAA 120
 GGAAGAGCTG CTCCTGCAC AGGATATCAA AGCTCTGTTT GTGTCTGAGG AGGAGAAAAA 180
 GCTGACTCGG AAGGAGGTCT ACATCAAGAA TGGGGATAAG AAAGGCAGCT GTGAGAGAGA 240
 TGCTCAATAT GCCCAGGCT ATGACAAAGT CAAGGACATC TCAGAGGTGG TCACCCCTCG 300
 GTTCCTTTGT ACTGGAGGAG TGAGTCCCTA TGCTGACCCC AATACTTGCA GAGGTGATTC 360
 TGGCGGCCCC TTGATAGTTC ACAAGAGAAG TCGTTTCATT CAAAGTTGGT GTAATCAGCT 420
 GGGGGAGTAA GTGGGATGTN TGCAAAAACC AGAAGGCGGC AAAAGCAGGT ACCTGNTTCA 480
 NGGCCGAAC TTTCACATCA NCTNTTCAA GGTNTTNCCT GGNTGAGGNG GAACNTCCAN 540
 GTTGGGGGTT TTGGGTTTTT TTAAGGGGTT CNTGTTNGCA AGGGGGTTGG GNTTNTTTA 600
 NNCCTGTTNN GNACCN 616

SEQ ID NO:6

SEQUENCE LENGTH:615

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00006

SEQUENCE DESCRIPTION:

5 GATCTCTGCT ATTTTANCCC CCCAAATAAG TTATTTGTCC TTAAAGGTTG GTTACNNATA 60
 ATACCCCTCA GTAAGATTCC AGTATTAATT TCTGGGCAGT TTGTTCTCTG TATACAATTG 120
 CAAATGATAA GCATTTTGT GAGTGACCAC CTTTGCAATA TGTTTGTAA TTNTTCATGT 180
 TGGGTTCTTT CTGAAATGTA CATCTTTACA TAAAAACCTC ACATTCTACT TGATTACAC 240
 TTCCTAGTCT ACATTACATG TGGTTGAAGG TTTTATACAT TCTATATGCT TTTACTAAAT 300
 10 ATACAAGATT TACTACTAGA AATTTGGAGA AAGAACAATA ACACATGTAC TTGTGATTG 360
 TTCATGTTAT ATTAACCT TGAGATTGT GTATTTATGT AGGGGGGGG ATTGNCCAGG 420
 NCTGNTGGTT TTTTGTCCN TGGGGCTATT NTAATAAANC NGGGGTATNG GGTGNTGGC 480
 CTNGGTTTGG GCCTAAANTT GGATATATNT GGGGTTTCCT NGNTTTTACC AAAATNGNTT 540
 15 TTGGTTGGTA GGGTTNTTAT TGGACCCNNT CCTGGGCCTG GGATAATNG GCNGNTTCCC 600
 NGGANAAAAAN NCCCN 615

SEQ ID NO:7

SEQUENCE LENGTH:608

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00007

SEQUENCE DESCRIPTION:

25 GATCAACCA AAGGAAAAGT GTTGCTAGAG AAAATTGGGG AAAAGGTGAA AAAGAAAAA 60
 TGAGTAGTAAT TGAGCAGAAA AAAATTAATT TATATATGTA TTGATTGGCA ACCAGATTTA 120
 TCTAAGTAGA ACTGAATTGG CTAGGAAAAA AGAAAACTG CATGTTAATC ATTTTCCTAA 180
 GCTGTCCITT TGAGGCTTAG TCAGTTTATT GGGAAAATGT TTAGGATTAT TCCTTGCTAT 240
 TAGTACTCAT TTTATGTATG TTACCCCTCA GTAAGTTCTC CCCATTTTAG TTTTCTAGGC 300
 30 TGAAAGGATT CTTTCTACA TTATACATGT GTGTTGTCAT ATTTGGCTTT TGCTATATAC 360
 TTTACCTTCA TTGTTAAATT TTTGTATTGT ATAGTTNCTT TGGNGGTATC TTAACCCCT 420
 ATTTTGTAAA ACCAACCTTG GCTTTGNTAA NCATTGGGC CGCTTGGGTA NGTCCGGACC 480
 TNNCCTTINC CCCNAGGGCC TGTACAGGAGN GCCGGNTTN CCGGGGNGTT GGNCCCGNNG 540
 35 CCTTCCCGAT TTTTNGGGGT TGGGTCCCTN GGTNCCGGC NTCTGTANGG GGTNCNCCTT 600
 TTNNNCCN 608

SEQ ID NO:8

SEQUENCE LENGTH:606

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00008

SEQUENCE DESCRIPTION:

45 GATCGCTTCC TAGAAATAAG CAACACCTCT CCCAAAAAGC AGCCACAAG GCAGGGGCCA 60
 GCAGCCCAGC CATCACTCAT CTTNAGGAA ATNAGTTGGT AGCCTCTGTG CACTGTTTGG 120
 TGGCCACATC ANNGGTGATG TCCTGTTTAC ATACCTGCTT GTATTTAAAG CCCTCAGTCT 180
 GTCCTGTTGT GTGGGCGAA GTGATGGACT CTGCCAGGTG GACATGCTGT GGGTGGATGT 240
 TCCCGGCGTG TGCCGGCCTG AATGGACAGG GGTCACTTCA CAAGCATGTC AGGGAAAAATC 300
 50 ACTGTCACAC AATTCCAATG GATTTTGTGC TCTTTTGTAA AAAAAAAT TCTTAGCGT 360
 AAACCATGNA TTTTTTTCA ATGTAGNCCC TTGGGGANTG AANTGAAATT TTGGGCTTCT 420

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EP 0 679 716 A1

TCANATNCGN AAAATNAAAT TTTTACCCCT GAGGGGGGGA GCCCCTTTCT GAAAGAAGGT 480
NTGGGCCAAA AGCCCTTTTA ATGNTTGCTG GCCNTTGNTG GTTTTNANNG TCCANTTTC 540
TTGGGGCGAA NGCCGNNNTG ANAAAGGTGG GTTTCNCTGG NGGNTTAAAG GNGGTGGTTT 600
GNTTTN 606

SEQ ID NO:9

SEQUENCE LENGTH:606

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00009

SEQUENCE DESCRIPTION:

GATCTTCANN NGTTAAGCAC TTGCTCTNAA GATTAATAATT CCTTTTCTTT TTAAGGTAA 60
GGGTGTGTAC GTATGGCAGT GATGTCTATG TTGAGATTAA CTTATGTATT GAGGAAAATT 120
TGAAGTTTAT TTTTTCGATG AATAAGGCTG TCAAATNATT TAGTATAGAT TAATGACATC 180
TTTTTTAGAA ATATTAAAGT GAGTATTCCT CATTATGTCA TCATTCTGA TAATTAGAGT 240
GCTAATTGTA ATGTTAGATA ATGNTTCCAC ATCTATACCT ATTTCTTTCT AGGGCACTTC 300
TGACCCTGGG GCTTGGGGAT GGCCTTTAGG CACAAGTAGT GTCTGTGTTA AGTTCACATA 360
ATGTGTATTT AATGAGAAAC ATTCNATGT AAAAATGTGT GTATGTGAAC GTATGCNNAC 420
ATTGTTATTG TGCACCNGTA CATTGTGAAG AAGTAGTTTN GAAATTTTGT AANGCACAAC 480
CCTTAANGNG GTGTGGAGTT ATTAAANTGN TGTAGGCNCA AATGTAATGT TTAGCCTATA 540
AAAGGCCCTC CTATTGTCCN TNGCAAGGC TTTGNCNCTT GNAANTAAAN CCCGTNTTTG 600
TTTAAA 606

SEQ ID NO:10

SEQUENCE LENGTH:606

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00010

SEQUENCE DESCRIPTION:

GATCAGGGGA GACCCCAACT GCCAGATATA TTTAATGTA CAAAAGTGA ACCAGATGAA 60
ATAATGTTCT GTCACGTGAA ATATTTAAGT ATATAGTATA TTTATACTCT AGAACATGCA 120
CATTTATATA TATATGTATA TGTATATATA TATAGTAACT ACTTTTATA CTCCATACAT 180
AACTTGATAT AGGAAGCTGT TTATTTATTC ACTGTAAGTT TATTTTCTCT ACACAGTAAA 240
ACTTGTACTA TGTTAATACC TTGTCCTATG TCAATTTGTA TATCATGAAA CACTTCTCAT 300
CATATTGTAT GTAAGTAATT GCATTTCTGC TCTTCAAAG CTCCTGCGTC TGTTTTTAAA 360
GAGCATGGAA AAATACTGCC TAGGAAAATG CAAATGGAA ATAGGAGAGA GTAGGTTTTC 420
CAGCTTAGTT TTGAGGGGGG CCGGTTACCT TGTATATTCC CCCATTACA TTTGGTGTCC 480
ATGTGTAGGG GAAGGTAAAG GGGTGGTTCC ATAATCAAGT TCCCCGTGGG GTGTNCCCCC 540
TGTTAAATGT CCCTGGTTTG GTGTTACCCG GGCTTTATGG GGNCTTTTCA TTATTCCGG 600
TNGGGN 606

SEQ ID NO:11

SEQUENCE LENGTH:598

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00011

SEQUENCE DESCRIPTION:

5 GATCAACAAA AGATAAACAA ATTTGCACGG AATACAAGTA GAATCACAGA GCTGAAGGAA 60
 GAAATAGAAG TAAAAAGAA ACAACTCCAA AACCTAGAAG ATGCTTGTA TGACATCATG 120
 CTTGCAGATG ATGATTGCTT AATGATACCT TATCAAATTG GTGATGTCTT CATTAGCCAT 180
 TCTCAAGAAG AAACGCAGAA ATGTTAGAAG AAGCAAAGAA AAATTTGCAA GAAGAAATTG 240
 ACGCCTTAGA ATCCAGAGTG GAATCAATTC AGCGAGTGTT AGCANGATTG GAAAGTTTCA 300
 10 TTGTATGCAA AATTCGGGAG CAACATAAAC CTTGAAGCTN GATGAAAGTT AAACATTTTA 360
 TAATACTTTT TTTATTTGNT TTAATAANCT TGATTATTG TTTAANATGG TAATTTTCC 420
 TTCTTCANAT GGCNNNGGT NAGCAAANCT TTCTTTTTT AAAAAATTT CCANTTGT 480
 AATGGGGAAC TTGCCCNTT TTCCNCATGG CNTGNTNATT NATTTNTNT TTTTAAAGGG 540
 15 GGGCCAGTTT TCCCCNNGG TTTTGTGCT TNNCGGTTNT TNCAGGNNTN GGGGGTCN 598

SEQ ID NO:12

SEQUENCE LENGTH:597

SEQUENCE TYPE:nucleic acid

20 TOPOLOGY:linear

CLONE:HUMGS00012

SEQUENCE DESCRIPTION:

25 GATCGACAGA CCTGAAGCCA TCAGTGAAGA GAGGTTGCGA GAGATGTTG GTTTATATGG 60
 TCAGACAACA GGAAAGGGGA GTATATCTCT GAAAGAACTG AATGCCCGAC CCTTAGAAGT 120
 TTTCAATGTG AGTGTGCTCA AAAGACAAGG TTACGGAGAA GGCTTCCGCT GGATGGCACA 180
 GTACATTGAT TAACACAAAC TCACATTGGT TCCAGGTCTC AACGTTTCAGG CTTACTCAGA 240
 GATTTGATTG CTAACATGC ATAACCTGAA TTCAATAGAC TTTTGCTNGG TTATAAAACA 300
 30 GATGTTTTT AGATTATTAA TATTAANTCA ACTTAATTG ANTNGAATT NGAAANCTGA 360
 TTCAAGTAAG NTTTGAGTAT CACANTGTTA GCTTTCCTAA TTCCATAAAN GTACCTTGGG 420
 TTTTTTNCAG NTTTATAAAT CTGGCCATCA NCCCCNGCGG CCTTTTNGTA AAGGGGCACC 480
 TTTTCCNGCA GGCCATTTGG NAGCNCNTT TTAACCACCT TGGGNTTTT AACCCTTTT 540
 TNAAGGGNCN NCNTGGTTAA NTTTTTNTT GGGCCTTNC NGGGCCTGGT NTTTAAN 597

35 SEQ ID NO:13

SEQUENCE LENGTH:593

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS00014

SEQUENCE DESCRIPTION:

45 GATCTTCCAA AGCACTATTT GTTGTAATAA CTTTTCTAAA TGTAAGTGCCT TTAAAGGAAA 60
 AATGAACACA GGGAAAGTGAC TTTGCTACAA ATAATGTTGC TGTGTTAAGT ATTCATATTA 120
 AATACATGCC TTCTATATGG AACATGGCAG AAAGACTGAA AAATAACAGT AATTAATTGT 180
 GTAATTCAGA ATTCATACCA ATCAGTGTG AACTCAAAC ATTGCAAAAG TGGGTGGCAA 240
 TATTCAGTGC TTAACACTTT TCTAGCGTTG GTACATCTGA GAAATGAGTG CTCAGGTGGA 300
 TTTTATCCTC GCAAGCATGT TGTTATAAGA ATTGTGGGTG TGCCTATCAT ACCANTTGT 360
 50 TTCTGTATCT TGA AAAAGTA TTCTCCACAT TTTANATGGT TTTATATNG GGGATTCCTT 420
 TAATGCCCCC TTGGNCAAT TTATATATAT GGGCCCCATN GTTNCNTTT NAATTTTNG 480
 GTTTTNGGTT GTAAGGGNCN TGCNCNTATG GTGGGGGCT CCCAAAANTG GGANCANGNT 540

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TTTNCCTNNG GACNCCCNT TGGTTGTTNA GGGGGGCCAA TTTTCNTNC CCN 593

SEQ ID NO:14

SEQUENCE LENGTH:574

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00015

SEQUENCE DESCRIPTION:

GATCGTNCCTG CAGTGGGAGC GTGTGACTGC GGAAGTTGTG AAGCCACGGG AAACCTCGGAG 60
 CCTAGAGCAG CAGCTCAGCG CTTCTATGGG AAGCGGTCTC GAGCAGAAGC CCCACTGAAG 120
 TGTCCCCCTGG CAGACACCCA CATGAACTCT TCCGAGAAAC TCCAGTTCTA TAAAGAGAAA 180
 GCCCCAGATT GCCATGGGCC AGTNTTGAAA CACGAAGCTA TCTCAAGCCA GGAGTCAAAG 240
 AAGAGCAAGA AGAGACCTTT TGAGGAGTCA GAGACAGAAC AGAATAACTC TTCACAACCT 300
 TCAAAGCAGA AATATGTATG TTTTGTCTGT GAAGACTGGG GACTTGTAA ATTCTATTG 360
 ATTAAGTAGA TACAAGTTGA CCTTCTCTCTG GCCCCCAGCT CTAGTGTGTTG AGTAAAGGGA 420
 GACTNAGGCT GGGTTTACTT TTTTNGGTTT GNATTANCC TATTGGCATT TAGNCATAGG 480
 TAAGCGCGTN TTTTCNNCT TTTNTGGNT TTGGGNGGGG GATTNTNTNN GGGGNNNNAA 540
 AAAANTTNC ANGGGNTTTT TCCAAANCAAT NGGN 574

SEQ ID NO:15

SEQUENCE LENGTH:573

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00016

SEQUENCE DESCRIPTION:

GATCAGCCCA GAGGAATGCT GAGAAATCAC CTGGAGGAGG GAGCAGAAAG AGAAGGTTTT 60
 TAAGGAGGGG CTTCTGAATA CTTGGGAGAT ACGGAACGGA CCAAGGACCA CACTCCAGGG 120
 TGCATTGCTT GCTCCCTGGG GCACCACTTC TGGATTACAG TGTGCCAGGT CCTTTGGAGG 180
 CCCTACCCCT TCCCCATTCA TTGCCACCAG TGAGAAATNG GGGTGCCCT GTGTAAAGAA 240
 ACCTACCAAA GGTTTACATT TGCACCTTAG CCTCAATAGC TACGAACCCT AGAGAAGCAG 300
 CTAGCTGGAG CTCATGTGCA ACTCCTGATT CTCAGGAGAA AGATGGATTT TAACCNAAAA 360
 TTATGAGTNA GCTGTAACT CTAAATGTA CTTNGGGAGA TAGGGCCAAG NGAGAGGTCA 420
 TGGGCCAACT TAAGTGTTAT CCNGTAGGAA AGNNCAGGTA NCACTGGNTT TTTTTTNNA 480
 GGGTTGCTNT TNCCTTNTNC TAAANGGATT TGNTANTTCC NTGGGGNTNG NATTTAAATT 540
 GGGTTNTAAA AAGNTTNGAC GTGANAAAAA TTN 573

SEQ ID NO:16

SEQUENCE LENGTH:567

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00017

SEQUENCE DESCRIPTION:

GATCAAAACA GTCTCACCAG CACCATATCC ACATTCTAGC CCATGGAAAG GGTAAAGAAA 60
 AGAAAGTGGA AGATATTAGT TTCCATTTAA GGAAGTGACA TGGAGNTAAT ATAAGTCACC 120
 TGTGTTTACA TTCCACTGGC AAAAATTCAG TCACAGGAAT GTACTTAGCT GCAGAGGAGG 180

CTAGGATATG CCCTCCAAAA ACTCAGGGGG GATGTCCTAC TTGTAAAAGG AAGAAATGAA 240
 AANTGGACAC TGAGAGGAAA TCAGCAGTCT CAGAGGTAAT ATACTTACAC AAGTTTTTTA 300
 AAAACCATAA AATGATGCAG AATGAAGTTT CCACTCTATT CACCATCTAT CCAGTCCTCA 360
 TGCCTCCCAN CANGNGGTAA ATNCTTTATT ATTGTGTCAT GGTATCTTTC CAGGGTTTTT 420
 CTAAGCAATT TTGCAACNGN TTTTAATTAT GTATCCTNAT TTCCTACNTT ACCCCNTTTT 480
 TGTCCATGNA NGGNANANTN TCCTGNGGNN TAACCTTCNT GTNTCTTTTT TTCCCCTNAT 540
 ATTTTTTGGC GGTNCCNTNN NTTTGGN 567

SEQ ID NO:17

SEQUENCE LENGTH:552

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00018

SEQUENCE DESCRIPTION:

GATCTTACCC GTGACAAAAT GTGTTCCATG GTCAAAAAAT GGCAGACAAT GATTGANGCT 60
 CACGTTGATG TCAAGACTAC CGATGGTTAC TTGCTTCGTC TGTNCTGTGT TGGTTTTACT 120
 AAAAAACGCA ACAATCAGAT ACGGAAGACC TCTTATGCTC AGCACCAACA GGTCCGCCAA 180
 ATCCGGAAGA AGATGATGGA AATCATGACC CGAGANNNGC AGACAAATGN CTTGAAAGAA 240
 GTGGTCAATA AATTGATTCC AGACAGCATT GGAAAAGACA TAGAAAAGGC TTGCCAATCT 300
 ATTTATCCTC TCCATGGNTG TCTTCGTTAG AAAAGTAAAA ATGCTGAAGA AGCCCAAGTT 360
 TGAATTGGGA AAGCTCATGG AGCTTCATGG TGAAGGCAGT AGTTCTGGAA AAAGCCACTT 420
 GGGGNCNGNG ACAGGTGCTT AAAGGTTGAA CCGNGCTNGA TTGGTTNTGA ACCCACCAGT 480
 CCCAGGAATT CTTGTTTAAA GTTCCAGNCN TTCAATTAGT TGGCAAATTA AAAANGTGCT 540
 TTTTGGNGGA AA 552

SEQ ID NO:18

SEQUENCE LENGTH:581

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00019

SEQUENCE DESCRIPTION:

GATCGCCGTT CTGGTAAAA GCTGGAAGAT GGCCCTAAAT TCTTGAAGTC TGGTGATGCT 60
 GCCATTGTTG ATATGGTTCC TGGCAAGCCC ATGTGTGTTG AGAGCTTCTC AGACTATCCA 120
 CCTTTGGGTC GCTTTGCTGT TCGTGATATN AGACAGACAG TTGCGGTGGG TGTCATCAAA 180
 GCAGTGGACA AGAAGGCTGC TGGAGCTGGC AAGGTCACCA AGTCTNCCCA GAAAGCTCAG 240
 AAGGCTAAAT CGAATATTAT CCCTAATACC TGCCACCCCA CTCTTAATCA GTGGTGGAA 300
 AACGGGTCTC AGAACTGTTT GTTTCAATTG GCCATTTAAG TTTTAGTAGT AAAAGACTGG 360
 TTTAATGATA ACAATGCATC GTAAAACTT CANGAAGGN AANGGAGGAA TGNTTTGTG 420
 GGCCCACTTT GGGTTTTNCT TTTTNCGGT GTNGGCAGTT TTTAAGGTTN TTAAGTTTTT 480
 TNAAAATNCA GGACCTTTT TAANTGGNAA CCAACTTTGG CCAAAAAATT TTGTACCAG 540
 ATTTTTTNGG GCCCNTTTA AAAANGTNTT NATTNGGGA A 581

SEQ ID NO:19

SEQUENCE LENGTH:556

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00020

SEQUENCE DESCRIPTION:

5 GATCAGCAGG GTTCTTTGTA AATAGTATTT TGAGACACTA AGATGTTTCT ACTGCTACGG 60
 AATGTATTTT AAACACATAT CGTTTCTTTT TCTTGAAAA AAAGTTGATT AGGACCACAG 120
 NNNNGGTTTA GAAAGGGTAA TATTTTGAAA TACTACAAGG TTAGACAGT CCATGAAATC 180
 GACCTGTTTA ATAATTACC ATCCTGAAA TCCAGAATTA AAATATGGAA GCAAGAACTA 240
 10 TATAATTGAT TAGGATGCTT GGTAGGTTTT TTTCATTGTT CAAATATTCA TTGCACAGTG 300
 GATTGTTTTG ATTAGTTAGT ATGCTTTTTT TTTAATTAAT TCAGTCTTCT GTTAATTTTT 360
 AAGNTTGGT TAGTGCCACA AGGAATTNA CTTNTTGATT TGTATAATNG GAACCTGACC 420
 TNGGGATTNG TAGCGGGGNT TTGAAGGGTG GGGACCTNCC CNCAAAATAA GGGGGAGGTT 480
 TCCAAANNTT CCNCTGGCCG NCCNNNNATC CCAGGTAAAG GGGGTNGAAA TANTNNGGNN 540
 15 NCCCCCAGG GGAAAN 555

SEQ ID NO:20

SEQUENCE LENGTH:555

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00021

SEQUENCE DESCRIPTION:

25 GATCTGGTAC GAGTGTGTGA AAACATCCCC ATTGTGTTGT GTGGCAACAA AGNGGATATT 60
 AAGGACAGGA ANATGAAGGC GAAATCCATT GTCTTCCACC GAAAGAAGAA TCTTCAGTAC 120
 TACGACATTT CTGCCAAAAG TAACTACAAC TTTGAAAAGC CCTTCCTCTG GCTTNCTAGG 180
 AAGCTCATTG GAGACCCTAA CTTGGAATTT GTTGCCATGC CTGCTCTCGC CCCACCAGAA 240
 GTTGTCAATG ACCCAGCTTT GGCAGCACAG TATGAGCAGC ACTTAGAGGT TGCTCAGACA 300
 30 ACTGCTCTCC CGGATGAGGA TGATGACCTG TGAGAATGAA GCTGGAGCCC AGCGTCAAGA 360
 AGTCTAGTTT TATAGGGAAG TTGTCCTGTG ATGTCAGCGG TNCAGCGTGT GTNCCACNTC 420
 ATTATTATCT AGCTAAGCGG ACATGTNTTC ATCTGTGGGN TCTTAAGGAG NTGAGTNGNN 480
 TNGGNGTNAT NTGGANTTAA AAATAACTTC ATNTTNGGC CNNTATTTA NGTNTTTTNG 540
 35 CCCGNTTNT CCCTN 555

SEQ ID NO:21

SEQUENCE LENGTH:544

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00023

SEQUENCE DESCRIPTION:

45 GATCGATACA TGCAAAATTA ATGTAGTAAC TCACTTTTCC ATATATTTTN AATGTATATT 60
 TCTATTTATG AATACCAATT TATAAAAAAT AATTACACAG AAAAAATGG AATAGGAAAA 120
 ATTATGCATC TAGCACATTT AAAGTGTGCA AATATGAAAA TTTTCGAGG ATTACATTTT 180
 NTNNNTAGGC TGCATATTTT AACTGGCTTT AAAACTGTAA CACATCATAT AAAAGTACTT 240
 TACCCGGTAT GTATTGCATT ATATCATTGC AATAATTATT GGAGTCTAGA TATCGAGCCA 300
 TCCCAGGTGT TGGGCGGGGG GAGGGTTGTG GCAAGTTGTC TTTTCAATTT NGNGNGTTTT 360
 50 CCTGTNGCTC CAGGGCAAGT ACCGGGTTGG AAAGCTGCCT GTAAGCGTTG GCACCTTCAT 420
 AGNGTAGTGT TTNGGTGNCT TTTTTNTCG GTTCTTGTA ATNGGTNCG GTNGGTGGTG 480

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TTCAGATGNT TTTTNCNCT NGTTCAGCAA CTTNCCCNNT NNCTTGTCTT GATAGGGNAC 540
NTCN 544

SEQ ID NO:22

SEQUENCE LENGTH:538

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00026

SEQUENCE DESCRIPTION:

GATCTCTATC CAGTTGGACA CTTAATTGCT TTCTTCATTG AGAAAGATAG TCATGTTTAC 60
TGGTATATTT GGTCACCTCTT AGAACCTGTC CTTACATAT GTTTTTTATG GGACCCATGA 120
ATGGTTAGCC TTTCTGTACT ATTGTAGAAG GAAATAAATA GGCGTAAAAA GACCATTGTA 180
GTAAATAAGT TCAAGGGGAA CTTGGGACCA GAAACCACTG GTATGTACAA AAAAGCTGGC 240
AATTTGAATA ACCTCAAGTT TGACAATAAT TTTTAAATT GAACAGTTAT GATAAATTTT 300
AGTAGTTTTA TACACTAGAT GTGCCTAGAT GGTTCCTCAAG GCTTATAGGA CTGGCTCACA 360
GTTACCACTT TCTAGTGGCT TTTCTTGGT TTGGGTCTGG GGGGCTGGGG GCAATGGGCT 420
TTTTTCCTTG GGTGCGCAAT CGGTTTCTCT GGTGGTTCAG TTTCCAATCC TTNGGGGGGT 480
CNTTGTGNTN TTNNCNGCCC NGNNNGGTNN GTCCNGGGTG TTNGCCGGGN NCNTTTTN 538

SEQ ID NO:23

SEQUENCE LENGTH:535

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00028

SEQUENCE DESCRIPTION:

GATCCTGGAA TATGTCGAGG TTATATTACC AGGTATTTTT ATAACAATCN GACAAAACAG 60
TGTGAACGTT TCAAGTATGG TGGATGCCTG GGCAATATGA ACAATTTTNA GACACTGGAA 120
GAATGCAAGA NCATTTGTNA AGATGGTCCG AATGGTTTCC AGGTGGATAA TTATGGAACC 180
CAGCTCAATG CTGTGAATAA CTCCTGACT CCGCAATCAA CCAAGGTTCC CAGCCTTTTT 240
GAATTTACAG GTCCCTCATG GTGTCTCACT CCAGCAGACA GAGGATTGTG TCGTGCCAAT 300
NNGAACAGAT TCTACTACAA TTCAGTCATT GGGAAATGCC GCCCATTTAA GTACAGTGGA 360
TGTGGGGGGA AATGAAAACA ATTTTACTTC CAAACAAGGA ATGTCTGAGG GGCATGTAAA 420
AAAGGGTTTC ATCCAAAGGA TTTCANAAGG GNGGCTNATT TAAAACCANA NGGAANNNGN 480
AGGAGGCNGG NNGTGAATTT GNNTTTTGGN GGAANTTTTT GNTTNAANNT TNTGN 535

SEQ ID NO:24

SEQUENCE LENGTH:528

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00029

SEQUENCE DESCRIPTION:

GATCTACACT TGGATGGATG CAACTTTGAA AGAACTGACA AGTTTAGTAA AAGAACTCTA 60
CCCAGAAGCT AGAAAGAAGG GCACTCACTT CAATTTTNC AATCGTTTTA CAGATGTAA 120
AAGACCTGGC TATCGAGTTA AGGAGATTGG CAGCACCATG TCTGGCAGAA AGGGGACTGA 180
TGATTCCATG ACCCTGCAGT CGCAGAAGTT CCAGATAGGA GATTACTTGG ACATAGCAAT 240

TACCCCTCCA AATCGGGCAC CACCTCCTTC AGGGCGCATG AGACCATATT AAATTCTATT 300
TACTATTGTG TGAATTTATT TTTCCGTCAG TTATGTAAAA TAAACATACT CTNCCCTCCT 360
CCCCCTGGATT TATTGCCATT TAAGGCTTTT AAAATTCTAA TCAANNTTTG TNANTGCAAT 420
CATCTGTTTN GGGNGTTNNG TTTTGGGATG TGCTTTTGN NTGGNTTNCG GNTTAGNCTT 480
GGNTTGTTTT AATGGCCNTT CNNGTNANAT TTGGNGGNAA NGNGCTTN 528

SEQ ID NO:25

SEQUENCE LENGTH:528

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00030

SEQUENCE DESCRIPTION:

GATCAAGGTA TAATGGAAAA ATATACCTAT TCTGAAGTA GTTTATTATN GTTTTCAAAT 60
TGATTTATAC CATTATTAAC CTGATGTGGT CTGCTTAAAA AATGAATATA TCAGTATTTA 120
GAAATAAAAT GCAAAGGTGG GAATATATAC TTAAATAATT TGTCTAAGT AAATTAGCAT 180
TTGGTAGTCT GANATGGTGA CAGATTACTT GTTAAAATTG TGAAANCTCT GTTGTGTCCT 240
CTCTNCCTAC ATTTGTCCCT GAGAGTNTC CACGATTACT AGGTTCTTGA TTCCCTTATA 300
TGGCAATCAG GCAGAGGCGT TCCTTAAGCA TTAGAGAGTT CTGAAGCTTA AGATTGTITT 360
TGGTTGGATG AANGTCCTTA GTACAGTTGA AAANCAGAGC ATTAAAGNCT ANTANTTTG 420
TTTTGNCCTC ACCAGTCATT TTAAATNNG TNGGAATNCT TNTNNCTCA GTGCTTAAAN 480
NTTCCNTTG TTTCAANCTG NNGGGGGTTN GGATTAAACC AGGCCNCN 528

SEQ ID NO:26

SEQUENCE LENGTH:527

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00031

SEQUENCE DESCRIPTION:

GATCAGAATG CCCCTCCACT CATGAGACTC TTCATTTTGT CCACTTTGAC AGGAAAAGTG 60
GGAATGTATG CAGAGCTCTC AAAAGAAACA AAAAAGGCCA AAACGGTGCC TTCAGCCACA 120
TCCTCTGAAT TGGCCCTGAC TTGGACTAAA TGCCTAATG CAAAATCCCT TGACAAAAGC 180
GCATAGGTTA TTTCAAACCA GCATTGTTTT TTATGTAACC TGTTTTACCG CATCTTCTCA 240
GCAGCTTCTG ACCACTGCTC AATTTTCTCC TTTACAGCCA TTGTTCTGGT GGACAAATAA 300
CCTAGGTACT CCAAATCCTG GCAGGAAAAA TATACAGCAT TATGAANCAG CACTCANGTA 360
ATCCTAAAAT GGATTTCCTA AGCTGGTTAC ACATGGCCCT GGNAANGTCN TATTGANTTT 420
ANANGGGCTT TCTTCNTTTC AGGAGTTTNG GTCAACGGTG GCAAATCCNT GGGGTNNTTA 480
ANTGGNNNGG TTNNTTAANT TNTGNTANTT TCNTNGGGGC CANAGGN 527

SEQ ID NO:27

SEQUENCE LENGTH:520

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00033

SEQUENCE DESCRIPTION:

GATCAAAATG GTTGGTGAAC CTCCACATGT CCAGTTCTGT TGCCAAACTT TCCATTGAGA 60

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5 GTATTTGGTG GAGTTTGAAT TTGAGCAAAC TAAATGCCTT CATCTTAGGT AGAAAGGGCC 120
 TGAATCTTCC ATTTTATATT CAAACCTCAT TGTATTTTGG CCTAAGTAAA AAGTCAGATT 180
 TCATTTCAT TTACCTGAGT TCGCTTTAAA GAGCTTTTCA AAGAGAGCTT TATAGACACC 240
 CACAATTGTC CCCAATCTCT TCATGATGTT GCATTAATAG TTGTTTTTGT CCCTTTCTTG 300
 GAAATGTAA TGCCAAAGNT TGCCTGAACA TTNGGGCGGG TTTTCTTAAA TTGAANGTN 360
 TAAAANTTTT NTAANGGGGG AATTNCCAAA NGGGTATTTA AAAGGGTTNG TTTTAACCAG 420
 GTATTGNGT GGGGGGATGG TCCAATAATC CTCCNGGGGG AGGGCTTTCA AGGGAAATCC 480
 10 CNTTTTNGGG GAAATAAAAA NNGGGTTAAA ANNNNTTTN 520

SEQ ID NO:28
 SEQUENCE LENGTH:514
 SEQUENCE TYPE:nucleic acid
 15 TOPOLOGY:linear
 CLONE:HUMGS00034
 SEQUENCE DESCRIPTION:
 GATCAGCGAG GCCGACAAGA AGAAGGTGCT GGACAAGTGT CAAGAGGTCA TCTCGTGGCT 60
 20 GGACGCCAAC ACCTTGGCCG AGAAGGACGA GTTTAAGCAC AAGAGGAAGG AGCTGGAGCA 120
 GGTGTGTAAC CCCATCATCA GCGGACTGTA CCAGGGTGCC GGTGGTCCCG GGCCTGGGGG 180
 CTTCGGGGCT CAGGGTCCCA AGGNAGGGTC TGGGTCAAGC CCCACCATTG AGGAGGTAGA 240
 TTAGGGGCTT TTCCAAGATT GCTGTTTTTN TTTTGGAGCT TCAAGACTTT GCATTTCCTA 300
 25 GTATTCTGT TTGTNAGTTC TCAATTCCT GTGTTTGCAA TGTTGAAATT TTTTGGTGGA 360
 AGTACTGAAC TTGCTTTTTT TCCGTTTCT ACATGCAAGA GATGAATTA TACTGCCATC 420
 TTACCGGCTA TTTCTCTTT TTTAATTCCA CTTAACTCAG GCCATTTTTT AAAGTTGGGT 480
 ACTTGCAAAG TAAAATAAAC TTAAAAATT CAAA 514

30 SEQ ID NO:29
 SEQUENCE LENGTH:513
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 35 CLONE:HUMGS00036
 SEQUENCE DESCRIPTION:
 GATCATCATT CTTCTGACTC TAGATGGGAC ACTTGACAGT GACTTGAAAC ATTTGCATAT 60
 TCAGGAATGC ATGAGATTTC AAGAGAGCCT ACAGTATGAA ATCATTITCA CAAAATAAGC 120
 AGCTTGCTTC TGAATGCTG TCTTTCCAG TAGCTACTCA CCTGCCTCTG GTGGCTGGGA 180
 40 TTCAGATGCC ACAAACCTGT CAGTATCTAT AGACCAGGTC TGTGCCACCT CCTCTCTCCT 240
 CTGTGCTCAG TGAGGAGGCA GTAAATGAAG TTACAGGCTA GCACAATACC TAACTCATGT 300
 TTCCAGTAC ACCTGTTGGA TATTNCTGT NCCTTTTAAT GGTTCCTAAG GGANTTAGGT 360
 TTTGNCCTG TTTCCAGNGG TTTCCAGGTT TTCTTTGGGT NCTTTTNA TTTTNAANTT 420
 45 CCNAGGGGGG GGGNNTTTT GGNAAGGGG GGGCAAAGGG GNTTTTTTTT TTNTTGGGCC 480
 NNGNTTTTGG GGGGAAANC CTTTNNGGTN NCN 513

55 SEQ ID NO:30
 SEQUENCE LENGTH:512
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00037

SEQUENCE DESCRIPTION:

5 GATCTAAATT GTTACATTTT ACCATTTTCAT TCCGAAGTTG GTTTTACTTT ATTAAATGAA 60
 GATTTAGTTT TCATATCGTA TACATAGCTG TATAGATTTC AAAATNAGGT TGTTAATTG 120
 TGTCACTTAC TATTTTTGTG TTGGTAATGC TTAAATGCA TACTTAAAAA TGAAGTACTG 180
 TTATCTAAGC TACTGTGTTT AGAAAATGTT AAGAATGAGC AGAAATTTT ATAGAAAAGT 240
 ATAACCGGAA GANGAGAGAA GATACTGCCA ATAGGCCCTC AANCTTAAAA NAGAAAAACC 300
 10 TTTGCCAGTT TTANGGACAT ATTTTGATTC TTTCNGTATT CTTAACACCT TTTTAAACAA 360
 NGTTCCTGAT AGTACCCACT ATTATTGGGT TTGTTTATG CCATTATTG ATTCTTGGAT 420
 ATCAAGCAT TTNCAATGTG GCATATTTNG NTTCCNNTN NCCTTNCNTT TTTTNGGNCN 480
 NCNTTACCCT TTCCNTTGA AAGNCANTN GN 512

SEQ ID NO:31

SEQUENCE LENGTH:510

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00038

SEQUENCE DESCRIPTION:

20 GATCAGCCAG GCACAGAATC TCCAGAACAA CCTAGAGAGT GAATGCTAAT TTGTAGAGCG 60
 AACTTCCATT TGGCCCATNA TTTGTAACG TGTAAGTCT CCAAGTGCCA GANTGCTTAC 120
 ACGTTAAAGC AGCACCTTTC CATTTGCCCA CATATTCTTC TTGCACACCC CTTCATTAC 180
 25 TGCTGAATAG GACATTGCAT GGGAAAGAGTA CAGAGGTGGC AGANTGANGC TAGAGTGGGC 240
 AGGNCTAAAG ACTGAGCCCC AGAGTGCTCC CAGCAACCGC CACGTACANG GTCTGNAATG 300
 NCANGGGCAN GNGTGAGATT GGAANCTGTG TGTGAANGGT AAGCCCTTGC AGTNTTCTG 360
 CCTCCCTTTC TTTCTGCCTT TCACCCCNCT TANTTGTNTG GTTNTTGGTT TGCCCGTTCT 420
 30 TCTCTTGGTG GNTGCNCATT TGTANATGG TGTTAGGGGT GTGGGGNTGA GGTTCCTCCC 480
 TTTGATGTGG GNTTNTCCN TTGGGTTTAN 510

SEQ ID NO:32

SEQUENCE LENGTH:507

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00039

SEQUENCE DESCRIPTION:

40 GATCGTGAAG CCAATGGCG AGAAGCCGGA CGAGTTCGAG TCCGGCATCT CNCAGGCTCT 60
 TCTGGAGCTG GAGATGAAC TCGACCTCAA GGCTCAGCTC AGGGAGCTGA ATATTACGGC 120
 AGCTAAGGAA ATTNAAGTTG GTGGTGGTCG GAAAGCTATC ATAATCTTTG TNCCCGTTCC 180
 TCAACTGAAA TCTTCCAGA AAATCCAAGT CCGGCTAGTA CGGAATTGG AGAAAAAGTT 240
 45 CAGTGGGAAG CATGTCGTCT TTATCGCTCA GAGGAGAATT CTGCCTAAGC CAACTCGAAA 300
 AAGCCGTACA AAAAATAAGC AAAAGNGTCC CAGGAGCCGT ACTCTGACAG CTGTGCACGA 360
 TGCCATCCTT GAGGGACTTG GTCTTTCNA AGCGGAAATT NTNGGCAAGA GGANTCCNGN 420
 GTCAAACCTT GNTTGGCANG NCGGGCTCAT AAANGGTTCA TTTTGGNNCA ANNGACNAGN 480
 AGGNCCAATT NTGGGNCAAA NAGGNNTN 507

SEQ ID NO:33

SEQUENCE LENGTH:508

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00040

SEQUENCE DESCRIPTION:

GATCAGAAAC TCACCCATAA TCTNAACGGG TGCCGCTATA ATTNGTNACA TCTGGCAAGA 60
 TTTCCCTTTA TGTATATATT TAAACAATCC GCTTGGACAC GAACAAAGCC ACACCTCTAA 120
 CTGCTTCTGG CGAACTGATT TAATTTTNA TTTTNTNCA TAAAGATATT CTTAGATACT 180
 GAAAGAAATA GTTAATGAGT TTNCATTGT CCTTGAGAAA ATTTGGCTCA AGTCCATTG 240
 GCTGTAGTGT CAACGATGTT TCCAGTAGTG TTTAGGATTT GGTGTCTTCA AAGGTAGTTG 300
 ATTAAACCAA GTGTGTCTTT AATATCTTGT ATCAGAATAA CTTTGTATGT TACCAACTTA 360
 AATTGCTAGA ATAAGGGTAA ATTGGATACA CAACTGCTGA TTTTAAATTT AGGANCTTTG 420
 ACCNNATTTT GGGGTTTCA AANCCGTTT TGGNTGCTNT GTATCCTTAT GCTGTTTGGT 480
 TNATTTCCAN TAAAAANTTC ACNCGNGN 508

SEQ ID NO:34

SEQUENCE LENGTH:505

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00041

SEQUENCE DESCRIPTION:

GATCTGTAAG TAACTTCACA TTAATAATG AAATATTTT TAATTTAAAG CTTACTCTGT 60
 CCATTATCC ACAGGAAAGT GTTATTTTAA AAGNNAGGTT CATGTAGAGA AAAGCACACT 120
 TGTAGGATAA GTGAAATGGA TACTACATCT TTAACAGTA TTTCATTGCC TGTGTATGGA 180
 AAANCCATTT GAAGTGTAAC TGTGTACATA ACTCTGTAAA ANCACTGAAA ANTTATACTA 240
 ACTTATTTAT GTTAAAAGAT TTTTTTTAA CTAGACAATA TACAAGCCAA AGTGGCATGT 300
 TTTGTGCATT TGTAATGCT GTGTGGGTA GANTAGGTTT TCCCCTCTTT TGTAAATAA 360
 TATGGCTATG CTTAAANGGT TGCATACTGG GGCCAAGTAT AATTTTNTG GTAATGTGTG 420
 GNAAAGGATG NCCAGTTATT GGTACCNT TTANGNNATC CNNTAANGGG AACCTTCCCC 480
 TNGGTAAAA NCANGNNGTA NANNN 505

SEQ ID NO:35

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00042

SEQUENCE DESCRIPTION:

GATCTGGAAA GAGCTGTTTT GGATGAATGC AGTATAAAAT GTAAAANCCC TGCTAAATGA 60
 AA 62

SEQ ID NO:36

SEQUENCE LENGTH:503

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00043

SEQUENCE DESCRIPTION:

5 GATCGAAAAGG CACTCCATGA GCTAAAAGTGA GAAGAGTGGG AAGGCAGACT ACAAGTTACT 60
 GAGCACCTCC CTGAGAAAAAT TGAAAGTAGT TTACAGGAAG ATGAACCTGA GAATGNTGCT 120
 AAGAAAATTG AAGCACTGCT AAACCTTCCT AGAAACCCTT CAGTAATAGA TAAACAAGAC 180
 AAGGACTGAA AGTGTCTCTGA ACTTGAACT CACTGGAGAG CTGAAGGGAG CTGCCATGTC 240
 CGATGAATGC CAACAGACAG GCCACTCTTT GGTGAGCCTG CTGACAAATT TAAGTGCTGG 300
 TACCTGTGGT GGCAGTGGCT TGCTCTGTGN TTNTTCTNGN CTNTTTAACT AAGAATGGGG 360
 10 CTGTTGTACT CTCACCTTTAC TNATCCTNAA ATNTAAATAC ATACTGATGN TTTGTATTAA 420
 TCGNTCCAAT ATATGNNTAC ATGNANTATA TCNACNCNC TTNATNTTT AAGCANGTAA 480
 ATAAAACCAT TNNGCAATGG AAA 503

SEQ ID NO:37

15

SEQUENCE LENGTH:497

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00044

20

SEQUENCE DESCRIPTION:

GATCGATAAA GAATTGGCTA GTGGTGAATA CTTTTGAAG GCAATCAGA AGAAGCGGCA 60
 /GAAAATGGAA GCAATAAAGG CTAACAAGC AGAAGCCATC AGTAAGAGAC AAGAGGAAAG 120
 AAACAAAGCA TTTATTCCAC CTAAGGAAAA ACCAATTGTG AAACCTAAGG AAGCTTCTAC 180
 25 TGAAACTAAA ATTGATGTGG CCAGCATCAA GGAAGAGTT AAGAAAGCAA AGAATAAGAA 240
 ACTGGGAGCT CTTACAGCTG AAGAAATTGC ACTTAAGATG GAGGCAGATG AAANGAAAN 300
 GANGAAAAAN NAGTANCATA CCCAAANCTC CTTGNCNNGG ACCTATCTCC TTTTNGTAA 360
 AGGGGTTTTT TGGGGTTTTT AGGCCTTTAG GTTNCCTTT TTTGNGGGA AANTTTNTT 420
 GGGGGGGTTT TTTNNCNTTT TTTNGGGGGG GNGGGGGTT TTNNTCCTTG GNGGGGGTT 480
 30 TCTTTNAAA AATTTN 497

SEQ ID NO:38

35

SEQUENCE LENGTH:498

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00045

SEQUENCE DESCRIPTION:

GATCTTATGG ATGCTGAGCA TGTCTGCAC TGGTGCTAAT GTCTAATATA ATNTTATATT 60
 40 TACACACATA CGTGCTACCC AGAGATTAAT TTAGTCCATA TGAATATTG ACCCATTGTT 120
 CATTGAGACA GCAACATACG CACTCCTAAA TCAGTGTGTT TAGACTTTTC AAGTATCTAA 180
 CTCATTTCCT AACATGTACC ATGTTTTATA AACCTCTTGA TTTCCAGCAA CATACTATAG 240
 AAAACACCTG CTACTCAAAA CACAATTCT CAGTGTGATC CATTGCTGTC GTGAGAGACA 300
 45 ACATAGCAAT ATCTGGTATG TTTGCAAGCT TTCAAGATAG CCTGAACTTA AAANGTTGGT 360
 GCATTAGTTG TATCTGATGG NTATAAATTT TGCCTCCTAG GTTCACTTTG GTGTCCAGGN 420
 GCTAAACCTG TGGANCCTAA CTTTCCCTN ATTGGGGGGG GAATAACCTG GAAAAATAAG 480
 GGTTTTTTTC CAGGGNTN 498

50

SEQ ID NO:39

SEQUENCE LENGTH:494

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00046

SEQUENCE DESCRIPTION:

GATCTGTGCT GTAGAAAAC ATTAACCCCTT GTTCAAAAAA GAAATGGATA ANCTTGGCCT 60
 TTCTAAGTGG TAAGAATGAC CTGTCACTAT AATATACTGT ATGTTTACAT TTNATTAAA 120
 TTTAATCTCT TATGTATAGG GTGATAACCT TCCCAGAAA CAACAGTGAT TGCNATTGTT 180
 TTCTAGAAAC TNCTTTAAAG TGCCACATTT GGCAGTACAA ATGAGTCTGA GTGTAATAGC 240
 CCAGAGATTT ATATATAGTT GAATGTCTAA NATGGTAAAA TGTGCCACTG TGTCAAGTTA 300
 CAGTGGCTTA TGTTTTTCAT AGTAATTCAN ATGANCTTCC TATTTTGTNT AGTAAATGGC 360
 CATTTAATAG NATTCCTTGG CCATTTGAGG CTCACTGGCA AATTTTAGGT GCNGGGGGNG 420
 GAANCCANTT TTTTANATGG NAATCCTTGG GTTTTNNCCN CCNTNNTNCC TGGNCCNTTC 480
 CCCCCAAAAN CCTN 494

SEQ ID NO:40

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00047

SEQUENCE DESCRIPTION:

GATCAGTTGA CAGTGGCAAT TAAACTGTAA ATAACCTGCC CTGGGGGCCT TTTTTTAAAA 60
 AACAAAAACC AAAAAATTC CCAAACCATA CTTGCTAAAA ATNCTGGTAA GTATGTGCTT 120
 TTNTGTGGGG GTGGGATTG GAAGGGGGGT TGGGTTGGGC TGGATATCTT TGTAGATGTG 180
 GACCACCAAG GGGTTGTGA AAATAATTG TATTAATGT CTTTGTATAA GCCTTCTGCT 240
 CAAA 244

SEQ ID NO:41

SEQUENCE LENGTH:283

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00048

SEQUENCE DESCRIPTION:

GATCACTGTA AATGAACCTC CCTGTTGGCC GCTCTGTGGA TGANACTTTA AGACTAGTTC 60
 AGGCCTTCa GTTCACTGAC AAACATGGGG AAGTGTGCCC AGCTGGCTGG AAACCTGGCA 120
 GTGATACCAT CAAGCCTGAT GTCCAAAAGA GCAAAGAATA TTTCTCCAAG CAGAAGTGAG 180
 CGCTGGGCTG TTTTAGTGCC AGGCTGCGGT GGGCAGCCAT GAGAACAAAA CCTCTTCTGT 240
 ATTTTTTTTT NCCATTAGTA AANCACAAGA CTTCAGATTC AAA 283

SEQ ID NO:42

SEQUENCE LENGTH:486

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00049

SEQUENCE DESCRIPTION:

GATCAGTTTT CNTTGTAACA CTGGGTTTAA TCTGAATGGC GCTGATTCTN CCAAGTGCAC 60

EP 0 679 716 A1

5
10
TGAGGAAGGA AAATGGAGCC CGGAGCTTCC TGTCTGTNCT CCCATCATCT GCCCTCCACC 120
ATCCATACCT ACGTTTGCAA CACTTCGTGT TTATAAGCCA TCAGCTGGAA ACAATTCCT 180
CTATCGGGAC ACAGCAGTTT TTNAATGTTT GCCACAACAT GCGATGTTG GAAATNATAC 240
AATTACCTGC ACGACACATG GAAATTGGAC TAANTTACCA GGAATGCAAG GGAAGTAAAA 300
TGCCCATTC CATCAAGACC AGNCAATGGA TTTGTGNAC TATCCTGCAA ANCCCAACAC 360
TNTNTTCCA AAGGNTTAAA GGCCACATTT TGGGTGGCC ATTGGTNGGG TTATTTNTCT 420
TGGGAGTTGG GCCCCGGANG GAANTTTGNN TNTGTNCCN NAANCTTGGG GAACCCTTGG 480
GTTTNN 486

15
SEQ ID NO:43
SEQUENCE LENGTH:470
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00050

20
SEQUENCE DESCRIPTION:
GATCCACCAG CTGAGAATTC GTCCGCTCCC GAGGCTGAGC AGGGCGGGGC TGAGTAAATG 60
CCGGCTTACC ATCTCTACCA TCATCCGGTT TAGTCATCCA ACAAGAAGAA ATATGAAATT 120
CCAGCAATAA GAAATGAACA AAAGATTGGA GCTGAAGACC TAAAGTGCTT GCTTTTGGCC 180
CGTTGACCAG ATAAATAGAA CTATCTGCAT TATCTATGCA GCATGGGGTT TTTATTATTT 240
TTACCTAAAG ACGTCTCTTT TTGGTAATAA CAAACGTGTT TTTTAAAAA GCCTGNGTTT 300
25
TTCTCAATAC GCCTTTAAAG GTTTTAAAT TGTTCATAT CTGGTCAAGT TGAGATTTT 360
AAGNCTTCA TTTTAAATT GTAATAAAN GTTACCACC TTGGATTTT TCAANAAAGG 420
TCAACCAANC TGCAANGCAC CTGTTAATAA NGGGTCTTA ANTAATTTAA 470

30
SEQ ID NO:44
SEQUENCE LENGTH:479
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00051

35
SEQUENCE DESCRIPTION:
GATCTGTAAG TAACCTCACA TTAAAAATG AAATATTTT TAATTTAAAG CTTACTCTGT 60
CCATTATCC ACAGGAAAGT GTTATTNTNA AAGGAAGGT CATGTAGAGA AAAGCACACT 120
TGTAGGATAA GTGAAATGGA TACTACATCT TTAANCAGTA TTTCATTGCC TGTGTATGGA 180
AAANCCATTT GANGTGTACC TGTGTACATA ACTCTGTAAA ANCACTGAAA AATTATNCTA 240
40
ACTTATTTAT GTTAANNGAT TTTTTTAAAT CTAGACAATA TACAAGCCAA AGTGGCATGT 300
TTTGTGCATT TGTAATNCT GTGTTGGGTA GAATAGGTTT TCCCCTCTTT TTGTTAANTA 360
ATATGGCTAT NCTTTAANGG GTTGCNTACT GGGCCAGGTN TAATTTTTTG TAATGGNGTG 420
AAAGGGTGCC ATTTTTTGT CNCACTTNGG GGGTCTCANT GGGGGGNTTC TNNCNGGGN 479

45
SEQ ID NO:45
SEQUENCE LENGTH:477
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
50
CLONE:HUMGS00053
SEQUENCE DESCRIPTION:

55

5 GATCTCTAAG GAACTCCTGT TGCTAAATAT GAAGAGTATG GAACATTCAT ATAGTCTCTG 60
 TGAAGCATGG GGGGAGGGAA GACATTTCTT TTTCTTATAG GCTTTATGCT CAAATGTCAT 120
 AGTCTCCTTT CAAAGAATTG TGTTCGATTT TAAATGCACC CAGCTTAAGT AGAAGACATT 180
 GAAGGATGCA TTAATTTTCA GGAACATTTT TGAATTATGA AAAGATTCCC AATTGAAAAA 240
 NTTATTCAAC AAGTAAAAGC TAAGAAATTT CATTGAAATC ATAAGGCAGT TTAAGCATAA 300
 NTTGATAAAA ATAGCTGTGT ACTACTAATT AATAGAAAAAT CATTCAACCA AGAGANGAGT 360
 10 CANGTGAATA TCGTTTGTGTT ATTTGCTAGT GAGTTTCTTT GTAACGTTGG ATTTTATTAA 420
 NTGGTTAATN TTTGGTTAGG TATGTCCTAT GTTANTNAAA ANTGGNCCAA NTTTAAA 477

SEQ ID NO:46

SEQUENCE LENGTH:476

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS00055

SEQUENCE DESCRIPTION:

20 GATCACCATT AGCAAATGGA AATNACATTT GAAAGCCATT AGACTTATAG GTGATGCAAG 60
 CATCTAAGAG AGAGGTTAAT CACACTATAG AGGCATAAGT GGTATCAGTT TTCATTTTCN 120
 TAATTGTTTA ANCTGTGTTT TATACCAGTN TTTGCAAGTA ATTGGGTGTT AGCTTGAGAT 180
 GGTAAAGGT GGTTCGGGA GGGACTTCGT TGAATGGTT TTCCTGTAAA ANATGTTTCC 240
 AACTCCNCTG AAATGTTGCT GAAAAGCATG GTGCTGGTAA CAGTTCAACA ATCCCGTGGC 300
 25 TGCTCATTCT TGGCTACTT TTA CTCTCCC ACTTGNNAGC AGGTTAGCGT TTGAAGGGTG 360
 GTATGGGAAA AGCCTNGCAT TGCCTGGGCC AAATTCCTTT TGGGGTTCTN CTCCTNTCCC 420
 CNCTTCNCCN TNTCTTCCT TCCCCCN TN ANGTCCNNCC NCTTNCNTTA GGTTCN 476

SEQ ID NO:47

30 SEQUENCE LENGTH:472

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00056

SEQUENCE DESCRIPTION:

35 GATCAAATCT GCACTGTGTC TACATATAGG AAAGGTCCTG GTGTGTGCTA ATGTTCCCAA 60
 TGCAGGACTT GAGGAAGAGC TCTGTTATAT GTTCCATTT CTCTTTATCA AAGATAACCA 120
 AACCTTATGG CCCTTATAAC AATGGAGGCA CTGGCTGCCT CTTAATTTTC AATCATGGAC 180
 CTAAAGAAGT ACTCTGAAGG GTCTCAACAA TGCCAGGTGG GGACAGATAT ACTCAGAGAT 240
 40 TATCCAGGTC TGCTTCCCAG CGAGCCTGGA GTACACCAGA CCTCCTAGA GAAATCTGTT 300
 ATAATTTACC ACCCACTTAT CCACCTTTAA ACTTGGGGAA GGNNGCNTT CAAATTAAAT 360
 TTAATCNTNG GGGGNTTTTA AACTTTAACC CTTTNCNT TNTNGGGGTN GGNANTTGNC 420
 CCCNTAAAG GGGGNNCCCC TNCNNGGGG AATAAAACAA NTTNNTTTT TN 472

45 SEQ ID NO:48

SEQUENCE LENGTH:472

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50 CLONE:HUMGS00057

SEQUENCE DESCRIPTION:

5 GATCAAANCT GCACTGTGTC TACANATAGG AAAGGTCCTG GTGTGTGCTA ANGTTCCCAA 60
 TGCAGGACTT GAGGAAGAGC TCTGTTATAT GTTTCATT CTCTTTATCA AAGATAACCA 120
 AACCTTATGG CCCNTATAAC AATGGAGGCA CTGGCTGCCT CTTAATTTTC AATCATGGAC 180
 CTAAAGNNGT ACTCTGAAGG GTCTCAACAA TGCCAGGTGG GGACAGATAT ACTCAGAGAT 240
 TATCCAGGTC TGCCCTCCAG CGAGCCTGGA GTACACCAGA CCCTCCTAGA GAAATCTGTT 300
 NTANTTTAGC AACCCAGTTA TCCNCNTTAA NNCTGNGGAG AGTGGTCTTT ACATCTTAAT 360
 TTTATTCTNTG TGGTGGTTNT TACCTTTAAC CCGGTTTCTT ATTTTGGGT TTGTTATTGG 420
 10 CCCTTTTATG GGGTGGTCCC TTTTCCNGGT TGGNTTCCC TTTTTTGTG TN 472

SEQ ID NO:49
 SEQUENCE LENGTH:319
 SEQUENCE TYPE:nucleic acid
 15 TOPOLOGY:linear
 CLONE:HUMGS00060
 SEQUENCE DESCRIPTION:
 GATCTCATGG TCCGGAATGA CACCCCTGT GGAACCACCA TTGGACCTAT CTTGGCTTCT 60
 20 CGGCTGGGGC TGCGGGTGCT GGATTTAGGC AGCCCNNAAC TGGCCATGCA CTCTATCCGG 120
 GAGATGGCCT GCACCACAGG AGTCCTCCAG ACCCTCACCC TCTTCAAGGG CTTCTTTGAG 180
 CTGTTCCCTT CTCTAAGCCA TAATCTCTTA GTGGATTGAG CCCTCTTGA AAGACTTCTC 240
 TGCCATCCCT TTGCACCTGA GAGGGGAAGT TCTCAGCTGA GCTGAAGCTG GATTATTAAA 300
 25 GTGGATTGTC ACTCAGAAA 319

SEQ ID NO:50
 SEQUENCE LENGTH:461
 SEQUENCE TYPE:nucleic acid
 30 TOPOLOGY:linear
 CLONE:HUMGS00061
 SEQUENCE DESCRIPTION:
 GATCTTCCTC TAATTGACAG CCTCATTACG GGTCTTACAA AATATGGAAC AGTGTCAGAA 60
 35 AAAACCAGAG AACTCGGCAG AGTCTAACAC AGAGGAAACC TAAAAGGACT GATTTAACCC 120
 AAGATGATTT CCACTTGAAA ATCTTAAAGG ATATTTTATG TGAATTTCTT TCTAATATTT 180
 TTCAGGCATT AACAAAGGAG ACGGTGGCTC AGGGAGTAAA GGAAGGCCAG TTGAGCAAAC 240
 AGAAGTGTTT CTCTGCATT CAAAACCTTC TTCCTTTCTA TAGCCCTGTG GTGGAAGATT 300
 TTATTGAAAA TCCTACGGTG AAGTTGATAA GGCCTTTGC TGGATGGGCT TGGGATAAAA 360
 40 ACCCTTTCCC AAGTTTAAA GGGTTTCAGG TCTTTAAATC CCTGAAATTT TGGGATTCT 420
 TTCTTGTTCC AGGTGTTTA AACCTTTTAT TTTTCCTCC N 461

SEQ ID NO:51
 45 SEQUENCE LENGTH:458
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00062
 SEQUENCE DESCRIPTION:
 50 GATCTAGCAT ATTTCACTAT TCTGTGGATG AATACATAGT TTGTGGGGAA AACAAACGTT 60
 CAGCTAGGGG CAAAAGCAT GACTGCTTTT CCCTGTCTGG CATGGAATCA CGCAGTCACC 120

55

TTGGGCATT AGTTTACTAG AAATNCTTTA CCTTAAGCAG CACACACATT TACTACACAC 180
 ACAGNCCTAA CAAAGCACTG TGCTTAGAGG GTAAAAAGGA ATCACAAAAC AAGAATCTTT 240
 CCAAAGTTGT CTCATTGAGC AATGTTAAGG CATCTGTATC AAATTATTTT GGATGTAAAG 300
 ATTCTGTGT CTCATAATAT GAATGTATTT TTTGATATAC AAGGAACTG GCCATAAAAA 360
 TGGTGNGGNA ANCCGCCNN TAATTTNCC CCTGGGGCCC CAATTGGTNN NNTCNANTCT 420
 NGGNTNAGC NTTGTCTC AAATGGGATN CANTNNN 458

SEQ ID NO:52

SEQUENCE LENGTH:459

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00064

SEQUENCE DESCRIPTION:

GATCTATCAC CCAAACATCG ACGAAAAGGG GCAGGTCTGT CTGCCAGTAA TNAGTGCCGA 60
 AAAGTGAAG CCAGCAACCA AAACCGACCA AGTAATCCAG TCCCTCATAG CACTGGTGAA 120
 TNACCCCGAG CTGAGCACC CGCTTCGGGC TGACCTAGCT GAAGAATACT CTAAGGACCG 180
 TAAAAAATTC TGTAAGAATG CTGAAGAGTT TACAAAGAAA TATGGGGAAA AGCGACCTGT 240
 GGACTAAAA CTGCCACGAT TGGTTCAGC AAGTGTGAGC AGAGACCCCG TGCAGTGCAT 300
 TCAGACACCC CGCAAAGCAG GACTCTGTGG AAATTGGCAC GTGCCACCGN CTGGCGTTTCG 360
 NTTGTGGCAG TTACTAACTT TTCTACAGTT TTCTTAATCA AAAGTGGTCT TAGGTAANCC 420
 TGTAAGGNA AGGGGTTTAN NAATTTTANG GTTGGTCTN 459

SEQ ID NO:53

SEQUENCE LENGTH:458

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00065

SEQUENCE DESCRIPTION:

GATCAGCTGG CCAACTCAGC CAATCCGCAC ATTAGCTCT CCAACTACCA TACAACGTGC 60
 TTGGTTTAGG TCGGAGCGCA AATNTNCTTG ACCATCTCTA CGTTGGTATT CCCCCTCCAT 120
 CTGGAGAAAA ATCTATACGA AANCAAGAGT GGACTGCAAT NATTCAAAT NCCAGCTAA 180
 TTGTCAATCC ATACCTCAC AATGTCCCTC GAAGTTGGAG TGCCAACTG TATCTTACAC 240
 CAAGTAATAT TGTNCTGCTT ACTGCTATAG CTCTCATCGG TGTCTGTGTT TTCAATCTTT 300
 GGCAATAAAT TGGCATTTTA CCATTTGNCA GGGAAAAGGA AAGGCNCGTT GGNTTGGGGG 360
 GAAAACCGGC CAAGGGANGG CCCCCCGGG TTTTCNATTT TTGGNCGGNT TTTTGGGNNT 420
 TTTGCCTTTT TAAANTTTT CCNAANAAAN NGGGANTN 458

SEQ ID NO:54

SEQUENCE LENGTH:454

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00066

SEQUENCE DESCRIPTION:

GATCAGTTNC GTGTCCGNG GAGCAGGCCT TGCTGAGTGA AGACACTGGN ACTAGCTGGG 60
 TCCTGGGGTG ACTTGGAGGC TTTGGCCTA AAAGGGCAGC CTGAACCTGG AGTCTTATCT 120

CCCCCAGGAG CCGAAAGCAC TTTTCTTGAT TTCCCCCAGG AAATCAAGCG CTGCTTCTCA 180
 GCTCCTGTGG TTTTAGTATT TATATATCTG TATCTTCTTT GTAGAAATTT ATTTATTTTT 240
 GAATAAGAAT ACCTGCCTGG AAAAAATTTA AAAGGACGGG AGGGCGAANT GCAAGGGAAG 300
 GCCTCTCCTA TGCCGNCCCA GAGNAGCACT GTACCAATTT CATGTGATTC CTTAACTCTG 360
 TTTAAGGAAG CTCTGAAACT GTCATTTCCT TTGCAGATTG TTNTGAACCT GGAAACCCNG 420
 AATTTATNGN TAANNCTCAN TTNCCACCNG GAAA 454

SEQ ID NO:55
 SEQUENCE LENGTH:505
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00067

SEQUENCE DESCRIPTION:
 GATCGTTGGG GAACCCAGCC CCTTGGAAC TGGGAAGACCC GTGTTTCCTG GACCGCGAAT 60
 CAGTGTGTGG GGCATCAGTG TTTTCTGCAA GGGTTGTGAC CTGAAACTTT TAAAAACCA 120
 CCCACCTTTG GGAAGCATT TCTGAATTTA TCCATCACC ACCATTTCTT CTTGGATACC 180
 ATCAAGTAAC AGCTATTATT TGCCAAGTGG AGCTGTCATT TAATTTGATG CACCTCTGGN 240
 TTCAGATGAA ACATTAAAT GTCTTCCTCG ATTCTCCATC GGGTGTAGAG TTTTAAACT 300
 ATCANTGGCA TTTCAAGTCT TCTGANACAA CATGGCTGTA TGTGCGTGGT CCATAGCACA 360
 GTACATGCAG CATCTAATAA GNGTTTCCAT TTGTAGAATT NTTTTCNCA NACTTNTAGT 420
 TAAANNCAA ATTTTTTAAT TTGNAAANAA GNGNTGNGTT GGTATTNNN GNTGTTNTTT 480
 GTNTNTGGTT GNTNTGTTTA TTNTN 505

SEQ ID NO:56
 SEQUENCE LENGTH:450
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00068

SEQUENCE DESCRIPTION:
 GATCAGAGAC TGGAGAGGTG GAGTGAGAAG TCTCCGCTGC TCGGGCCCTC CTGGGGAGCC 60
 CCCGCTCCAG GGCTCGCTCC AGGACCTTCT TCACAAGATG ACTTGCTCGC TGTACCTGC 120
 TTCCCCAGTC TTTTCTGAAA AACTACAAAT TAGGGTGGGA AAAGCTCTGT ATTGAGAAGG 180
 GTCATATTTG CTTTCTAGGA GGTGTTGTTG TTTGCCTGTT AGTTTGAGG AGCAGGAAGC 240
 TCATGGGGGC TTCTGTAGCC CCTCTCAAAA GGAGTCTTTA TTCTGAGAAT TTGAAGCTGA 300
 AACCTCTTTA AATCTTCAGA ATGATTTTAT TGAAGAGGGC CGCAAGCCCC AAATGGAAAA 360
 CTGTTTTTAG AAAATATGAT GATTTTTGAT TGCTTTTGTA TTTAATTCTG CAGGTGTTCA 420
 AGTCTTAAAA AATAANGATT TNTANCAGGN 450

SEQ ID NO:57
 SEQUENCE LENGTH:447
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00069

SEQUENCE DESCRIPTION:
 GATCTTTGAT AGTNGAGAAA ATTATGCAAA GTTCCTCAGA AGTNGGTTAT NATGCTATGG 60

CTGGNGATTT TGTGAATATG GTGGAAAAAG GAATCATTGA CCCAACAAAG GTTGTGAGAN 120
 CTGCTTTTATT GGATGCTGCT GGTGTGGCCT CTCTGTTAAC TACAGCAGAA GTTGTAGTCA 180
 CAGAAATTCC TAAAGANGAG AAGGACCTG GAATGGGTGC AATGGGTGGA ATGGGAGGTG 240
 GTATGGGAGG TGGCATGTNC TAACTCCTAG ACTAGTGCTT TACCTTTATT AATGANCTGT 300
 GACAGGAAGC CCAAGGCAGT GTTCCTCACC AATAACTTCA GAGAANGTCA GTTGGAGAAA 360
 AATGANGAAA AAGGGCTGGC TTGAAANTCA CTNTTAACCN NTTANGGTG CTTGGGTTTC 420
 ANGTTGGCCA NAGTTTTNNN TNNTGGN 447

SEQ ID NO:58
 SEQUENCE LENGTH:445
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00070

SEQUENCE DESCRIPTION:

GATCACTGAG CAGTTTTCCC AGAGCTCCAT GGGAAGGCAA GCTCTCCCTC CCAATGGGAG 60
 CCCCACTGTC ACTAACTGTA AACTCAGGCT CAGGCTTCAN CTGCCTACCC CCATCCTCAT 120
 ATTTCTGTCT GTCCCAGCAC CTCAGGAGCA TTCTCATTGT GGCCGGCTAA CTCCGCCTGG 180
 ATGTGAACAG GCAAGCACAG TGGGAAATNA GTCACGTACT TGTATTGCAC AGTGGACACC 240
 TCTAGAGGTC CATTGGTTTA AAGGGATAGG GAAGGAGGAG GGATGAGACC ATCTCCCCCT 300
 CCCAGGAAGT AAATCTAAGT ATCTAAGGTT TTCTTTATNG CCTTNGAGTC AAACANTAA 360
 CTGGCTAGTA CGGGAGGTGT NTGCTNGGTT TTTTTCGGGT GGTTTTTTCC TAATGNAATA 420
 AACTTCATTT NTTGCNTGNT TGGNN 445

SEQ ID NO:59
 SEQUENCE LENGTH:459
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00071

SEQUENCE DESCRIPTION:

GATCTTCGGT GGCCTCATGT AAACGTGGCA GCCAGCCTCT TCTAGAACCC TAGCCCAGGG 60
 ACTGGAGCAG GAAAGGGACC TTCAAAGTGA AGACTGCCTT GTCCCGCAGC TCCTTCTGGC 120
 TTAGATTGAA ACATGGGCTT CCTAATGGGT TAAATCCTTT AAAACAAGGA GTTGTGGGGG 180
 AAGGGTGTG TGCACCTCA GAGAAAGGTA CACAGTTGCC CGGTTGGGAA TGTGCTTGGC 240
 GCTGACCCTG CGGGCATCTG ACTGGTCTTC CAGCTCAGGA AAAAGAATT GAAAGAGGCT 300
 TAGCGTGAAG GGGAAATCAA GAGGAGGTTG TNATTTNGGT CGAAGGTGCC TTGGTTTAAG 360
 TCCTNGTAAT TTGTNCTTAT TAATTTTTTT TNATATAATA TNATTTTNTT GGGGGGTAAA 420
 CCATTTTAA ATTAACCAA CCATTGTCT TNCTNGAAA 459

SEQ ID NO:60
 SEQUENCE LENGTH:441
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00072

SEQUENCE DESCRIPTION:

GATCAGACAC TTCAAGGTCT AGGCTAGACA TGGCAGAGAT GAGGAGGTTT GGCACAGAAA 60

ACATAGCCAC CATTTTTTCC AAGCCTGGGC ATGGGTGGGG GGCCTTGTCT GCTGGCCACG 120
 CAAGTTCACA TGCNATCTAC ATTAATATCA AGTCTTGA CTCTACTTCC CGTCATTCC 180
 CACAGGACAG AAGCAGAGTG GGTGGTGGTT ATGTTTGACA GAAGGCATTA GGTGACAAC 240
 TTGTCATGAT TTTNACGGTA AGCCACCATG ATTGTTTCT CTGGCCTCTG GGTGACCTT 300
 AAAAAACCC ATTTGGAAC TGNNGACTTT GAAANGGTGC TCTTTGCTTA AGGCTTTNAT 360
 ATNGNGCCTT GTTTAATTGG GANGGTCNCT TNAAGGCC NTTCCTTTA NTTAANGNG 420
 GGGTTNTTAN GGNTGTAGAA A 441

SEQ ID NO:61
 SEQUENCE LENGTH:436
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00073

SEQUENCE DESCRIPTION:

GATCCGTCAC TCTTCCTTGT GGTAAATCCCT AGACTGGGAG CTCAGGTACT CTTTATAGTCA 60
 TCTTTGTATG TCTTTAGCAG AGTCTTGAC ATGTGGTAGG TGCTTAATAA ATNTTGTG 120
 TTTATCAAAT TTTATGGTAG GGAGAGTAAG TCAGCATCGG TATAAATCG CTTACTCCAC 180
 GTAACCTTC TTCTGATAGG GTTTGATTTT CTATTAGAAG CTCAATTTA GTTTTTTTC 240
 ATATTATAAC TAAATATGTT TCCTGAGAGA TAAGAGAAAT AATGTTCTTA CAATAGTTGT 300
 ATGTATCTAA GATAAGACAT ATAGATGCTT AAGACATTT GTTTCACCTG CTATTCAC 360
 GTGTA CTGA ACCATGGTCA TTTTAGCCC TTTTCCTAGG GACCATGCTT ATTTCTCAAT 420
 AAGGAAATAC CTTCN 436

SEQ ID NO:62
 SEQUENCE LENGTH:434
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00074

SEQUENCE DESCRIPTION:

GATCTTTTTC CATCCAGCAG TGGAGTTTAG TACTTAAGAG TTTGTNCCCT TAAACCAGAC 60
 TCCCTGGATT AATGCTGTGT ACCCGTGGGC AAGGTGCCTG AATTCTCTAT ACACCTATTT 120
 CCTCATCTGT AAAATGGCAA TAATAGTAAT AGTACCTAAT GTGTGGGGTT GTTATAAGCA 180
 TTGAGTAAGA TAAATANTAT AAAGCACTTA GAACAGTGCC TGGANCATAA AAACACTTAN 240
 TAATAGCTCA TAGCTAACAT TTCCTATTTA CANTTCTCT AGAAATAGCC AGTATTTTGT 300
 TGGAGTGCCT ACNATGTTAG TTCCTTNTAC TAGTTGCTTT ACATGGATTA TCTTNATATC 360
 CTGTTTTAAA GNTTNTTAC AGGTACCAGG TTTTCATGGA ATTTTCCTTT NANTAAANG 420
 GGAGGNNAAN GNTN 434

SEQ ID NO:63
 SEQUENCE LENGTH:433
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00075

SEQUENCE DESCRIPTION:

GATCTGTGAA TCTTGGCTGG GACTTCCTCT GAGTGATGCC TGAGGGTCAG CTCCTCTAGA 60

EP 0 679 716 A1

CATTGACTGC AAGAGAATCT CTGCAACCTC CTATATAAAA GCATTTCTGT TAATTCATTC 120
 AGAATCCATT CTTTACAATA TGCAGTGAGA TGGGCTTAAG TTTGGGCTAG AGTTTGACTT 180
 TATGAAGGAG GTCATTGAAA AAGAGAACAG TGACGTAGGC AAATGTTTCA AGCACTTTAG 240
 AAACAGTACT TTTCTATAA TTAGTTGATA TACTAATGAG AAAATATACT AGCCTGGCCA 300
 TGCCAATAAG GTTCCTGCTG TGTCTGGTGA GGCAGCATTN CTTTGTATGC AAATTTCTTA 360
 TTGGNCCCTN TNTTNNTCCA AAAAGGTAAA TGNCTTNNAT TNCCCAGGTTA AAAAATNNTT 420
 CCCNGGNNAT TTN 433

SEQ ID NO:64
 SEQUENCE LENGTH:432
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00076

SEQUENCE DESCRIPTION:

GATCCTGGAG GTCTTTTCTA GTCTGAGCTT CTTTAGCTAG GCTAAAACAC CTTGGCTTGT 60
 TATTGCCTCT ACTTTGATTC TNATAATGCT CACTTGGTCC TACCTATNAT CCTTCTACTT 120
 GTCCAGTTCA AATAAGAAAT AAGGACAAGC CTAACCTCAT AGAAACCTCT CTATTTTAA 180
 TCAGTTGTTT AATAATTAC AGGTTCTTAG GCTCCATCCT GTTTGTATGA AATTATAATC 240
 TGTGGATTGG CCTTAAAGCC TGCATTCTTA ACAAACCTCT CAGTTAATTC TTAGATNCAC 300
 TAAAACTCTG AGGAACTCTA CATGTAACCTA TTTCTTCAGA GTTTGTCATA TACTGNTTGG 360
 CATCTGAATG GCTACTCAGC ATTTGGTTAA CATTNGNGTA AATTGGGAAT AAANTTCCCC 420
 AGTAAGCCAT TN 432

SEQ ID NO:65
 SEQUENCE LENGTH:459
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00077

SEQUENCE DESCRIPTION:

GATCCATCGC AGAGTCCTAA AGAAGAACCC ACTGAAAAAC TTGAGAATCA TGTGAAGCT 60
 AAACCCATAT GCAAAGACCA TGCGCCGGAA CACCATTCTT CGCCAGGCCA GGAATCACAA 120
 GCTCCGGGTG GATAAGGCAG CTGCTGCAGC ANCGGCACTA CAAGCCAAAT CAGATGAGAA 180
 GGCGGCGGTT GCAGGCAAGA AGCCTGTGGT AGGTAAGAAA GGAAAGAAGG CTGCTGTTGG 240
 TGTTAAGAAG CAGAAGAAGC CTCTGGTGGG AAAAAAGGCA GCAGCTACCA AGAAACCAGC 300
 CCCTGAAAAG AAGCCTGCAG AGAAGAAACC TACTACAGAG GAGAAGAAGC CTGCTGCATA 360
 AACTCTTAAA TTTGNTTATT CCATAAAGGT CAAATCATT TGGNCAGCTT CTTTTTTGAA 420
 TAAAAGNCCT GNTTTATACC AGGGCAGTGA GGAACCAAA 459

SEQ ID NO:66
 SEQUENCE LENGTH:626
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00078

SEQUENCE DESCRIPTION:

GATCTACAAA GGCCATGGGA AAAATTCAGA GAGTTAGGAA GGAAAAACCA ATAGCTTTAA 60

AACCTGTGTG CCATTTTAAG AGTTACTTAA TGTTTGGTAA CTTTATGACC TTCACTTTAC 120
 AAATTCANGC CTTAGATAAA AGAACCGAGC ANTTTNTGTC TAAAAAGTCC TTGATTTAGC 180
 ACTATTTACA TACAGGCCAT ACTTTACAAA GTATTGCTG AATGGGGACC TTTTGAGTTG 240
 AATTTATTTT ATTATNCCCG TTTNGTTTAA TGTCTGGTGC TNCTATCAC CTCTTCTAAT 300
 CTTTAAATGT ATTTGTTTGC AATTTTGGGG TAAGACTTTT TTATGAGTAC TTTTCTTTG 360
 AAGTTTTAGC GGTCAATTTG CCTTTTAAAT GANCATGTGA AGTTATACTG TGGGCTATGC 420
 ACCAGCTCTC ACCTACNGGG GGNCTTACCT TGGGGGTAGN GNCCATACCA GNCCACTGTA 480
 TGTTTACTTC CTCACCCATT TGGNGTTGCC CCANCTTGGT TNAACACTNG GGCANCATTN 540
 TGGTTTNAGG GGNCCTTAGG GTTNACCAGN TCNTTTTAAAC NGGNTATTTN CCCGGGGTTT 600
 TTTNAAANTG GCCCAAAATN CTAAAA 626

SEQ ID NO:67
 SEQUENCE LENGTH:534
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00079

SEQUENCE DESCRIPTION:
 GATCAACAGT TCTAGTACTC TTCTTTGTCA GTATA¹CAAC CTACAGCTAT TGAATGCAAA 60
 GCCACAAGAG TGTTTAAATGG GGACAGTGGG CACTCTCTG CTTGAAAACC CACTTGGGCA 120
 GAATGGACTC ACCCACCAAG GTCTTCTGTA TGAAGCAGCC AAGGTGTTTG GCCTTCGGAG 180
 CAGGAAGCTA AAGCTGTTTC TGAATGAGAC CCAAACGCAG GAAATTACAG AAGACATCCC 240
 CGTGAAGACT TTGAATATGA AGACTGTGTA TGTTTCTGTG TTACCAACAA CAGCAGACTT 300
 CTAGCATGTA CTTATCAATG TTGTTCCGGTC AGCCCTTCCC TAATTACACC TATCCCCTAC 360
 ACATACATGC ACATAGNCAC ACACATGNAC ACACTTGAAG GTATTTCCTT CAAGGTGTGT 420
 GTAAAAATAT GCTGCTTGGN TTTGAATTCA AATGGGGTTG NTTAGGTCAA GACTTTGNG 480
 GCCTNANAGG NATCTTCACA CTTAACCTTA GGCACTTTGT ANGCAATTGT GGGN 534

SEQ ID NO:68
 SEQUENCE LENGTH:417
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00080

SEQUENCE DESCRIPTION:
 GATCTTAGTT GATATTTTGG GCTTGGGGCA GTGAGGGCTT AGGACACCCC AAGTGGTTTG 60
 GNAAAGNAGG AGGGGAGTGG TGGGTTTATA GGGGGAGGAG GAGGCAGGTG GTCTAAGTCC 120
 TGAATGGCTA CGTAGTTCNG GGCAATCCT CCAAAGGGA AAGGGAGGAT TTCCTTAGAA 180
 GGATGGCGCT CCCAGTGACT ACTTTTGGAC TTCTGTTTGT NTTACGCTT TCTCAGGGAA 240
 AAACATGCAG GTCCTCTAGT GTTTCATGTA CATNCTGTNG GGGGGTGACA CCTTGGTTCT 300
 GGTTAAACAA GCTGTACTTT TAATAGCTGT TNCAGGAAGG GTTAAGGCCA ACTACAAATT 360
 AATGTTGGTT GCAATGTAG TGTGGTTCCC TAACCTTNCG GGGTTTTCCT GAGGAAA 417

SEQ ID NO:69
 SEQUENCE LENGTH:417
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00081

SEQUENCE DESCRIPTION:

5 GATCTGCCTG CCCACCAACT GGTGATGGAA GGTTACAAGT GGCACCTCAA TGAGACGGTG 60
 CTCACGTGTGT GGTCTGGCACC AACTACTGCT ACCGTGTGGG AATGTGGCAG CATCTTGGAG 120
 CTGGACGAGC ATCTCCAGAA AGATTTTCATC ATCTTTGAGC TGCTCCCAAG AGCACGGGGC 180
 ATCCCTCCAA GAGCCGTGCC GCTATTCTTG TGACCCGCCG GCCTGCCCTC ACCTTTGGCT 240
 CGACATGTGC TTGCATTCT AGCGAGCTGG CGTGGGGGCT GTCTGGTTGT GTCCCAAGAG 300
 10 GTGTTGAGGT AGGTNTTGAG AGCTGAGACT AGTCATGTCT CTCTTTCCAT TACATGAGTT 360
 CATATTTTNN TTTTCTNTTT TGTGTTAGTA ATTTGGAAAT GAAATTATAA GGAATGN 417

SEQ ID NO:70

SEQUENCE LENGTH:415

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00082

SEQUENCE DESCRIPTION:

20 GATCTTTCTG GGAACACAGC CCNGCTGGCG GCTAACCTGC TGTTTGAGAT GCTATGTGCT 60
 CTCCCAAAAG TGACAACCGT CTGAGTCTTG TGCTCTTCAA GACAAAACAG ATTGCGTCGC 120
 TGACAAGTTC TCAAGAAGAA CTTATGAGTA AGCAGTCTGA GAACTAAAGA GTTTATGCCA 180
 AGAAAACCTT CTGCTGAAAG TGTCATTGCT GGCTGTGAAG TCGGGATAAT CAGTAGAATT 240
 25 CTCACCCAAA CAGCAACATT TCTAAGGAAC TTGGATTAAT TGGGGGAAAA AAAANGGGGT 300
 ACTTGACTG CTTTGATTTG TTTTCCTTTG GNTGAAAAGN TGGGGGGTTA AANGGGGGAT 360
 NGTGAGGGGG ANTTTNCCTN TNNAGGGNTT TTTNTNANC CCATTNNGN NTNCN 415

SEQ ID NO:71

SEQUENCE LENGTH:415

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00083

SEQUENCE DESCRIPTION:

35 GATCAGAATC ATTAAAAAAT ATTTTGTGTT AGTAAGTTTG AAGATTTCCN GCTTTNAGGC 60
 CTTTCCTATT TTGTCCCAT TATTTTNC A GGCAATCTTT TCCATGGAGG GCAGGGTATC 120
 CATTCCTTAC CATGGGTGTA CCTGCTTAGG TTAAAAATCA TACCAAGGCC TCATACTTCC 180
 AGGTTTCATG TTGCGTCTTG TTGAGGGAGG GAGAGCAGGT TACTTGGCAA CCAATATTGTC 240
 40 ACCTGTNCCT GTCACACATC TTGAAAAATA AAACGATAAT AGANCTAGTG ACTAATTTNC 300
 CCTTACAGTT CTGCTTGGN CCCACCCNAC TNGGGGTNGG CTCCATTGGT NNGTTCCGGG 360
 GCCGTNNNTT AGGGGGNANT TGGGGGNTCG GTTAGGCCTN TNGGTTTGGG GAAAN 415

SEQ ID NO:72

SEQUENCE LENGTH:410

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00084

SEQUENCE DESCRIPTION:

50 GATCTCCCN CTCTAGGGGT CAGGCTCCAT TAGGATTGTC CCCTTCCAN CTCTTCCTAC 60

55

CCAACCACTC AAATNAATCT TTCTTTACCT GAGACCAGTT GGGAGCACTG GAGTGCAGGG 120
 AGGAGAGGGG AAGGGCCAGT CTGGGCTGCC GGGTTCTAGT CTCCTTTGCA CTGAGGGCCA 180
 CACTATTACC ATGAGAAGAG GGCCTGTGGG AGCCTGCAAA CTCACTGCTC AAGAAGACAT 240
 GGAGACTCCT GCCCTGTTGT GTATAGATGC AAGATATTTA TATATATTTT TGGTTGTCAA 300
 TATTAAATAC AGACACTAAG TTATAGTATA TCTGGACAAG CCAACTTGTA AATACACCAC 360
 CTCACTCCTG TTACTIONTACCT AAACAGATAT AAATGGCTGG TTTTAGAAA 410

SEQ ID NO:73

SEQUENCE LENGTH:406

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00085

SEQUENCE DESCRIPTION:

GATCGTGACG CTGAATAAAT GTCTTTTTTT TAATGTGCTG TGTAAGTTA GTCTACTCTT 60
 AAGCCATCTT GGTAATTTTC CCCAACAGTG TGAAGTTAGA ATTCCTTCAG GGTGATGCCA 120
 GGTTCATTTT GGAATTTATA TACAACCNCG TTGGGTGGAG AAGCCATTGT CTTGGGAAAC 180
 CTTGGTGTAG TTGAAGTAT AGTTACTGTT GTGACCTGAA GTTCACCATT AAAAGGGATT 240
 ACCCAAGCAA AATCATGGAA TGGTTATAAA AGTGATTGTT GGCACATCCT ATGCAATATA 300
 TCTAAATTGA ATAATGGTAC CAGATAAANT TATAGATGGG AATGAAGCTT GTGTATCCAT 360
 TATCATGNGT AATCAATAAA CGGNTTNAAT TCNCTTGGAN TGGAAA 406

SEQ ID NO:74

SEQUENCE LENGTH:408

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00086

SEQUENCE DESCRIPTION:

GATCACATTG TAAAACTATG GATGGTCTGA TAAGGCTTTN ACTGACCCCA CTGACTTCAG 60
 AGTTATACTC TGTTTGCNAC ATCATAATGC TGGTTTTCTT GACTTTTTGT NTTTTAATAT 120
 ATTTATAAAA AAAGAAAAAG TTGGTGATTG CATTGGGAAA TTCCAGGGT ATTACTGGAC 180
 CTATGTGGTG TATTGTTAAA CCAGTGTCTT TGTNATACTG TTGCTCTTGA TGTTCCTGAT 240
 ACAGGTAAGG ANGCAAGTTG TCAACTCTNA TACAAAGTAT ATATACAGTT CAGTATTGTC 300
 TCTGTTTATT TTGTTTTAAT TTCATTGGNC AAANTCAANC CAGCATTCCC CATTGTGTGA 360
 AATAAATGAT TTTCTGGAA TAAAAGGNA AGGNCTTNA ATTCCAAA 408

SEQ ID NO:75

SEQUENCE LENGTH:407

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00087

SEQUENCE DESCRIPTION:

GATCAAACTA GCTCAGGCCA AACTTTAAGT TCATACCTGA GCTAAGAAGG ATAATTGTCT 60
 TTTGGTAACT AGGTCTACAG GTTNCATTT TTCTGTGTTA CACTCAAGGA TAAAGGCAAA 120
 ATCAATTTTG TAATTTGTTT AGAAGCCAGA GTTTATCTTT NCTATAAGTT TACAGCCTTT 180
 TNCTTATATA TACAGTTATT GCCACCTTTG TGAACATGGC AAGGGACTTT TTTACAATTT 240

TNATTTTATT TTCTAGGTAC CAGCCTAGGG GATTTCGGGT TAGGTACTCA TTTTGTATTC 300
 ACTGTCACTT TTTCTCATG GTCCTAATTA TAAATNGNCC CAAAATCAAG GNTTGCCTNA 360
 AAAAGGGGGN AAAATGGTTG GCCCCNNGGT TNTTNGNNNC CCCNGTN 407

5

SEQ ID NO:76
 SEQUENCE LENGTH:413
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00088

10

SEQUENCE DESCRIPTION:
 GATCTACCGA CTCACTTCTG AGAATATTTT TNACAGATTA TCTTTGGGCC TTTCCATTAG 60
 AAAGCTGTTT GTTTGTCCCC CTGTTGGTAC ATTGGTTAC CTCATTTTGC CGTTTCAAAT 120
 TGTAAGGCT CACAGGGGTG TTTTGGAA TCATTTGCTG AGTCATTTTC TCAAATCATA 180
 TTCCATTGTA TCAGTTAACA TATAGTTTAA AATGTATGTA TTATAAATNT CTGTANCCAA 240
 ATCATTGTA GGCCTGATAA ATTTNTAACA ANGTTGTAC ATTTNTCATG AAAGTCACTA 300
 GTAATGCTNG GNGNGGTAGT GCAATGGANT TTTCCNTTTT TCNTCCCTGT GCCCATTTTG 360
 GAGTTGAGAG GGTGTNGGT AATNAACTGT ATGGTGTAACA NTGNANCCNA NNN 413

20

SEQ ID NO:77
 SEQUENCE LENGTH:417
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00089

25

SEQUENCE DESCRIPTION:
 GATCGGCAAG CCNCNCACTG TCCCTTGCAA GGTGACAGGC CGCTGCGGCT CTGTNCTGGT 60
 ACGCCTCATC CCTGCACCCA GGGGCACTGG CATCGTCTCC GCACCTGTGC CTAAGAAGCT 120
 GCTCATGATG GCTGGTATCG ATGACTGCTA CACCTCAGCC GGGGCTGCA CTGCCACCCT 180
 GGGCAACTTC GCCAAGGNCA CCTTTGATGC CATTTCTAAG ACCTACAGCT ACCTGACCCC 240
 CGACCTCTGG AAGGAGACTG TATTCACCAA GTNTCCCTAT CAGGGAGTTC ACTGACCACC 300
 TCGTCAAAGA CCCACACCAG AGGTCTCCGT GCAGNGGACT TCAGGNTNCA GNTTGTGGTT 360
 ACAACATAGG GGNTTTTAT ACAANGGAAA NGTAAAGGTG NNNTTAAAGN GGTGAAA 417

35

SEQ ID NO:78
 SEQUENCE LENGTH:404
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00090

40

SEQUENCE DESCRIPTION:
 GATCAGAAGA AACACTCCAA AAATTGAGAT GAAATGTTGG TGCAGCCAGT TATAAGTAAT 60
 ATAGTTAACA AGCAAAAAA GTGCTGCCAC CTTTATGAT GATTTTCTAA ATGGAGAAAC 120
 ATTTGGCTGC ATCCACATAG ACCTTTATGT TTTGTTTCA GTTGAAACT TGCCTCCTTT 180
 GGCAACATTC GTAAATNAAG CAGAAATTTT TTTCTCTTT TTTCCAAATA TGTTAGTTT 240
 GTNCTTGTA GATGTATCAT GGGTATTGGT GCTGTGTAAT GAACAACGAA TTTTAATTAG 300
 CATGTGGTTC AGAATATNCA ATGTTAGGTT TTTAAAAAG TATCTTGATG GTTCTTNTTC 360
 TATTTATAAT TTCNGACTTT CATAANGTGT ACCCANGANT TTCN 404

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SEQ ID NO:79

SEQUENCE LENGTH:622

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00091

SEQUENCE DESCRIPTION:

GATCCCCGCA ACTCGCTTGT CCTTGGGTCA CCCTGCATTC CATAGCCATG TGCTTGTCCTC 60
TGTGCTCCCA CGGTTCCTCAG GGGCCAGGCT GGGAGCCAC AGCCACCCCA CTATGCCGCA 120
GCGGCCCTAC CCACCTTCAG GCAGCCTATG GGACGCAGGG CCCCATCTGT CCCTCGGTCG 180
CCGTGTGGCC AGAGTGGGTC CGTCGTCCCC AACACTCGTG CTCGCTCAGA CACTTTGGCA 240
GGATGTCTGG GGCCTCACC A GCAGGAGCGC GTGCAAGCCG GGCAGGCGGT CCACCTAGAC 300
CCACAGCCCC TCGGGAGCAC CNCACCTCTG TGTGTGATGT AGCTTTCTCT CCCTNAGCTG 360
CAAGGGTCCC GATTTTGCCA TCGGAAAAAG ACAACCTCTA CTTTTTCTCT TTTGTATTTT 420
TGATAAACAN TTGAAGNTTG GAGCNTGTTA AAATTTATTN TTTGGGGGGA AACCTNAAGA 480
ACTGGGNTTT AATTTNGNG TTCGTGGGAC CCTNTTANNT GGTTTTNAAT NAANCGGTTA 540
NGGAATTAAA CTGTTTGGGA ANANTTGGTT TAAAGNTTAA AAATTTTGGG AAAAAAAGGG 600
GCTTTTAAAA TTTTGGGT TN 622

SEQ ID NO:80

SEQUENCE LENGTH:400

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00092

SEQUENCE DESCRIPTION:

GATCTTCCTT TTTCTNTGA ATGNGCTCTG TTGNCTTTT CTCTTTTTC TCATGTGTTT 60
TTCCCTCCAC CTCCACCCCT TTCTTTCTTT CTCTCTCTGA TTGAGAGGCA TTNAATTACG 120
TTTTAGTAG TACAGGCTTC TTGCCGATAT GAAGGGAAGG TTTGAGAAAG AGACCTACTC 180
TGGGTCAATT AATTTTGAAT ACAGTTTCA ATCGTTCAAG TTTGGNNNG NTTATATCTA 240
ATGTGTGTTT CATTTTGTG GAAAGCTATA TTTTGTATTT AGGAAATGGT ATACTATTTT 300
GCTATTTGTA CTGAGTGAGT ACATTGGCAT AAATATAGAA ATTTATATAT ATACATATAT 360
ATAACTGTGC TNNTTGCCCT TTTTNTGNG GGAAATTGGN 400

SEQ ID NO:81

SEQUENCE LENGTH:396

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00093

SEQUENCE DESCRIPTION:

GATCAGACTG TGGCATTGTA AATGTCAACA TTCCAACAAG TGGGGCTGAG ATTGGAGGTG 60
CCTTTGGAGG AGAAAAGCAC ACTGGTGGTG GCAGGGAGTC TGGCAGTGAT GCCTGGAAAC 120
AGTACATGAG AAGGTCTACT TGTACTATCA ACTACAGTAA AGACCTTCCT CTGGCCCAAG 180
GAATCAAGTT TCAGTAAAGG TGTTTTAGAT GAACATCCCN NAATTTGAGG GTGTTCCAGC 240
AGCTGTTTTT GGAGAAGACA AAGAAAATTA AAGTTTTCCC TGAATAAATG CATTATTATG 300
ACTGTGACAG TACTAATCC CCCTATGACC NNAAGNCCT GATTAAATCA AGAGATTCTT 360

TTTTTAAAAA TCAANTAAAA TTGTNACACC ATAAAA

396

SEQ ID NO:82

SEQUENCE LENGTH:400

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00094

SEQUENCE DESCRIPTION:

5 GATCGATGGT TGACAATCCA GAGTGGTGAA CAGCCCTACA AGATGGCTGG TCGATGCCAT 60
 GCTTTTGAAA AAGAATGGAT AGAATGTGCA CATGGAATNG GTTATACTCG GGCAGAGAAA 120
 GAGTGAAGA TAGAATATGA TGATTTTCGTA GAGTGTTCG TTCGGCAGAA AACGATGAGA 180
 CGTGCAAGTA CCATCAGGAA GCAGCGGGAT AAGCTGATAA AGGAAGGAAA GTACACCCCT 240
 15 CCACCTCACC ACATTGGCAA GGGGGAGCCT CGGCCCTGAA CAGAGCAGCT GCTGATGTCT 300
 GGAGGCTGAT TTTCTGTTC TCTGTTCTCC ACTGGAAGG TTGTTTACGA CAAACCTCCT 360
 TGTCAAAGTN TGTAATAATA AAGGATTGCT CCATCCTAAA 400

SEQ ID NO:83

SEQUENCE LENGTH:397

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00095

SEQUENCE DESCRIPTION:

25 GATCTGGGCA CTGTACTTNA GCCTGGGCGA CAGAGAGACC CATCTCAAAN AAAAAATTGG 60
 AACCTGAGAA GGGGGTCGTG GGGTCCCGG GGGCCACCGT CTGCACTTGG NATCTNAAGT 120
 CGGGGTGGNC TTGTGGGACT NACCCNTTAC CCTGTGGGTT CTGTACTAGC TCCGGGNAAT 180
 TGGTGACAGA NTCGAGTTAA ATTGTAGGAC ATCGCGTTGG TGTCTGAGAG GGAGTTGGAG 240
 30 AGCTGGTTGG TGTGGAGGGA AAGGNTTACA CACATGTNAT TTCAGAAGCG TTCTGTGGGT 300
 AGAGGAATCG TTTTCTCTTT GAGACTGTTA TGAGTATGTA CAAATTTTAT TTCCTGTAAA 360
 AATATTNCA TTTTATAAN TGGTTATTTT CTAGAAA 397

SEQ ID NO:84

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00096

SEQUENCE DESCRIPTION:

40 GATCGAAGAT TTATCCCAGC AAGCACAACT AGCAGCTGCT GAGAAATTCA AAGTTCAAGG 60
 TGAAGCTGTC TCAAACATTC AAGAAAAAC ACAGACTCCA ACTGTACAAG AGGAGAGTGA 120
 AGAGGAAGAG GTCGATGAAA CAGGTGTAGA AGTTAAGGAC ATAGAATTGG TCATGTCACA 180
 45 AGCAAATGTG TCGAGAGCAA AGGCAGTCCG AGCCCTGAAG ANCAACAGTA ATGATATTGT 240
 AAATNCGATT ATGGAATTAA CAATGTAACC ATATGGANGC AACTTTTTTT TGGTGTCTCA 300
 NAGGNGTAAC TGCAGCTTGG TTTGAAANTT TGTTACCTTG TTTCTTATCA TAAATNAAN 360
 NGTTATTNGC TTCCTTTTTT GGNTTGGAAA 390

SEQ ID NO:85

SEQUENCE LENGTH:392

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00097

SEQUENCE DESCRIPTION:

GATCACTTTC ACTNTCAATT ATTTGCCAGG NCTCACAGAA CTCAGAAAAG CTCAGANCAC 60
TCATGGTTAC TATTTAGTAA AGCAAAAAGA CACAAATNAA AATNAGCAAG TTTGGCCGGG 120
ATTGCAGGCA TGAGCCACTG AGCCCGGCCC CCAACTGTTA CATCAAAATA TTATTTGAGA 180
GTATATGTGT CCTCACGTCC CTAAACACT AGAAACTGTC AANCTTTTAA TCTTTGTCAA 240
ACTCTCAAAA GTAGTATCTC TGCATTTGCA TGCCTTTGNG TNCTAATAAG GTTGAGTACT 300
GCTTTAAAAG TTTGCTGGNC ATCTNTTGN TTTTTTAAAG GACCTGCGGT GGNNAGGCC 360
NTTCAANANA TTNTTTCNTT AATTNGGGCC TN 392

SEQ ID NO:86

SEQUENCE LENGTH:393

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00098

SEQUENCE DESCRIPTION:

GATCAGTCTG GCTGGTGGTT TAACAGGTGT CACTCTGCAA ACCTGAATGG TGTATACTAC 60
AGCGGCCCTT ACACGGCTAA AACAGACAAT GGGATTGTCT NGNACACCTG GCATGGGTGG 120
TGGTATTCTC TGAATCTGT GGTATGAAA ATTAGGCCAA ATGATTTTAT TCCAAATGTA 180
ATTTAATTGC TGCTGTTGGG CTTTCGTTTC TGCAATTCAG CTTTGTTTAA AGTGATTGTA 240
AAAACTACTCA TTCTGAACAT ATCCATGCGC AATCATGATA ACTGGTTGTG AGNAGTGCTT 300
TTCATTCTTC TCACTTGCCT TTGTACTTA ATGTGCTTTC AGGACAGCAG ATATGCAATA 360
TTCACCAAAT AATGTAGGC TGGTGGTAAT AAA 393

SEQ ID NO:87

SEQUENCE LENGTH:391

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00099

SEQUENCE DESCRIPTION:

GATCCAGAAA TACTTAACAC GTGAATATTT TGCTAAAAAA GCATATATAA CTAFTTNAAA 60
TATCCATTTA TCTTTGTAT ATCTAAGACT CATCCTGATT TTAATATCA CACATGAATA 120
AAGCCTTTGT ATCTTTCTTT CTCTAATGTT GTATCATACT CTNCTAAAC TTGAGTGGCT 180
GTCTTAAAAG ATATAAGGGG AAAGATAATA TTGTCTGTCT CTATATTGCT TAGTAAGTAT 240
TTCCATAGTC AATGATGGTT TAATAGGTAA ACCAAACCCT ATAANCCTGA CCTCCTTTAT 300
GGTTAATACT ATTTANGCAA GGANTGCAGT ACAGATTGG NTACAGTACG GATTGNCCA 360
AATAANTTCA NTAAGGCCT TAAAGCTGAA A 391

SEQ ID NO:88

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00100

SEQUENCE DESCRIPTION:

5 GATCAACCCA CAGAACAAAG CGGATTTCCT AGGCATCTCC CCAGAGCGAG CCTTTGCTGA 60
 TTTTCTCTTT GCCAGCACCA TCCTGCACCT TGTGTGTCATG AACTTTGTTG GCTGACTCAT 120
 TCTCATTAC TTAATTGAGG AGTAGGAGAC TAAAAGAATG TTCACTCTTT GAATTCCTG 180
 GATAAGAGTT CTGGAGATGG CAGCTTATTG GACACATGGA TTTTCTTCAG ATTTGCACTT 240
 ACTGCTAGCT CTGCTTTTGA TGCAGGAGAA AAGCCCAGAG TTCACTGTGT GTCAGAACAA 300
 10 CTTTCTAACA AACATTTATT AATCCAGCCT CTGCCTTTCA TTAAATGTAA CCTTTTGCCT 360
 TCCAAATTAA GGAATCCATG CCACTCCTCN 390

SEQ ID NO:89

SEQUENCE LENGTH:390

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00101

SEQUENCE DESCRIPTION:

20 GATCTTTCTN AATGTGTATT GATTGGTCTT TTCAGCTACT CTGAACAGAT TACTAAGGCC 60
 ATCTCCTCAT CTCTAAGGGA GAAAAATAGT CTGTAGATGA ATAATGTAAG GTAAAGAGTT 120
 GCATGTCAGT CTTTGTAAATN ATTTACACTT TAACTTTCTC CAGAACTCAG ACATGATTTC 180
 AACATGGTGT TAGATTTGTG CATTTNATTT TCCTGACCAC CTCATTCCAG CCAATGTATG 240
 GTTATCCACT CTGTGTGCNA AANCCAATCA TGCNTTTCAC GGCCCTTTAG TTCAGAGAAG 300
 25 TTCTGCACTG ATTTTATGTC TCTTGATGTC TCAATCTTAC ATGTATACCA ATCACAATGG 360
 AATAAAAAGT GTTTGAGGTT GTACTGTGGN 390

SEQ ID NO:90

SEQUENCE LENGTH:391

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00102

SEQUENCE DESCRIPTION:

35 GATCCGAGGA GGCAGAACAA GTCCACGGAG TCCCNNGCAG GCCAACGTGC AGCGGCTGAA 60
 GGAGTACCGC TCCAAACTCA TCCTCTTCCC CAGGAAGCCC TCGGCCCCCA AGAAGGGAGA 120
 CAGTTCTGCT GAAGAACTGA AACTGGCCAC CCAGCTGACC GGACCGGTCA TGCCCGTCCG 180
 GAACGTCTAT AAGAAGGAGA AAGCTCGAGT NATCACTGAG GAAGAGAAGA ATTTCAAAGC 240
 40 CTTTCGCTAGT CTCCGTATGG CCCGTGCCAA CGCCCGGNTC TTCGGCATAC GGGCAAAAAG 300
 AGCCANGNAN GCCGCAGANC AGGATGTNG TAAGGAAANN ATTTANAGCC CCTCCTGGGN 360
 GACCTTTGGG ATTCAGTCGN CAGTCAATAA A 391

SEQ ID NO:91

SEQUENCE LENGTH:391

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00103

SEQUENCE DESCRIPTION:

50 GATCTGTGCC AAGCTCAGGG TGTAGCGCTG CAAACGATGA AGCAAGAGAT TCTCATTAAC 60

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CTTGTGAAGC AAAAGCCACA AATAACAGAG GAACAACTTG AGGCTGTCAT TGCAGATTTT 120
 TCAGGCCTGT TGGAGAAATG CTGCCAAGGC CAGGAACAGG AAGTCTGCTT TGCTGAAGAG 180
 GGACAAAAAC TGGNGNCAAA AACTCGTGCT GCTTTGGGAG TTAAATTAC TTCAGGGGAA 240
 GAGAAGACAA AACGAGTCTT TCATTCGGTG TGAACTTTTC TCTTTAATTT TAACTGATTT 300
 AACACTNTTT GGTGAATTAA TGAAATGNTA AAGACTTTTT ATGTGAGATT TTCCTTATCA 360
 CAGAAATNAA NTNTCCTCCA AATGTTAATA N 391

SEQ ID NO:92
 SEQUENCE LENGTH:385
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00104

SEQUENCE DESCRIPTION:
 GATCTTTTCC CCTGGCCAAA GGGAAATTGT ATTAGTCTGT GACATCTTGT GATGCTGTTT 60
 ATCTTGGTTT GACATTGGAG ATACGCTAGT AACTGTGATA CCATACTATA AAACAGAAGA 120
 ATTTTCTGCT ACTAAAACT GCCTTTTAC AAAATGACTG TAAATATTG TAAAAATAAA 180
 TAACACTAAA CTTAAGCCC AAAAGGAGAG ATAGAGCCAT GTGTTTCACT GTGGACCTGT 240
 CCGTGGGGCA CAGTGCCACC CCATCACAGT GTTGCTGTCA TCAGGCAAAAN GTGAATGTTT 300
 GTTTATGGCA AATTGCNCTT TTGCGAATGG CTTANTTCTG ACACTACCTT TCTGGGAAAT 360
 GTTAATANAT TTTTAATTNT TCAAA 385

SEQ ID NO:93
 SEQUENCE LENGTH:381
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00105

SEQUENCE DESCRIPTION:
 GATCTTTGAT AGTTTTGGTG AACTCTCTAA AATACATTCA CTGTGGGTCC GACGCAATTT 60
 ATAAAAATNA TGTACTCAAG AAGGGAGACC TGTTTGTTTC ATTTCTCATC TGTTTGGGAG 120
 ATGATTTTAG AGCACTAGAA AGGCACTGGG GAGATTCTCA GCTTAAACA TCCAGCAGTT 180
 TGAAGTATGA TTAGGTACAT CAGGGCTGCA TTGTCAATNT TCTCITTAAG TCTTTTAACA 240
 TTTATAGCAA TTTTTTTTTT CCCGGAGAGT TTAGGTTGCA AGTTTGGGT TTCTTGTTTG 300
 TTTTGTGTTT GCTTCCTGCT TTAATNCTTN AATTNCACT CATTACTGGT ATTGAAAAAT 360
 AAAATATCTT TAAANCANNG N 381

SEQ ID NO:94
 SEQUENCE LENGTH:380
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00106

SEQUENCE DESCRIPTION:
 GATCTAAGAG ACTCAAGAGC TGGGTTTCTT TCAGCACTCT GTACTGTCCC AAATAGCAAA 60
 CAAATNACTT TGTAGCCAGA TTTCTGAATG GAAATNAGAA ATTGAATTCT CCATGGACTT 120
 TTAGGTTTAT GGGGGAGTTT TAGCTGTGTT TCTTGGTTTT ATTTAGCCA AACATGTCTG 180
 CTTTGTATTT TTTTTTAAA GTATAAGTG TCTATATATA TGTTACCTT TTAATGTAA 240

EP 0 679 716 A1

ATGTTTAAAA AGTAAGCATT TATGTGTTTC CATAACTGAC ATCTGATGCA GACCTCATT 300
TCTCCCCCTC TTCTACCCTC CTCTTTTCCC CCTTTTCAAT ACTCTTGAT TGGGTTCTAA 360
TAAATGGGT TGCTTTTCN 380

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SEQ ID NO:95
SEQUENCE LENGTH:379
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

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CLONE:HUMGS00107

SEQUENCE DESCRIPTION:

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GATCCATACT TGGATGATAT TGATGATGAG ATGGACCCAG AGATAGAAGA AGCTTATGAA 60
AAGTTTTGTT TGGAATCAGA GCGTAANGNA NAACAGTAAA GTTAAATTTC AGCATATCAG 120
TTTTATAAAG CAGTTTAGGT ATGGTGATTT AGCAGAACAC AAGAGAGCAA GAAAATGTGT 180
CACATCTATA CCAAATTGAG GATGTTGAGT TATGTTACTA ATGTATGCAA CTTTAATTTT 240
GTTTAACTACT ATCTGCCAAA ATAACTTTA TTCCCTATAA CTTAAATGT GTATATATAT 300
ATAATAGTTT ATTATGTACA GTTAATTCTA CTGTTTTGGC TGCAATAAAA TCGATTTTGG 360
AAATAAATGG AATGTTGNN 379

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SEQ ID NO:96
SEQUENCE LENGTH:384
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

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CLONE:HUMGS00108

SEQUENCE DESCRIPTION:

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GATCTTTGCT GGCAAGCAGC TGGAAGATGG ACGTACTTTG TCTGACTACA ATATTCAAAA 60
GGAGTCTACT CTTCATCTTG TGTTGAGACT TCGTGGTGGT GCTAAGAAAA GGAAGAAGAA 120
GTCTTACACC ACTCCCAAGA NGAATAAGCA CAAGAGAAAAG AAGGTAAAGC TGGCTGTCCT 180
GAAATATTAT AAGGTGGATG AGAATGGCAA AATTAGTCGC CTTGTCGAG AGTGCCCTTC 240
TGATGAATGT GGTGCTGGGG TGTTTATGGC AAGTCACTTT NGNCAGACAT TATTGTGGCA 300
NATNTTGCT GACTTACTGG TTNCAACAAAN CCCAGAAGNC ANGTTAACTG TNTGANGTTN 360
ATNAAAAGNC ATGTNCTGAA CAAA 384

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SEQ ID NO:97
SEQUENCE LENGTH:583
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

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CLONE:HUMGS00109

SEQUENCE DESCRIPTION:

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GATCCTCATG AATGACTATC CTAAATTAA GTATGCAGTT CTNTTTTTCG TGGGTTTATT 60
CGTGCTGGTT CATCGNGAGT NAGANGCCTG CCTTGCTGTT CCTGGGAAGA TGCCATAGTT 120
TTCGTTACTG GATGTTTGGG GTAGATACTG GTCTGTNATT GGTGGAATGG AGAACACACG 180
TGTTGGTGCT TCTGGGTAGC ACTGGTTTGC ATTAGTTTAT GTTTCCATGC CAGAGTTTGT 240
GTGGGCGGGC GCATGTCCAC CACAGAGTGC ACTCGAGGGG ACTTTCAGTC ACAGGATTTT 300
ATAATTGTNA TTGTCACACT TTCAAATTTT TGTACATCAG TGAATTTTTT TTATATTTAA 360
AGGTTGAGCC AAAGCCCCCA GTGTTTTGTA TTTTGAAGCC AAGCTTCACT TCTAAAAGTG 420

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CCTACAGAGG ACTTGTA AAA TGGAAAATGC AGCTCTGCAC GGAGTTTGAA ACCGTCATAC 480
 CTCCTTCTAT TAGGGAAATNG GCATATACTG AGGGTGGTCC GGAAGNNNTT AACTTCCTAA 540
 AATTTTAAAA TAAAAGGCCT TTGCACCATT GGACCCCNNT AAA 583

SEQ ID NO:98

SEQUENCE LENGTH:370

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00110

SEQUENCE DESCRIPTION:

GATCAAGAAA AGCAACTTAT GGAAACAACT ACAGAATTTA CAAAAAGGA TACTCAAACC 60
 AAAAGTATTA TTTCAGAGAC CAGTAATAAA ATTGACGCTG AAATTGCTTC CTTAAAAACA 120
 CTGATGGAAT CTAACAACT TGAGACAATT CGTTATCTTG CAGCTTCAGT GTTTACTTGC 180
 CTGGCAATAG CATTGGGATT TTATAGATTC TGGAAAGTAGT ATTAATGCTC ATCCTGCTGT 240
 GGCTGTTGGC TTCTTAGAAC ACCAAACCGG GAGAGATTTA CTTTGAACAT TGTCAAGTTGC 300
 AGCAAAAATT TACTACACAA GATTATTCGA AGTGTATACG GACTAAAAGA GGAAGTGTTT 360
 TAGAATGAAA 370

SEQ ID NO:99

SEQUENCE LENGTH:384

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00111

SEQUENCE DESCRIPTION:

GATCTGAAGA GCGTCCTGGG TCAACTGGGC ATCACTAAGG TCTTCAGCAA TGGGGCTGAC 60
 CTCTCCGGGG TCACAGAGGA GGCACCCCTG AAGCTCTCCA AGGCCGTGCA TAAGGCTGTG 120
 CTGACCATCG ACGAGAAAGG GACTGAAGCT GCTGGGGCCA TGTTTTTGA GGCATACCC 180
 ATGTCTATCC CCCCCGAGGT CAAGTTCAAC AAACCCCTTG TCTTCTTAAT GATTGNCCAN 240
 AATACCAAGT CTNCCCTCTT CATGGGAAAA GTGGTGAATT CCACCNAAAA ATAAGTGNCT 300
 GTNGGTNCTC AACCCCTTNC NNTTCATCCN TGGGCCCN TN GGCTTGATN GANAATTA 360
 AGAAGGGGTT GNGGCTNGGG NAAA 384

SEQ ID NO:100

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00113

SEQUENCE DESCRIPTION:

GATCTTTGAA ACCTTGGTCC CGTTAACTTA CTAGTCACAT TGACCAATGT TTTATAGAAA 60
 TGCCTAGAAT TTTGAGACTA ATNGTAGTTA TCCATTAACTA TTCCAAAAGT TTTGTNCTTT 120
 TNAAAATTTG TTTGGTAAT TATCACATTT NTNCCTCTTA CCTTCCTTTA AATGGCCACA 180
 GTGTGTACTG CTGGANTGTN CCATCCAAAA GATGTAGCTT CAGANGCACA GTGATTGCCC 240
 CAGGGTCCAT GAGATATTGT TTGTATTATG ANGTTGGAGT GCTGTCTACT GAAATTATAC 300
 TCTTAAATAA NTATGTATGT NGTGTGTAAT ATTCCTAAT AAATNCTTTN GATAAACTAA 360
 AAAACTNNNG CTNN 374

SEQ ID NO:101

SEQUENCE LENGTH:382

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00114

SEQUENCE DESCRIPTION:

GATCTGTGCA AGGTATTAAC GTGTCAGGGC TGAGTGTCT GGGATTCTC TAGAGGCTGG 60
 CAAGAACCAG TTGTTTTGTC TTGCGGGTCT GTCAGGGTTG GAAAGTCCAA GCCGTAGACC 120
 CAGTTTCCTT TCTTAGCTGA TGTCTTTGGC CAGAACACCG TGGGCTGTTA CTGCTTTGA 180
 GTTGGAAGCG GTTTGCATTT ACGGCTGTAA ATGTATTCAT TCTTAATTGA TGTAAGGTTT 240
 TTTTTGTAC GCAATTCTCG GATTCTTTTG AAGNAGATGA CAACAAATTT NGGTTTTCTA 300
 CTGTATTGT GAAGACCATT AAGGCCCCAA GCAACAAGNC AATTNTGTAA GGGAAANTNA 360
 AAGTTCCTTG CNGTAANCCA AA 382

SEQ ID NO:102

SEQUENCE LENGTH:368

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00115

SEQUENCE DESCRIPTION:

GATCTGTCTC TGCTGTTTAA CTTCAATTGA TTAATCAGCT GGTTCAACT CTAAGCGAA 60
 AAAAAATAG CTCCTTAAAA GTACTGTTCT CCTTCAGTGG CATGTAGTTA TCTAATCAAG 120
 ACACCTCATT CAAACAAAAC CTGCCTTAGG AAAATTTAAT ATATTNAAA TNATTTTAAA 180
 AGAAATACAA CATCTTATTC TTTAGCTTTC TTAATCGGTG CTTTATGGAG GCCAGTGTA 240
 CGNTACATGA CTCGTTGAGA AAGTTGAGGA ATTTCTCTA CCACCTTTGT TGCTTGAAGA 300
 AAAACATGTC TTTTCAAAAT GAGAGGCTTT CATTGAAGAA AAGAAAAAAA CAACAGTTAA 360
 AAGCTAAA 368

SEQ ID NO:103

SEQUENCE LENGTH:367

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00116

SEQUENCE DESCRIPTION:

GATCTCGGAT GACCAAACCA GCCTTCGGAG CGTTCTCTGT CCTACTTCTN ACTTTACTTG 60
 TGGTGTGACC ATGTTTATNA TAATCTCAA GGAGAAAAA AACCTTGTA AAAAAAGCAA 120
 AATGACAACA GAAAANCAAT CTTATTCCGA GCATTCCAGT AACTTTTTTG TGTATGTNCT 180
 TAGCTGTACT ATAAGTAGTT GGTGTGTATG AGATGGTTAA AAAGGCCAAA GATAAAGGT 240
 TTCTTTTTTT TCCCTTTTTT GTCTATGAAG TTGCTGTTTA TTTTTTTGGG CCTGTTTGAT 300
 GTATGTGTGA AACANTTGTN GTCCAACATT AANCAGGANT TTTATTTTNC NGAGTNGTNC 360
 TANCAAA 367

SEQ ID NO:104

SEQUENCE LENGTH:366

EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00117

SEQUENCE DESCRIPTION:

GATCTTAGTA ACTATGNATG AAGATGGTGC TTGGCCTGTN CTTCTTGATG AATTGTGTTGA 60
GTGGCAAAAA GTCCGTGAGA CATCATAGCA AGAACTATGT GAAGAAAAATG CAAACCTTTC 120
AATTCCCACG TGTATACAAG CTAATGTGAT GAGGGGGAAA AAAATCCAAC GGGTGCATTT 180
TCATTCATAT GAAAGACTTC TCATAGTACT TTTTTTCCN TTTTTTAAAA GGAGGTTTTT 240
CTTGTTACAT GTGATGGGCA TTGAGCCACA CCNNTTCTTA GACTGAATAT NGAAGTTTTT 300
GTTTTGAGTT ATGTTTATAA CATTATTTTC AGAACANTAA TGATTCAGAT TTGTGACAAA 360
GGCAAA 366

SEQ ID NO:105

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00118

SEQUENCE DESCRIPTION:

GATCCCCGAA ATTGGTGGGC TTGACCTCCT GGCAAATTGC TGGCTCTTTC CACTTGCTGT 60
TCAGGACCAC TAAATGCTGA AATNTGGATG CATACCGAAA TAAAAGNAAT TCATTGTGTA 120
AA 122

SEQ ID NO:106

SEQUENCE LENGTH:364

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00119

SEQUENCE DESCRIPTION:

GATCTTCAAT ATGAAGACAT GAGCTTTTCT CGCAGGAAAT TTTCTTTTTC ACAGAACTGG 60
TGTCAGGAAT CACTGAAGGG CTAACCGTGA TAGTCCTTGC AAGTAAGTCA AGGTTTTATC 120
CTGATTGGAA ATAGAAGACA TTCCGGTTG AGAGAACAGA TTCGTTGGAA GCTTAACTTT 180
TGTTGCCTCT TAACGCCACC AAATTTTAGG GTAATTTGAT TATGAAAGAG TGAATTTTTC 240
TGGACAGAAA AGGGAGAGCT ACCAAATTGT TTTTCTTTT TTAAGGAA GTTAAATGTC 300
CGTTGTATCA CAAATCAGTG TTAACACACC AGAACTTTAG CCAAAATAAA TGTCTTACAT 360
TACN 364

SEQ ID NO:107

SEQUENCE LENGTH:358

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00120

SEQUENCE DESCRIPTION:

GATCAGCAGG GAGTTTATTT GAGGACATCA GTCACCTTTG GGGTTGCCAT GTACAATNAG 60
ATTTATAATC ATNATACTCT TCGGTGGTAG TTCAAAAGA CACTACTAAT ACGCAGGAAG 120
CGTTCAGCT ATTTAATGCT GGCAACTACT GTTTAATGGT CAGTTAAATC TGTGATAATG 180

GTGGGAAGTG GGTGGGGTTA TGAAATTGTA GATGTTTTTA GAAAACTTG TGAATGAAAA 240
 TGAATCCAAG TGTTCATGT GAAGATGTTG AGCCATTGCT ATCATGCATT CCTGTCTCAT 300
 GGCAGAAAAAT TTTGAAGATT AAAAAATAAA ATAATCAAAA TGTTCCTCT TTNCTAAA 358

SEQ ID NO:108
 SEQUENCE LENGTH:430
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00121

SEQUENCE DESCRIPTION:
 GATCTGTCTC TGGGGTCCCN CATACAGAGA AATGCATCTT GCTGAACAAG TGACCAATAA 60
 TCTTAAAGAA CTTCACAGC AAGTAACTCC AGGTGATATC GTAAGCACGT ATGGAGTTCG 120
 AAAAGCAATG GGGATTTCCTTTCCTTCCCC CGTCATGGAA AACAACCTTN TGGATTGAC 180
 AGANGNNCT GAAGAACCTA AAAAGACGGA TGTGCTGAG TGTGGACCTG GTGGAAGTTG 240
 AGGCTGCCTG GTATTGATT ATATATTATG TACATACTTT TTCATTCTTA ACTTAGAAAT 300
 GCTTTTCAGA AGATATTAAA TATTGTAAA TTGTNTTTT AATTAACTT TGGAACAGCG 360
 AATTTGGNTG TTCCAGAGGT TGGGCCTTGT ATTAGGGAAA TAAAGCTTG GACCTGGGGC 420
 CTCGTGAAAA 430

SEQ ID NO:109
 SEQUENCE LENGTH:357
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00122

SEQUENCE DESCRIPTION:
 GATCACTNGA TATTTAGTC ATTCTGCTTC TCATCTAAAT ATTTCCATAT NCTGTATTAG 60
 GAGAAATNA CCCTCCCAGC ACCAGCCCC CTCTCAANCC CCCAACCAA AACCAAGCAT 120
 TTTGGAATGA GTCTCCTTTA GTTCAGAGT GTGGATTGTA TAACCCATAT ACTCTTCGAT 180
 GTACTTGTIT GGTTTGGTAT TAATTNGACT GTGCATGNCA GCGGCAATCT TTTCTTTGGT 240
 CAAAGTTTTC TGTATTATTT GCTTGTCTATA TTCGATGTAC TTTAAGGGTG TCTTTTATGA 300
 AGGTTTGCTA TTCTTGGCAN TTAAGNTTTT TTAGGNCTTT TTAANGNGN ANNNAAA 357

SEQ ID NO:110
 SEQUENCE LENGTH:356
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00123

SEQUENCE DESCRIPTION:
 GATCAAGGGA CGGCTGAACA GACTTCCCGC TGCTGGTGTG GGTGACATGG TGATGGCCAC 60
 AGTCAAGAAA GGCAAACAG AGCTCAGAAA AAAGGTACAT CCAGCAGTGG TCATTGACA 120
 ACGAAAGTCA TACCGTAGAA AAGATGGCGT GTTCTTTAT TTTGAAGATA ATGCAGGAGT 180
 CATAGTGAAC AATAAAGGCG AGATGAAAGG TTCTGCCATT ACAGGNCCAG TAGCAAAGGA 240
 GTGTGCAGAC TTGTGGCCCC GGATTGCATC CAATGCTGGC AGATTGCATG ATTCTCCAGT 300
 ATATTTGTAA AAANTAAAAA AAAGCTAAAC CCATTAAAAA GTATTGTTT TGCAAA 356

SEQ ID NO:111

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00124

SEQUENCE DESCRIPTION:

GATCCTACCT ATCAAGCACT AAAAAAGTTGA ACCATTATAC TTTATATCTG TAATGATACT 60
 GATTATGAAA TGTCCCCTCA AACTCATTGC AGCAGATAAC TTTTGTGAGT CATTGACTTC 120
 ATTTTATATT TAAAAAATTA TGGAATATCA TCTGTCATTA TATTCTANTT AANGTTGTGC 180
 ATAATGCTTT GGAANAATGG GTCTTTTATA GGAAAAAACC TGGGATAACT GATTTCTATG 240
 GCTTTCAAAG CTNAAATATN TAATATACTA AACCANCTCT AATATTGCTT CTGTGTGTTT 300
 ACTGTCAGNT TAANTTACAG CTTTTATGGG TGGTTAACTT TTCGTNCATT TTCAAAAAAN 360
 CCNGGGGNNN NNNNN 375

SEQ ID NO:112

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00125

SEQUENCE DESCRIPTION:

GATCTCTGTT TTGTTGTTGA AAATTCATTT GTATACTTTT GTTTTNATCT AGGACTTCAT 60
 GTTTTTTNAA AGCACTGGCA GCCAGGAACA AAAATCAGGA GTGTGGTAGT GGATTAGTGA 120
 AAGTCTCCTC AGGAAATCTG AAGTCTGTAT ATTGATTGAN ACTATCTAAN CTCATACCTG 180
 TATGANTTAA GCTGTAAGGC CTGTAGCTCT GGTGTGATAC TTTTCCTTTT CAAATTATAG 240
 TTTATCTNCT GTATAACTGA TTTATAAAGG TTTTGTACA TTTNTNAATA CTCATTGTCA 300
 ATTTGAGAAA AAGGACATAT GAGTTTTTNC ATTATTAAT GNAACTNCCT TTGAAA 356

SEQ ID NO:113

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00127

SEQUENCE DESCRIPTION:

GATCACATTA TNATAAATAA ATGAAAAAAT GATTTAATCT GTAATAAACT GGTTTATTGT 60
 GCAGTGA CTG TAATATACTA GAGTTATAAT AAATTGTTTA CTCTGCCTCA CCAAACACAT 120
 GCTAGGATAT AACCCCAAAA ATAAGTATTT AACTTTGCAT TAGGTATAAA GGAGACTGGG 180
 TGCTATAATN AGATTATTTT GAGGCAGACA GAGAGCTGTT ATCCTAACTG ATTTAGTATG 240
 TTCTGTAATT GAGAAAATGT TCACCAAATN ATACTTTTTA GTGATTTACA TGTACATTTT 300
 ATAGGGGACA TGTTCTGTGT ATAGCGAATA AATAACTTTT ATAGTATCAC N 351

SEQ ID NO:114

SEQUENCE LENGTH:352

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00128

SEQUENCE DESCRIPTION:

GATCTTGAAC CTGGTGCTCC ATCCATGGNA GCNNAAGCC TTTGCATCCC CTTCAAACCA 60
 CTCTGTGAAC TGCAGCCTGG AGCCAAATNT GTCTGTGGCA AGAACCCCTGC CAAGTACTAC 120
 ACCTTATTTG GTCGCAGCTA CTGNGGGATG NACGAAAGCC CCCTCTTCAA CTCCTCTCAC 180
 TTTTAAAGC ATTGATATTA GTATCTTCTC AGATACAGAC CGTTTTATGA TTTTAAAAA 240
 AGTAAAGTT CTAAATGAA GTCACACAGG ACAATTATTC TTATGCCTAA GTTAACAGTG 300
 GATAAAGAC TTTTCTGTAA ACAACTCCAG TAATAAATAT CATGNACTNA AA 352

SEQ ID NO:115

SEQUENCE LENGTH:348

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00129

SEQUENCE DESCRIPTION:

GATCAAGTCG TGCTCCTGGC AGGCGCGCCC CTGGAGGATG AGGCCACTCT GGGCCAGTGC 60
 GNGGTGGAGG CCCTGACTAC CCTGGAAGTA GCAGGCCGCA TGCTTGGAGG TAAAGTCCAT 120
 GGTTCCTTGG CCCGTGCTGG AAAAGTGAGA GGTCAAGNTN NTNAGGTGGC CAAACAGGAG 180
 AAGAAGAAGA AGAAGACAGG TCGGGCTAAG CGCGGATGC AGTACAACCG GCGNTTTGTC 240
 AACGTTGTGC CCACCTTTGG CAAGAAGAAG GGCCCAATG CCAACTCTTA AGTCTTTTGT 300
 AATTCTGGGC TTTCTTCTAA TAAAAAGCC ACTTNAGTTC AAGTCAAA 348

SEQ ID NO:116

SEQUENCE LENGTH:344

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00130

SEQUENCE DESCRIPTION:

GATCTCCAC AATTAATTTA TCTTTTGACA AAGGGGATAA AGAGTTTCAG TTTAGCTCCT 60
 TTTGATTGTA TATNATTTT TCCTTTTNA TTGTGAAAAG AGGTAGGTTT TATTTGTGGA 120
 GAGAGAGTTG AAGATTAGGG AACCAAGTAT TTTAATTATG CTAATTTTCC TTCTAAGAGA 180
 TAAATTGATA TATCATTGAG TGTATGAAA AACATGAATG TNGTACAATT TTCTNCCTCA 240
 AAAAATTTT TAAATGTAAG TATCCTTATT TNNTTTTAA AAGAGCACAA TGTAGGTGTA 300
 TTTGGGTATT TCCAAGAAAA GANTAAANCC ATTAATGCAG TAAA 344

SEQ ID NO:117

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00131

SEQUENCE DESCRIPTION:

GATCTGGGCT CCAAGCCAGG AAAGGTGAAC AGAAACCACA AGTNTCCAGC CCTCGGTGCT 60
 GGAGTGGACG TTAATTGTNA GCCACCAGAC TGTCCCGGCA CCTACAGAGA ATGTTTCACA 120
 GTTCTGGCAT TTAATCCTT TGATAGTGGA TTGTGCTGCT GTTAGCCTTA GTTTCAGTGC 180
 TTTACAAGTC TCGCTTATNA TCTCATTGGT ATTTAGGTAT ACAAACAGT TGATTATTCA 240
 CCACGCCAAT ATCTGGGTCT CTGTATCTCA TGTAAGACAT AAGAAAATGG GAACTAATAG 300

GGAAATTTAT TTATAGCATG AAAATAAACCC TGGTGGCTGG AGTCTGCTAA A 351

SEQ ID NO:118

SEQUENCE LENGTH:343

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00132

SEQUENCE DESCRIPTION:

GATCCTAAGG CAATAAAAGA ATAAGGAGAT TTGGAAAACC ATTGTCTGTA ATCTCTGAAG 60
 AAAAGTGGAC ATTAGGGGAG TCAGTTGAAA AGCAAAGCTA TCACCATTTT CTAAAGAGGA 120
 AAAAGGTGAA CCTCACAAAC TATAGACCAA AAAAATAGGA CATCGAGAGA AAGAATATGA 180
 AGCTAGCATA GGTTCACAAA GAATGAGTCA AATCAAACAA CATGCATTTT TTATTATATA 240
 AGCATGACTT GTTCATTGTC AATTCATGTT AGCTTAATCA TTAGGCATTA ATGCCATCAC 300
 TGCAATGCAT ATGTCAGCAA TAAATAATCA AGGCCCGGCT TCN 343

SEQ ID NO:119

SEQUENCE LENGTH:345

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00133

SEQUENCE DESCRIPTION:

GATCTTCCCA CAACACCACA GGAAGTGCAGG GTGCACAACCT CCCCTGCCAA GGAAAACCAT 60
 GCAGTCCTCC CCTCCCTGGT CTCCTGCTTC AGCTCTGTAC AACGAGGGCA AAGATGCTAA 120
 ATCTTGCTTT GCATTACAGTA AAGTGTCAAG TGATTAAGTG TGTATTTGTA CCCTAGATGA 180
 TATGAACCAG CAGTCTTGTG TTGGCATCAT CCTCATCATG TTGTATTCCA GCTTCTTAAG 240
 TGGAAGGAAA AGAGTGTGTA GAAATGGCTC TGTATAATCT ATGGCTATCC GAATTCTCTG 300
 AAAANTANT AAAAGTCCCC TCTNTTATAT GAGCCTGTAC AGAAA 345

SEQ ID NO:120

SEQUENCE LENGTH:358

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00134

SEQUENCE DESCRIPTION:

GATCCCCCT CTCGAGGGCG ATGAGGATGC GTCTCGCATG GAAGAAGTCG ATTAGGTTAG 60
 GAGTTCATAG TTGGAAAACCT TGTGCCCTTG TATAGTGCC CCATGGGCTC CCACTGCAGC 120
 CTCGAGTGCC CCTGTCCAC CTGGCTCCCC CTGCTGGTGT CTAGTGTTTT TTNCCCTCTC 180
 CTGTCCTTGT GTTGAAGGCA GTAAACTAAG GGTGTCAAGC CCCATTCCCT CTCTACTCTT 240
 GACAGCAGGA TTGGNTGTTG TGTATTGTGG TTTATTTGAA TTNCCTTCAT TTTGTTCTGA 300
 AATTAAAAGT ATGCAANAAT AAAAGAATTA TGCCCNNTTT TNATAAANA NNAANAAA 358

SEQ ID NO:121

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00135

SEQUENCE DESCRIPTION:

5 GATCTTCATG CCCTGGGTTT TGCCCGNACG GACCCNCATC TCTGTGACTT CCTGGAGACT 60
 CACTTCCTAG ATGAGGAAAT GAAGCTTNTC AAGAAGATGG GTGACCACCT GACCAACCTC 120
 CACAGGCTGG GTGGCCCGGA GCTGGGCTGG GCGAGTATCT CTTGAAAAGG CTCACTCTCA 180
 AGCAGGACTA AGAGCCTTCT GAGCCCANCG ACTTCTGAAG GGCCCNITGC AAAGTAATAG 240
 GGCTTCTGNC TAAGGCTCTG CCTNCAGNCA ATAGGNANGC TTTTAAACN ATCCTAACAN 300
 10 GGNTTGGGAC CAAATGGNAA TAAAGNTTGG TNGATGCAGG AGATATGAAA 350

SEQ ID NO:122

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS00136

SEQUENCE DESCRIPTION:

20 GATCTGAGCT GAATTGAAG ACTATTAATA AGTTATGTTT GGAAGTTTAA ACTTCAATGA 60
 AGTAATTATT TGCTGTGAAA GAAACAAACA TTGAATTACT AAACAAAGAT GGTGCAATAT 120
 CTTTGTGTTT TTTTATGAG GCTCCTGAGA ATCAACCCAA CTGAAGCATT TCAATTCAGT 180
 TGAATGAGAA ACGTGTGTTAG TATCAAAAGA GCCCAAGAAG AACTGGGTGT GAAAGGTACA 240
 NTCTCAGAGG TTGGTCAATT ACCGTGGCAC ANTTCTGGT CACTTTGTAC AATGTAGATT 300
 25 TGAAGTACAG TGGTGAAAAC ATTAAATGTG ACATTTGN 338

SEQ ID NO:123

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS00137

SEQUENCE DESCRIPTION:

35 GATCAAAAAA CATGAGGNAG AAGAAGCCAA AGCTGAGCGT GAGAAGAAGA NAAAAAGAAC 60
 AGAAAGAAAA GGATAAATAG AATCAGAGAT TTTATTACTC ATTTGGGGCA CCATTCAGT 120
 GTAAAAGCAG TCCTACTCTT CCACACTAGG AAGGCTTTAC TTTTNAAC TGGTGCAGTG 180
 GGAAAATAGG ACATTACATA CTGAATTGGG TCCTTGTCAT TTCTGTCCAA TTGAATACTT 240
 TATTGTAACG ATGATGGTTA CCCTTCATGG ACGTCTTAAT CTTCCACACA CATCCCCCTT 300
 40 TTTTGGAATA AAATTTGGAA AATGGAAATN AAGGAAA 337

SEQ ID NO:124

SEQUENCE LENGTH:336

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS00138

SEQUENCE DESCRIPTION:

50 GATCACCATT TGAGATACGC GGCTTAACGC ACATGTGAGT GTAGCTTGCT ACATGAAAAT 60
 GCTAGGCTCT AGGGCATGTA AAACATGAAT ACAGAATACT AGATTGTTCT AAGTAATGTC 120
 ATTTGGGTTT GTGANTTTGA TTTTCCCTT CATTTTCATGT CATATTGNAA ATGCAAACAA 180
 ACTGCTCTCA AGAACACCCA GAAGCTATCT GTGTTACCAG ATGTGTTGTG NACACTCTAC 240

55

TNTTTTTCAT AGGTGCTACC TGGNAATATA TGTCCATTGT AGTGGTGGNG NGGGNCTNGA 300
CTCTNTCAGG CTCTTNTCTN GCCAGNTGNC TNCNGN 336

5

SEQ ID NO:125
SEQUENCE LENGTH:338
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

10

CLONE:HUMGS00139

SEQUENCE DESCRIPTION:

15

GATCTGGGCT GCAGGAGCTG GGGCCACCCA CAGCCCCCCT ACCGACCTGG TGTGGAAGGC 60
ACAGAACACC TGGGGCTGCG GGAACAGCCT GCGTACGGCT CTCATCAACT CCACTGGGGA 120
AGAAGTGGCC ATGCGCAAGT TGGTGCGCTC AGTGACTGTG GTTGAGGACG ACGAGGATGA 180
GGATGGAGAT GACCTGCTCC ATCACCACCA CGTGAGTGTA AGCCGCCGTT GAGGCCGAGC 240
CTGCACTGGG GCCACCNAGC CAGGCCTGGG GGNAGCNTTT CCCNAGNNTN CNNGTGCCAA 300
AANTTTTTTN ATTAAGAT TGTGTTGGGA ACTTTAAA 338

20

SEQ ID NO:126
SEQUENCE LENGTH:347
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

25

CLONE:HUMGS00140

SEQUENCE DESCRIPTION:

30

GATCAAGCAG ATTCCACGAA TCCTNCGGAC CAGGTTTAAA TANGGCAGGA AAGTTCCTT 60
CCCTGCTCAC ACACAACGAA AACATGGTGG CCAAAGTGGA TGAGGTGAAG TCCACAATCA 120
AGTTCCAAAT NAAGAAGGTG TTATGTCTGG CTGTAGCTGT TGGTCACGTG AAGATGNCAG 180
ACGATGAGCT TGTGTATAAC ATTCACCTGG CTGTCAACTT CTTGGTGTCA TTGCTCAAGG 240
AAANCTGGCA GANTGTCCGG GCCTTATATA TCANNNGCA CCATGGGCAA NGCCCCAGCG 300
GCTTATATTT AAGGCACATT TTNNATAAAT TCTATTNACC CGGTAAA 347

35

SEQ ID NO:127
SEQUENCE LENGTH:335
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00141

40

SEQUENCE DESCRIPTION:

45

GATCAGTTGT AATCAGAATA CAACTGNGTC TTGTAGTTGT AATATGTTCT ATCTTAACCA 60
CCACTTTCGT ACCAGGAACC TGCTCAGGTT TGTCTCTAG AAGCTCCCA CATAGATAGT 120
CTACATTCA GACTACTAAG TTATTAACAA ACCCTTTGGG CCCATGTTCA CTTTAGGGTT 180
GAGCATAGTG TGAGGAGATG TAAATTAAT TATAATCCTA TATGTGTGTG TAATAAATAT 240
TAAAGTGTAT AAATTAACA GCAGATTCTA AGTATCCAAC AAGAGTCAA TAAATGATAC 300
AAAGTCACCA AATAAATAAT ATTAATCTC ATCTN 335

50

SEQ ID NO:128
SEQUENCE LENGTH:356
SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS00142

SEQUENCE DESCRIPTION:

5 GATCTAGTTA AAGTTATTCA ACAGGAGTCT TACACATATA AAGACCCAAT TACAGAATTT 60
 GTTGAATGTT TATATGTTAA CTTTGACTTT GATGGGGCTC AGAAAAAGCT GAGGGAATGT 120
 GAATCAGTGC TTGTGAATGA CTTCTTCTTG GTGGCTTGTC TTGAGGNNNN CATTGAAAAAT 180
 GCGCGTCTCT TCATATTGA GACTTCTGT CGCATCCACC AGTGTATCAG CATTAACATG 240
 10 TTGGCAGATA AATTGAACAT GACTCCAGAA GAAGCTGAAA GGTGGATTGT AAATTTGATT 300
 AGAAATGCAA GACTGGATGC CAAGATTGAT TCTAAATTNA GGTCATGTGG TTATGN 356

SEQ ID NO:129

SEQUENCE LENGTH:333

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00143

SEQUENCE DESCRIPTION:

20 GATCAAAGNA CTCTGACTGC AGAACTGCCG CTCTCAGTGG ACAGGGCATC TNTNACCCTG 60
 AGACCTGTGG CAGACACGTC TTGTTTTTCT TTNATTTTTG TTAAGAGTGC AGTATTGCAG 120
 AGTCTAGAGG AATTTTNNNT TCCTTGATTA ACATGCTTTT CCTGGTTGTN ACATCCAGGG 180
 CATGGCAGTG GCCTCAGCCT TAAACTTTTG TNCCTACTCC CACCCTCAGC GAACTGGGCA 240
 GCACGGGGAG GGTTTGGCTA CCCNTGCCCA TCCNTGAGCC AGGTACCACC ATTGTAAGGA 300
 25 AACACTTNCA GAANTTCAGC TGGTTCCTCC AAA 333

SEQ ID NO:130

SEQUENCE LENGTH:332

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00144

SEQUENCE DESCRIPTION:

35 GATCTCTGTA GATATTCTGT TTTATTTTGG TCATCTTTAG AAGTTATCAG GAATGTGTTT 60
 AAAACAAGAA GAGAACTTTT CTAAGGAATG ATACATAGAA AAGATTTTAT TTTAAAAATGA 120
 GTTGTAAGC TTGTTTTTCT TTGTGCTGC AANTATCTGC CCAAGTTAAT GCAAATGGAC 180
 ACATTTTTTA TGTCAGAAAA ACACACACAC ACACACACAC ACACACACAC ACACACNCGC 240
 GNNACACAGN GANAAAAGTG CTTGNGCTTN NNCTCNCNTC CCCTTGCTGT CTGTTGTGTG 300
 40 CGCAGCCTGT TTATNTCTCT NNTATTGTGT CN 332

SEQ ID NO:131

SEQUENCE LENGTH:332

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00145

SEQUENCE DESCRIPTION:

50 GATCTGTGAC CTTACCCCA AACCTGTNCT CTCTGAAACA TGTGCTGTGT CCACTCAGGG 60
 TTAATGGAT TAAGGGCGGT GCAAGATGTG CTTTGTTAAA CAGATGCTTG AAGGCAGCAT 120
 GCTCCTTAAG AGTCATCACC ACTCCCTAAT CTCAAGTATC CAGGGAGACA AACACTGCGG 180

55

AAGGCCGCAG GGTCTCTGC CTAGGAAAAC CAGAGACCTT TGTTCATTG TTTCTTTGTT 240
 CACTTGTGTTA TCTGCTGACC TTCCTCCAC TATTGTCCTA TGACCCTGCC AAATCCCCNT 300
 NTGATGAAAA ACACCCAAGN ATANTCANTA AA 332

SEQ ID NO:132

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00146

SEQUENCE DESCRIPTION:

GATCGAGGTT GTTTGCAACG ACCGTCTGGG GAAGAAGGTC CGCNTTAAAT GCAACACGGA 60
 TGATACCATC GGGGACCTTA AGAAGCTGAT TGCAGCCCAA ACTGGTACCC GTTGGAAACAA 120
 GATTGTCTCTG AAGAAGTGGT ACACGATTTT NAAGGACCAC GTGTCTCTGG GGGACTATGA 180
 AATCCACGAT GGGATGAACC TGGAGCTTTA TTATCAATAG ATGAGAATCC TCATCTTNCT 240
 GCCCGCTNT CCNCTNCCA TCCTCATCCC CCACANTNGG GATAGATGCT TNGTTTGTA 300
 AAACCTCANCN NAATAAAGAC TTAGATGTTG AAA 333

SEQ ID NO:133

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00147

SEQUENCE DESCRIPTION:

GATCAGGTCT GTAAATGTGT ACTAAAAA TNAGAGTTTA TTTATAAACA AAATAGTTTA 60
 TTTAAAGAGA AGGTCTCTTC CTTATTGATA TCATGGTATG CATTAAATCC ATTTGTTACT 120
 ATTGTGCACA AAAGCCCTGT TCACAGGGGA ATGGTGTAAT CATTTATACT GTTTTGTTC 180
 CTGTATTAG TAGACATAAC TGTGAATAG TTAAGTGAATC ATGATGTAAA GAATATGTGA 240
 CCATCTTCAG GTATGGGATT TCTGAACGTT TCAAATTTCA ATCAATGAGC ACTGTCAACA 300
 CCCACAGGNG AGAATAAAAT TACCTGTGCN 330

SEQ ID NO:134

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00148

SEQUENCE DESCRIPTION:

GATCGAACCA CTGCACTCCA GCCTNGGTGA CAGAGAGAGA CACTGCCTTN GAAAAA 60
 GAATCTCACT CACTATCTAG AGAGGATTGT CAGANTATTC ACGATTGAGN TCTTGAACT 120
 TTGATTATGC AAAAGAGGTA TATATAAATA TTTCATTATG ATTCAGGTTT TAGGCTTTGC 180
 AGCTTCTATA AGGTGTTCTC AGGTGGCCCT TGTACNNCTN AAAGCATCCT TTAGGAAATN 240
 CTTAAGGNG GGCTTTNTAT AAGGAATAGG NGGNTGTTGA ATTTTACAG GGGGGTTTG 300
 GTCATTNAGN CCCCATTNT GTANGN 326

SEQ ID NO:135

SEQUENCE LENGTH:325

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00149

SEQUENCE DESCRIPTION:

GATCATGANC TCTGAAAAA AGAGAAACCT TATCTTTNCT TTGTGGTTCC TTAAACACA 60
 CTCACACACA CTTGGTCAGA GATGCTGTGC TTCTTGAAG CAAGGNCTCA AAGGCAAGGT 120
 GCACGCAGAG GGACGTTTGA GTCTGGGATG AAGCATGTNC GTATTATTA TATGATGGAA 180
 TTTCACGTTT TTATGTNAAG CNTGACAACA CCAGGCAGGT ATGAGAGGAA AGCAAGGCCC 240
 GTCCATNGCT GTCCGTACNC TTACGGNTTG CTTGTNGGAG NCATTNGGT ATTGTTTGT 300
 GTAANANCCA AAANGGGCTT TGGNN 325

SEQ ID NO:136

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00150

SEQUENCE DESCRIPTION:

GATCNAAGCT GTGCCTTGGC AGGGCACAAT GACCTTGTGC AAATCCACCT GTCAGGACGC 60
 CTAGGGGTCT GTACCGGGCT GGCCTGTGCC TATNACCTCT NATGCACACC TCCCACCCCC 120
 TGTATTTCCA CCCCTGGACT GGTGGCCCT GCCTTGGGA AGGTCTCCC ATGTGCCTGC 180
 ACCAGGAGAC AGACAGAGAA GGCAGCAGGC GGCCTTTGTT GCTCAGCAAG GGGCTCTGCC 240
 CTCCTCTCTT CTTCTTGCT TCTNATAGCC CCGGTGTGCG GTGCATACAC CCNACCTCC 300
 TGCAATAAAA TAGTAGCATC GGCAAA 326

SEQ ID NO:137

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00151

SEQUENCE DESCRIPTION:

GATCAAGNNG CCCTGGAGGC GGTGGGCGGC ACCGTGGTTC TGGAGTAGCC TCCAGCTCGG 60
 AGGACTTGTT TNCAGGGGTC CTGGGCCCCG GNCAAGGTCC CGCCCTCCCG TGGTCACTGG 120
 CTCCGCCCCA GCACCAGGCG CCCAGTGGAG CCGTTTGGAA GAATTGCCTG CNGCAGGAGC 180
 GGGGCCGGAC AGGCGCACAG ACCTACTGTN GCGGGAGGAA GGGGCGGCTG CTGCCTGGTG 240
 ACGGCACCCG GANGCCACC AGGACGCGCC ACCGGTNAAT GTNNCTCTNG TGGCTGCTGA 300
 GAAAAATACA CTGTGCAAGT CAAA 324

SEQ ID NO:138

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00152

SEQUENCE DESCRIPTION:

GATCTCAGCT TTTGGTTTCC CATGATACCA TCTCTAGGGG TAGCAGCTGG CTATAATAAC 60
 TAATGTCTGG ATTATCCTAA CTCTTCTGTT TGTNCTTCA GGTATTAAAC AATGTTGTGA 120

EP 0 679 716 A1

CTAATTGGCT TCCATTATTT CCCTAGAGTA GGTTCGTGTA TNACCCTGGA ATATGTTTGT 180
AATAGAGTGG GCTATTACAA TCATCTAGGA TAAAGATAAT CGTGGCTTGG AATAAGGGTG 240
GTAGCAATGG AAGTGATGAG AAGTCATTAG ATGCAGAATA TATTTTATAG ATGGANTGTG 300
ATAAANTAAA AAATAAACTG GGN 323

SEQ ID NO:139

SEQUENCE LENGTH:322

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00153

SEQUENCE DESCRIPTION:

GATCCATTCT CGGAATTCAC AGAATTTTNA TAACATCTNA CTCTCAGGGG GCATGAAGTG 60
CATAATCTTC CCTAGATTAC AAAAAACATA TAGATGACGG GTTTCCTAT NAACTTCAG 120
TACTACAAGA AACATAAAAT ATTTAAATAT ATGANATTTA AATATATTTA AAATTATTAA 180
AGTAATATAA ACATTTTNA GTGACTGTGT TATGTTTTTC TGGTTATTTT GTTTTCTACT 240
AGTATATTTT TCTGTAAAAA TTGTAAAACT ATATCAGCAA TTTCTAATGC CAANAANGTA 300
AAACCTNGTG TGTATAAATG CN 322

SEQ ID NO:140

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00154

SEQUENCE DESCRIPTION:

GATCAGAGGC ACAAGTNCAG AGGCTGTGGT CATGCGGAAC ACTCTGTTAT TTAAGATGGC 60
TATCCAGATA ATCCTGAACA CTGTGTATTT ATTTAATTTA GACTACCAGC AAAGATTAAA 120
GCATGAAATG TAAACATCT GATAAACTT ACAGCCCCCT ACACCAAGAG TGTATCTGTG 180
AAAGAGCTCC TACACTTTGA AAACCTAAGA NTCCCTTNTC ATGAAGTTTG CCTGTNCTAG 240
AATTGTAAGA TTGTTAATTT CCNTCAATCT CTAGTGACAA CACTTAATTT CTTTNCTAAT 300
ANAAAAAGCC TNGTNGGTGN AAA 323

SEQ ID NO:141

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00155

SEQUENCE DESCRIPTION:

GATCAAGTTT AAATGACTGT GCTGCCCCCT TCACATCAAA GAACTACTGA CAACGAAGGC 60
CGCGCCTGCC TTTCCCATCT GTCTATCTAT CTGGCTGGCA GGGAAAGAAA GAACTTGCAT 120
GTTGGTGAAG GAAGAAGTGG GGTGGAAGAA GTGGNGTGGG ACGACAGTGA AATCTAGAGT 180
AAANCCAAGC TGGCCCAAGG TGTCTGCAG GCTGTAATGC AGNTTAATCA GAGTGCCATT 240
TTTTTTTTTG GGTTCAAANG NTTTTTAATT TNTNGGAAT NGNNCCANTT TTTTNAATTT 300
NGCAANTAAA AANGTTTAAA ANCTTAAA 328

SEQ ID NO:142

EP 0 679 716 A1

SEQUENCE LENGTH:369

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00156

SEQUENCE DESCRIPTION:

GATCTCTGGC AGTGGAGGAA GTCTCTTTAA GAAAATAGTT TAAACAATTT GTTAAAAAAT 60
 TTNCCGTCCTT ATTTCAATTC TGTAACAGTT GATATCTGGC TGTCTTTTTT ATAATGCAGA 120
 GTGAGAACTT TCCCTACCGT GTTTGATAAA TGTNGTCCAG GTTCTATTGC CAAGAATGTG 180
 TTGTCCAAAA TGCCTGTTTA GTTTTTAAAG ATGGAAGTCC ACCCTTTGCT TGGTTTTAAG 240
 TATGTATGGA ATGTTATGAT AGGACATAGT AGTAGCGGTG GTCAGACATG GAAATGGTGG 300
 GGAGACAAAA TTATACATGT GAAATAAACC TCAGTATNTT AATAAAGTAG CACGGNTTCT 360
 ATTTGNAAA 369

SEQ ID NO:143

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00157

SEQUENCE DESCRIPTION:

GATCATGAAG GAACACATAG CACCAAGAGA GGCCATGCTA AATCTCGCCC TGTCAGANNN 60
 NTCCACACTT CTCCTTTGGG GAAGNCTTCC CTGTCCCCCT AGACTAAGTT AAATATTTCT 120
 GCACAGTGTT CCCATGGCCC CTTGCATTTC CTTCTTAACT CTCTGTTACA CGTCATTGAA 180
 ACTACACTTT TTTGGTCTGT TTTTGTGCTA GACTGTAAGT TCCTTGGGGA CAGGGCCTTT 240
 GTCTGTCTCA TCTCTGTATT CCCAAATGNC TAACAGTACA GAGCCATGAC TCAATAAATA 300
 CATGTAAAA TGGGATGAAT GAAA 324

SEQ ID NO:144

SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00158

SEQUENCE DESCRIPTION:

GATCATTGAA CGAGACAGAA AGCGACCATC CTGGTTCACC CAGAATTGAC ACCAAAGATG 60
 TTAAAAGGAT AACTTCACAG TAAATCATT CTCTGAAAT AGAGGAAGAT TCTTTACGTT 120
 GTTGTNCTTG TTTTAAATC ATCAGTATAG TTAAACACAT TCTTTCTAAG CAGTTTTGTG 180
 TGGGATAATT TGAAGAATAT ATTATGAGTA ANCTCCGAAA ATTTTGTTTA TCCAAAGGCT 240
 CANTGGATTA TGTTCTATT ATNTACAAGG TTTAAGTAA ACATANNTT TCCNGNNG 300
 AGNTTANAGN NATTN 316

SEQ ID NO:145

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00159

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

5 GATCTTCATT TTATTGCATT AGTTCATGTA GATGGGCATC TCTATGAATT AGATGGGCGG 60
 AAGCATTTCC AATNAACCAT GGTGAAACTA GTGATGAAAC TTTATNAGAG GATGCCATAG 120
 AAGTTTGCAA GAAGTTTATG GAGCGCGACC CTGATGAACT AAGATTTAAT GCGATTGCTC 180
 TTTCTGCAGC ATAGCTTGTC AATAATGGAA ACACCAAAAA CTGTATTATT TGCAACTAAA 240
 TTTTCTCTGC CATACACTAA CTCAAAAATT TTGATATTTT CATTAACTTG ATGATTAAAC 300
 TTTATGTGAG TTAANCTTTG AAA 323

10 SEQ ID NO:146
 SEQUENCE LENGTH:319
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00160

15 SEQUENCE DESCRIPTION:
 GATCTTACTG CTTGTNACTT GAATCCCGTG ATTGTNATAC ATCTCTGGTA TAAGCAACAT 60
 TTGATTTTTG AAGTGTGTAG ACCATCTCTT CATATTTTCA AGATGTAATT TTACATTNCT 120
 GCATTTTAA AACAGTTTGG CCATAATCCT AGATGCACGC TTCTAATTCA TGTACCTGCA 180
 20 CATGTGACCT TTGTGAACAG NAATTTGCAT GNATAATTNG TGTTTACTTG TAACTNCTCG 240
 GTTATATACT GCTTATATCT GTGGATTCAA GTTACTGAAG TGGANTNCCA ATAGAAAGNA 300
 ANCCCTAGGC CATGTAAA 319

25 SEQ ID NO:147
 SEQUENCE LENGTH:316
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00161

30 SEQUENCE DESCRIPTION:
 GATCTCTGAT TACCAGCCTG ACATCAACAA ATCCCTCAG TTACAACGTA TAGGTAAAC 60
 AAAGCTTTTA AAAGCTCATG TGGTATGACC TCAAGGTTGC TAACCTGGTC ACTCATGGTA 120
 ATNAGAAACT CTGATTGGCA GCTTTGTATT TCTTGACTAA AAACCTAAAT AAAGTATTA 180
 35 GGTTTTAGGC GTTCTTTCAA AGAGGTTCTT GAGAAGATTG AGAACTATCC TATTTGGTGC 240
 TTAGTGAAAA GATTTTGAAT TACTGTACGT ACCAGTTGTT GCCATTTCTT TATTAAATTC 300
 AGAAGTTTTT TTGCCN 316

40 SEQ ID NO:148
 SEQUENCE LENGTH:319
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00162

45 SEQUENCE DESCRIPTION:
 GATCTTGGAC AGCNTGGGTA TCGAGGCGGA CGACGACCGG CTCAACAAGG TTATCAGTGA 60
 GCTGAATGGA AAAACATTG AAGACGTCAT TGCCAGGGT ATTGGCAAGC TTGCCAGTGT 120
 ACCTGCTGGT GGGGCTGTAG CCGTCTCTNC TGCCCAAGGC TCTGCAGCCC CTGCTGCTGG 180
 TTCTGCCCT GCTGCAGCAG AGGAGAAGAA AGATGAGAAG AAGTAGGAGT CTNAAGAGTC 240
 50 AGNTGNTGNC ATGGGATTTG GCCTTTTTTG GTTAAATTCC TGNTNCNCTG CAAATAAAGG 300
 CTTTTTTTAC AGANGTAAA 319

55

SEQ ID NO:149

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00163

SEQUENCE DESCRIPTION:

GATCAATGCC CTCATTAAAG CAGCCGGTGT AAATATTGAG CCTTTTGGC CTGGCTTGTT 60
 TGCANAGGCC CTGGNCAACG TCAACATTGG GAGCCTCATC TGCAATGTAG GGGCCGGTGG 120
 ACCTGCTCCA GCAGCTGGTG CTGCACCAGC AGGAGGTCCT GCCCCCTCCA CTGCTGCTGC 180
 TCCAGCTGAG GAGAAGAAAG TGAAGCAAA GAAAGAAGAA TCCGAGGAGT CTGATGATGA 240
 CATGGGCTTT GGNCTGTTTG ACTAAACCT CTTTATAAC ATNGTNCANT AAAAAGGCTG 300
 GAGCTTTAAT AAA 313

SEQ ID NO:150

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00164

SEQUENCE DESCRIPTION:

GATCCAGAAT CCACGGGGTC TGGAGCATAA GGTTTATCTC AAGTNTCAAT TGANCTGCCT 60
 CCTCTTGTA GGCAGGGACA ACTGGGAGGA TGAGCCCCAA GAGCCTCAAG AACCCAACAA 120
 GGTGCCCCCTA GAAGACACAG AGACAGATGA NCTTGGGCA TCCTGGAGG CAGCTGCCAA 180
 GCGGANAGCT CTCGGGTTTG GAGCAGCCCC AAGGAGCTCT CCAAACGAGA CGGAGAAAGA 240
 AGAAGCGGCC TGGGTCCACC AGCCCTGAC GCCCCTGTNN CCACTTTGTA AATAAACTTG 300
 CTGAACACCC AAA 313

SEQ ID NO:151

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00165

SEQUENCE DESCRIPTION:

GATCATCAAC AAAGAAAGTC TGAGAAATTG TCCCGGAATA AAGGGGCCTA AGGAGACATA 60
 ACATCTAAAT GTAATGTAGT ATCCTGGATG GACTCCTGCA ACAGAAAAAG AACTTTAAGT 120
 AAAAATTAAG GGAATATTAA TAAAGTATGC ATTTGGTTA ATAATGTATC AATATTGGTT 180
 TATTAGTTGT GACAAATGTA CCAGAGGAAT GTAAATGTC AACAATAAAG GAATTGGATG 240
 TGGGGTCCAT GAGATGCTGT ACTATTTTG CACTTTTCTT AAATCTAAAC TCTTATAAAT 300
 TTAANCATAA AGN 313

SEQ ID NO:152

SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00166

SEQUENCE DESCRIPTION:

GATCTGGCCA TCTACGAGCC AAAGACTTTN AAATCTTTGG CTGCCTTGGC CAGTAGGAGG 60
 CGACACGAAG GATTNCTGC TGCCTTGGGG GATGGGAAGN AACCTGAAGG CATTNCTNCC 120
 AGAGTGGTGC AGTACCACTN AGGACTGTTG CTGTATTGAT TAGGAAAAGA GACAGAGTAA 180
 TTTNCAGTTT GTTTGATTTA TACTTTTGTT TATCTACAAC CCAATAACAG ACATGAGGGA 240
 TGGCCCTGTC TCTCTGGGAC AGAGCCTCAA AGATGATGTC CATGTTTTGT GTGAATGAAA 300
 CTCAAACACT CTTCAAA 317

SEQ ID NO:153

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00167

SEQUENCE DESCRIPTION:

GATCCCTGTC CCCCTGTCCC CTGCCTCTTT TCCCAATTCC CTTCCTTATG CTGGACTTTT 60
 AAAAGCTTAAA AAAAATCCGA TTGAATATAA ATGCCTAATT TCATTCTTTG TGAAATGGTT 120
 GCTTCCTCCT GATTCCCTAA TTGTGCTGTG TTCGTGTCTT GCACTGGAAT TCAACATTCC 180
 CTTCTCCTTT TGTACTGTGT TGTGCTTGCT GTCTCTCCCG GACANCCCTA AAGACTGTCT 240
 TTTTAGCAAA AAATTTCACT AAAGTGTTTT CTGTAATCTT TTTTAAAAG GTGAGAACTA 300
 ATTATTGTCN 310

SEQ ID NO:154

SEQUENCE LENGTH:309

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00168

SEQUENCE DESCRIPTION:

GATCACCACG GTTTTCAGCC ATGCTCAGAC AGTGGTTCTT TGTGTAGGTT GTTCAACAGT 60
 GTTGTGCCAG CCTACAGGAG GAAAGGCCAG ACTCACAGAA GGGTGTTTCAT TTAGAAGAAA 120
 GCAACACTAA TGATTCAAAC AGCTTCCTGA ATTTTAATTT TGTGTTGTCT CACAGAAAGC 180
 CTTATCATAA ATTCCATAAT TCTAATTAAT TTACCAAGAT AATGTAATTA CATTGTTGTT 240
 TGTAAGGTAT ACAGCAGTAA TCTCCTATTT TGGTGTCAGT TTTTCAATAA AGTTTGTATT 300
 ATGGGCAAA 309

SEQ ID NO:155

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00169

SEQUENCE DESCRIPTION:

GATCACATAC AGGGGAAAAG CCCTATGNAA TGTAACACAT GCAGGAAAAC CTTCTCTCAA 60
 AAGTCAAATC TCATTGTACA TCAGAGAACA CACATAGGAG AAAANCCCTA TGANTGATT 120
 GGATATTAGA AATTNCCAGC CACAAGTCAG CCTCCATAAT GCNTCAGAGT CTTCACTG 180
 TGGAGANGGG CCTGTTGACA TCCTGATTGT TCANTAATA TCCACAACCT CGCCTTATGT 240
 TACTCCANNG TAACAGTAGG GGTTAANCCC ATAGNCTACA ACACCTNTNG GNTGGCTTTT 300

NTTAGGN

307

SEQ ID NO:156

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00170

SEQUENCE DESCRIPTION:

5 GATCCACCAA CTTTGGCCTC CCAAAGTGTT CAGATTACAG GTGTGAGCTG CTACCATGCC 60
 TAGCCCCAGC TTCTACTGCT TGANGGCTCT CTTTGGCATC TCCACACATC ATCCTTAGCA 120
 GCCCAGACTG CATTCTGTGA GCAGCCTCTT CCCTGGTCTC TTCTTTCAGT CTCTCTGCCT 180
 CTAATCCAGT GGCTTTAAGA ATTTTTTGGC TGTGACTTCC AGTAAGAAAT ACAATTTACA 240
 15 TTGTGACCTA GTAAATATGT GTGTAAGATT TATTAAGTGA AATAAAAAATG TTATGATTTA 300
 ATTTTTN 307

SEQ ID NO:157

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00171

SEQUENCE DESCRIPTION:

25 GATCTGTCCC TGTGGTGGTG TCTAAGAATC GGACACCTTG GTTTTTGTGT TAGATTGAGC 60
 TGGGCAGCTG CAATCAGCTA CTAAATATGC AAATTAGGCA CGTCCCATCT GTGGGTCCTT 120
 GTTGGTGGCT AATGAAGTGA GGGGAGGGAG GGATGTCACC CCAAAAGTAG GCCCTCCCAT 180
 TGGCTTTGGC CAGGCCAGAC ACTTCACATC GTTTACATGG TTCTGTGTAA TTTTAAAGTT 240
 30 TATGTGTATA AAGCGACGGT TTTCTGTGAA CTGTATATTT TGTAAATAAA TATATTGCTA 300
 CTTTGN 306

SEQ ID NO:158

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00172

SEQUENCE DESCRIPTION:

40 GATCTTCAGA TAAATTCTGC CATTITNATT TCACTTCCTG AAAGTNAGGG TCGGCTTGTN 60
 AAAAGTTGTT AAACAACATG CTAAATGTGA AATGTCAACC CTCACTCTAA ACTTTCCTTG 120
 TTCAGAGCAT CAGATGAAGA CTTTATTGGG TTTTATAGTG GCTTTCCTGAT TTTNGGTAGT 180
 CCATTGAAGA AGGGAGTTTG AAAGTTGTTG TATACTGTGA ACGATTGTCT GCCCATGTCC 240
 45 TGCCTGAAAT ACCATGATTG TNTATGGAAA GTATCTTTAA TAAAGCTGGA TACAGTTTGG 300
 CTTGGAGAAA 310

SEQ ID NO:159

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS00173

SEQUENCE DESCRIPTION:

5 GATCTACTTT GGAAAAACAA AGGATATCGT CAATGGGCTG AGGTCTGTNC AGACTTTTGC 60
 AGACAAATCA AAACAAGAAG CTCTGAAGAA TGACCTGGTG GAGGCTTTGA AGAGAAAGCA 120
 GCAATGCTAA ACCTCTGTTT CATGCTAACC AGACACGCCG TGCACTCGTT AGATTCCCTT 180
 CTTAGAAAAC TCGTTTTCTG CTCCTTCCC TCGTCCCTC CCTCCCCGAC AGGTCACATA 240
 10 ACAGCTGCAT CATTGACCGC ACAGGCCCAT CTCTCCCTGA GAATAAGCC GATAGCCACC 300
 NTCAAA 306

SEQ ID NO:160

SEQUENCE LENGTH:329

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00174

SEQUENCE DESCRIPTION:

20 GATCTATTGG ACTTTTTTTT GCAGGAAGTG CATTCTCTGG TCCTTCCCTA TTTTCTGTTT 60
 TGGATGTGAG TGCAGTGAC TGCTTACTGT TTTATCCACT TGGCCACAGA CTTTTTCTAA 120
 CAGCTGCGTA TTATTTCTAT ATACTAATTG CATTGGCAGC ATTGTGTCTT TNACCTNGTA 180
 TACTAGCTTG ANATAGTGCT GTCTCTGATT TCTAGGCTAG TTAATTGAGA TATGAATTTN 240
 CCATAGAATA TGCAGTGATA CAACATTACC ATTCTTCTAT GGAAAGAGAA ACTTTTGATG 300
 25 ATGAAACAAT AAAGNTTTTA AATATCAAA 329

SEQ ID NO:161

SEQUENCE LENGTH:303

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00175

SEQUENCE DESCRIPTION:

35 GATCTGAATA AAGCAAATCT GCATAAATGG TAACCAGTAG CTCTACTTTN ATTTTNNATG 60
 TTGCTTAACT GTTTTATTTG AAGGAAACCT GTGTGATTTA AAAAGTTATA GCTTTTGCAA 120
 CTTTATTACT GGTATATAC ATTTGGCCAT TATNATGTGC AAGCAATTGG AAAAAAGTC 180
 AAGTAAATGC TTGTTTTTGT AGTAGTTTGT TCTTGTTAAA AATGTTTATA TGATAATGTC 240
 TGTAACAGC ATCACTTTGA TTACAATAGA TGTAGTGTTG TAATAAACTG TTTAATGGGG 300
 40 AAA 303

SEQ ID NO:162

SEQUENCE LENGTH:298

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00176

SEQUENCE DESCRIPTION:

55 GATCTCTCTA GCTTTGTCAT AGTTATGTGA TTTTCCTTTG TAGCTACTTT TGCAGGATAA 60
 TAATTTTATA GAAAAGGAAC AGTTGCATTT AGCTTCTTTC CCTTAGTGAC TCTTGAAGTA 120
 CTTAACATAC ACGTTAACTG CAGAGTAAAT TGCTCTGTTT CCAGTAGTTA TAAAGTCCTT 180
 GGACTGTTTT GAAAAGTTTC CTAGGATGTC ATGCTCTGCTT GTCAAAAGAA ATAATCCCTG 240

TAATATTTAG CTGTAAACTG AATATAAGC TTAATAAAN CAACCTTGCA TGATTAA 298

5 SEQ ID NO:163
SEQUENCE LENGTH:309
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00177
10 SEQUENCE DESCRIPTION:
GATCTCCTTC ATCCCTCTCC AGAAGAGGAG AAGAGGAAAC ACAAGAAGAA ACGCCTGGTG 60
CAGAGCCCCA ATTCCTACTT CATGGATGTN AAATGCCAG GATGCTATAA AATCACCACG 120
GTCTTTAGCC ATGCACAAAC GGTAGTTTTG TGTGTTGGCT GCTCCACTGT CCTCTGCCAG 180
15 CCTACAGGAG GAAAAGCAAG GCTTACAGAA GGATGTTCTT TCAGGAGGGA AGCAGCACCT 240
AAAAGGCACT CTGAGGTCAA GGATGAGGTG GGGAANCCAT CTCAATTAA CACCATTTTT 300
TGGGTAAA 309

20 SEQ ID NO:164
SEQUENCE LENGTH:295
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00178
25 SEQUENCE DESCRIPTION:
GATCTCGGTA AAAATCTACC ATTCCCTACA TATTTTCCTG ATGGAGATGA AGAGGAACTG 60
CCAGAAGATT TGTATGATGA AAACGTGTGT CAGCCCGGTG CGCCTTCTAT TACATTTGCC 120
TAACATCTTT GGACGTGGCA GAACCTTACA TATTCTGTGA GCTTCGATGA GCCAGAGTGA 180
TATCATAACC ACCAGAAATC ATACTCTCCT TTCTTAGTCA CAACAAAATC ACACATGTCA 240
30 TCTTTGTCAA GGCATAAAT ATATCATTCA TACCCCATTA AAATTTTGTT AGAAA 295

SEQ ID NO:165
SEQUENCE LENGTH:289
SEQUENCE TYPE:nucleic acid
35 TOPOLOGY:linear
CLONE:HUMGS00179
SEQUENCE DESCRIPTION:
GATCCCCACC CCATGTGTTT TAAAAAGGCA GTAGCCTTTG CAGGGACCTG TCTGTCCCAA 60
40 CTGTTTGAAC AGTGTGCTCC TCAGATTCTG TGTTCAGAAG NCCCCTGNTG CATTGAGACT 120
TGAAACCTTT GGATAGGGGA AAAAATTATA TATATATATA TNNNTTGTG CTGTTTGCAT 180
TTCTTAATTT GTGCTTGGA TGTGTTGATG TGCACAGCTA ATGATTCAAT GCGAGACAAG 240
ATTGGCGTCT GTGTTGTGGA GGTTCAAAT AAAGAGCACT CTTCATAAA 289

45 SEQ ID NO:166
SEQUENCE LENGTH:300
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
50 CLONE:HUMGS00180
SEQUENCE DESCRIPTION:

55

5 GATCTGTAAA ATGTGATTTT TTA CTTCAC TTATAACT TGTGATTGGG GAGGTTTGTG 60
 GAAATTCAAT TATGATGAAA AACCTATCTT TTTTGTAATG TTGGCATACT TGGGGAATTT 120
 AGTGGCAAAT ACATTCCCCA GCAGGCCTTT TGTGGTTGC ACTAACTGCA AGGTTGCTGG 180
 GAAGTAGAGT CCATTGGTT GATGAGCTTT GACTGCGGTT TTGGAACCTT ACCTCTCCTC 240
 CTTAGCCCAA TATGCTGTCT TGGGTCCTAT TCAAATAAAG TTATTCTCC TGGTCTCAA 300

10 SEQ ID NO:167
 SEQUENCE LENGTH:292
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00181

15 SEQUENCE DESCRIPTION:
 GATCAAAAAA CCATCTCCAC ATTTAAAAGA GATGTAAGGT GTATTCATAG GGATGGTGGC 60
 TCAACAAATC AAGCAAATG GAATCAAGGG GAGGGGGAAG GGAATNAAAT GGAAAGGGAG 120
 GCTGATTCCC TTCCCTGAC TTACCACTAA TTTACTAGGC TACCTACTTT NATGAGTAAC 180
 CTCTCACAGC TACCCAGCAC ATGCCACAAT CCTATGCTCT TGCCTTCTTT NATCTGCACT 240
 20 GTGTGAAGGG ACTCTTTAA ATAAATNAGC AAGTGTCTTA AGCTATGTCA AA 292

25 SEQ ID NO:168
 SEQUENCE LENGTH:292
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00182

30 SEQUENCE DESCRIPTION:
 GATCTTGGCT GTATTTAATG GCATAGGCTG ACTTTTGAG ATGGAGGAAN TTCTTGATTA 60
 ATGTTGAAAA AAAACCCCTG ATTATACTCT GTTGACAAA CCGAGTGCAA TGAATGATGC 120
 TTTNTGAAA ATGAAATATA ACAAGTGGGT GAATGTGGTT ATGGCCGAAA AGGATATGCA 180
 GTATGCTTAA TGGTAGCAAC TGAAAGAAGA CATCCTGAGC AGTGCCAGCT TTCTTCTGTT 240
 GATGCCGTTT CCTGAACATA GGAAATAGA AACTTGCTTA TCAAACTTA AA 292

35 SEQ ID NO:169
 SEQUENCE LENGTH:333
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 40 CLONE:HUMGS00183

45 SEQUENCE DESCRIPTION:
 GATCCACATG AACGCACGCC TGAGATTTGG CCACTCACCT ATGTTTTGGG TGGATTGCCT 60
 AGGAAAGCAA GTCATATGGC CATTGATAGT TCTCATGTAA TTAGTTTTCG TCACCACTAG 120
 TACAGATGAC CCGTTTACAC GTGGCTTCCC TCGGAAGCCT CCTCAACAGT AGCTGGTGTG 180
 AAAGACTAAA TCAGTAGAGT TGGAAAAGCT TTATAACCGG TGTGTCATAT GCTTGCTATT 240
 TAAAGCTGTG TGTGGTTTTT GTTTTCTGC CACATTCACCT AGTTTTTTAA TAAATATTTT 300
 CCAAAANTGG AAAAAAANA NCCCCNCCN CCN 333

50 SEQ ID NO:170
 SEQUENCE LENGTH:401

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00184

SEQUENCE DESCRIPTION:

GATCTGGANG GGACACGTCA TGCCTTGGGC CTAGAATACC CTGATGNAA AAGAGAAGAN 60
 AAAGGGAGGC CATATCTACA ACACAGCCTC TCGGCACTGC TGCTCCTTAT TTAACTTTG 120
 TTTTGCATTG TCCTGTATTT ATCACAGTTT CTGTTGAACA GCTTTTCAAG TATTTGGGGA 180
 GTTTATCTTG CCATCCTCCC CTCTGGGTC TCTGCACCCA CCTGTCCAC TGCAGTTCCT 240
 TCCGTGCTCT GTGACTTTAA GAGAAGAAGG GGGGAGGGGT CCCGGATTTT ATGTTTGT 300
 GNTNTTCTC CTTAGCAGTA GGA CTTGATA TTTTCAATTT TGGAAGAAGT AAAAGATGAA 360
 TAAACTGGGT TTTTTTGT GTTTGNNTTT GNAAATTC A 401

SEQ ID NO:171

SEQUENCE LENGTH:305

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00185

SEQUENCE DESCRIPTION:

GATCGAGCTC GCCTATNAGC AAGTGGCAAA CCCCTCAAA TAAGCCCTC CTGGGACTCC 60
 CTCAACCCCTC TCCATTTTCT CCACAAAGGC CCTGGTGGTT TCCACATTGC TACCCAATGG 120
 ACACACTCCA AAATGGCCAG TGGGCAGGGA ATCCTGGAGC ACTTGTTCCG GGATGGTGTG 180
 GTGGAAGAGG GGATGAGGGA AAGAAATGGG GGGCCTGGGT CAGATTTTGA TTGTGGGGTG 240
 GGATGAGTAG GACAACATAT TTCAGTAATA AAATACAGAA TAAAAATCAA GTGTTTTTAC 300
 GCAAA 305

SEQ ID NO:172

SEQUENCE LENGTH:289

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00186

SEQUENCE DESCRIPTION:

GATCTGAGGC AAGCTGGACA GGAGAGGTGG ATATTTNTTG ATGGAAGAAT TCAAGTTTAT 60
 AATCAATTCC CACTTAGCAC CTACTGTGTG CTAGGAACCT GAATGTGTAT GTTTGACAAG 120
 TCCTGCTTGG CCTGATGGGT GGGAGANGGA ACCTGAGCCT GGCTGAGATG GCTAGGCGGA 180
 GGGCTTTGAA GTCCAAGCAG CTGAAGTGGC TGGGTGGGT TCTACCTTTG AAAGTCAAG 240
 ACTTNTTTG GAGCTCTTAA TTACAATATC TGATATTTT ACAGTCTGN 289

SEQ ID NO:173

SEQUENCE LENGTH:286

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00187

SEQUENCE DESCRIPTION:

GATCCCTACC CTTNCCGTTG GTCTCTNTCG CTGACTCGAG GCACCTAACA TCCATTACACA 60
 CCCAACACAG GCCAGCGACT TCTGGGGCTC AGCCACAGAC ATGGTTTGTN ACTNTTGAGC 120

EP 0 679 716 A1

TTCTGTTCT AGAGAATCCT AGAGGCTTGA TTGGCCCAGG CTGCTGTNTG TNCTGGAGGC 180
 AAAGAATCCC TACCTCCTAG GGGTGAAAGG AAATNAAAAT GGAAAGTTCT TGTAGCGCAA 240
 GGCCTGACAT GGGTAGCTGC TCAATAAATG CTAGTNTGTT ATTTCTN 286

5

SEQ ID NO:174
 SEQUENCE LENGTH:290
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00188
 SEQUENCE DESCRIPTION:

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GATCGGGTTC TAAAGGAAAG GGTGGAGAGA TTCAACCAGT TAGCGTGAAA GTTGGAGATA 60
 AAGTTCTTCT CCCAGAATAT GGAGGCACCA AAGTAGTTCT AGATGACAAG NATTTATTTCC 120
 TATTTAGAGA TGGTGACATT CTTGGAAAGT ACGTAGACTG AAATAAGTCA CTATTGAAAT 180
 GGCATCAACA TGATGCTGCC CATTCCACTG AAGTTCTGAA ATCTTTCGTC ATGTAAATAA 240
 TTTCCATATT TCNCTTTNAT AATAAACTAA TGATAACTAA TGNCATCAAA 290

20

SEQ ID NO:175
 SEQUENCE LENGTH:284
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00189

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30

SEQUENCE DESCRIPTION:
 GATCAAGGCG CGGACGTATC TACGACCACA TCAACGAGGG GAAGCTGTGG AAACACATCA 60
 NGCACAANTA TGACAACAAG TAGTTCCTTG GNGGCCCTAT CCAGGCCAGA AGGCCANNGC 120
 CACCCAGCAG CTGTTTGCCA GAGCTGGAGC TCAGTTGAAG ATGATGCTCA AGGTACTCTT 180
 CATGCCACC ATTCGTGTTG GAAGAAGCNT TTACTIONNA CAGCTCTTTA CCTTCTGTGT 240
 GTTTNAGNTG TTAGNAGATN TCAGGAATAA TGTGATTGCC TTGN 284

35

SEQ ID NO:176
 SEQUENCE LENGTH:282
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00190
 SEQUENCE DESCRIPTION:

40

GATCAGAAC A TGAAATGCCC TCCTAAATGT CAGCTGTTGT CACACAGTAG CTCCAACACT 60
 TTGAGCATTT TTAAGGGAGT GGCCTCATTT CACTAGAGAC AAATCTTTAA GAATAGTTCT 120
 AAAATTGGGC TTGTGATTTC CATTTCTGAT GTCTCCAGAT TGGCACCCCT TTCTAGTTCA 180
 ATGCCTCACG AGATTTTGCC AGGGGCATCC AAGGCAACA ATCCCAATCT TTCTATATAA 240
 ANTGTATTCA AGCAAACATC AAATAANTTT CTGGGATATT TN 282

45

SEQ ID NO:177
 SEQUENCE LENGTH:278
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00191

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55

SEQUENCE DESCRIPTION:

5 GATCAGAGTT TGAAATGAAA TGTITGTCAG GGTGTTGGAA AAATTTTGGT GAGTTCTGCA 60
 CATTTCCTT GGTTCAGGCT GGGCATGGAC CAGCCTTCAG ATGCCAGAAG TGGAAGATGA 120
 GCCTACTTGT GAGCGATGTG ACTTTAAGGA AATGAAGACT GGGGAAGAAT AATTAGTGTT 180
 TATAAGACAT TTAAGAGGCC CTTTTTCATA TACTGACTCA CTGATGAATC AGCATTNGCA 240
 TTNTATGGAA NAATATAAAT CCAAAGAAAT AATTTAAA 278

10 SEQ ID NO:178
 SEQUENCE LENGTH:281
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00192

15 SEQUENCE DESCRIPTION:
 GATCAAAATA ACCCTCGTAA AAATATATGT ANGGGGTACA CAAAGTAAGC CTCTTTATGA 60
 AACAAATTGAG GATAATNATG TGAAAGGTTT TAATGATGAT GTTCTACTTC ANATAGTTCA 120
 CTTTCTACTG AATAGACCAA AAGAAGAAAA ATCACAGCTG TTGGAAAAC TAAAAAGCAT 180
 20 ATTTNATTGA GAACTGTGGG AATATTTAAA TTTTACTGAA GGACCAATAA TGATGAGATT 240
 TGTAAGTGTC AACTATTTAA TACATTGATT TTTGAGACAA A 281

25 SEQ ID NO:179
 SEQUENCE LENGTH:278
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00193
 SEQUENCE DESCRIPTION:
 30 GATCAGGCCC AGGAAGGGCA CAGGGGCTGA GCACTACAGA AGTCACATGG GTTCTCAGGG 60
 TATGCCAGGG GCAGAAACAG TACCGGCTCT CTGTCACTCA CCTTGAGAGT AGAGCAGACC 120
 CTGTTCTGCT CTGGGCTGTG AAGGGGTGGA GCAGGCAGTG GCCAGCTTTG CCCTTCCTGC 180
 TGCTCTGTT TCTAGCTCCA TGGTTGGCCT GGTGGGGGTG GAGTTCCCTC CCAAACACCA 240
 35 GACCACACAG TCCTCCAAA ATAACATTT TATATAGN 278

40 SEQ ID NO:180
 SEQUENCE LENGTH:278
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00194
 SEQUENCE DESCRIPTION:
 GATCTACATT AATATCAAGT CTTGACTCCC TACTTCCCGT CATTCTCAC AGGACAGAAG 60
 45 CAGAGTGGGT GGTGGTTATG TTTGACAGAA GGCATTAGGT TGACAACTTG TCATGATTTT 120
 GACGGTAAGC CACCATGATT GTGTTCTCTG CCTCTGGTGG ACCTCNACAA AAACCATTGG 180
 AACTGTGACT TTNAAGGTG CTCTTGCTAA GCTTATATGT GCCTGTAAAT GAAAGTGCCT 240
 GAAAGACCTT CCTTAATAAA GAAGGTCTA AGCTGAAA 278

50 SEQ ID NO:181
 SEQUENCE LENGTH:277

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00195

SEQUENCE DESCRIPTION:

GATCTCTCCC CCGTGAAGGA GTTGAGCACA TTAGCAACAA TGTACATTAA TTTTGGATT 60
TCATTTTCAT GTTTTATTTT GTAAATATTA TCTGATGTTT GGAGCTTGAG TATACAGACT 120
GTAAATATAG TTCTTGATT TGTACTAATT CTGATTCTTT TGCTNNCNG CCTTAGATGT 180
GCAATGCAGA CACTATCTAA CTGTGTGTGG TAACCTTGCG TCACGGAGCT GTTAGTGAAC 240
GAGGTAAAAA TAATAAAGGT ACAGCCAGTG CATCAAA 277

SEQ ID NO:182

SEQUENCE LENGTH:282

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00196

SEQUENCE DESCRIPTION:

GATCAAAACN GATTTACGGT GGGGGAGGAA TNTGAGCTGG AGACAATNAC AGGGGAGAAA 60
GTCAAGACAG TGGTTCAGTT GGAAGGTGAC AATAAACTGG TGACAACCTT CAAAAACATC 120
AAGTCTGTGA CCGAACTCAA CGGCGACATA ATCACCAATA CCATGACATT NGGTGACATT 180
GTCTTCAAGA GAATCAGCAA GAGAATTTAA ACAAGTCTGC ATTCATATT ATTTAGTGT 240
GTAAAAATTA AATGTAATTA AAAGTGANCT TTNGTTTTTA AA 282

SEQ ID NO:183

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00197

SEQUENCE DESCRIPTION:

GATCCAGATG ACCGTGGTNG TTGGGGTATA TCTCCTCGAG GAGCTGGTTA CACCTTTGGG 60
CAAGATATTT CTGAGACATT TAATCATGCC AATGGNCTCA CGTTGGTGTC TAGAGCTCAC 120
CAGCTAGTGA TGGAGGCATA TAACTGGTGN CNNGGCCCGG AATGTAGTAA CGATTTTCAG 180
TGCTCAAAC TTTGTTATCG TTGTGGTAAC CAAGCTGCAA TCATNGANCT TTTGCGATAC 240
TCTAAATAC TCTNTCTTGC AGTTTCACCN AGNNNNN 277

SEQ ID NO:184

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00198

SEQUENCE DESCRIPTION:

GATCTGAGAT TTCCGTGTTT GGCTGAACCT GGGAGACCAG CTGGGCCTCC AAGTAGGATA 60
ACCCCTCACT GAGCACCACA TTCTCTAGCT TCTTGTGAG GCTGGAAC TG TTTCTTTAAA 120
ATCCCTTAAT TTTCCCATCT CAAAATTATA TCTGTACCTG GGTCATCCAG CTCCTTCTTG 180
GGTGTGGGGA AATGAGTTTT CTTTGATAGT TTCTGCCTCA CTCATCCCTC CTGTACCCTG 240
GCCAGAACAT CTCACTGATA CTCGAATTCT TTTGGCN 277

SEQ ID NO:185

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

5

TOPOLOGY:linear

CLONE:HUMGS00199

SEQUENCE DESCRIPTION:

GATCGGTTTT TGTTCCTGC TTACCATATG ATTGTAAATT GTTTATGTA TTAATCAGTT 60
 AATGCTAATT AATTTTGCT GATGTCATAT GTTAAAGAGC TATAAATCC AACAACCAAC 120
 10 TGGTGTGTAA AAATAATTTA AAATTCCTT TACTGAAAGG TATTTCCCAT TTTGTGGGG 180
 AAAAGAGCCA AATTTATTAC TTTGTGTGG GGTTTTAAA ATATTAAGAA ATGTCTAAGT 240
 TATTGTTGC AACATAAAT ATGATTTAA ATTCTCN 277

15

SEQ ID NO:186

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20

CLONE:HUMGS00200

SEQUENCE DESCRIPTION:

GATCCTGACA CTGACATGAA GGCAAGCCTT GATTTCGTAT GAACGTTGCT GAAGTGGTAA 60
 TTGAGGAAAA CAGTTCCCA GATTGTTAAG AGTTCCTGA AGATATTGAC ACAATTTNNA 120
 AAAATCAGTA AAGGAATGTA TATAATATTG CNCTCGTGT TTACAGTAAG ATTTGTTGCT 180
 25 CTCAGACTGT GTAAACAAA ATTNATNGNT GTTTCTGCA TTTAAAAA TCTTATTGTA 240
 CCANCTGGTA ANCTATTAAN TGCCTATAAN NCTAAA 276

30

SEQ ID NO:187

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00201

SEQUENCE DESCRIPTION:

GATCAAGGAN GAAAGANTGA CTTCAAATAT GCCTTGTTAG TGTAATGTG ACTTNTNGAA 60
 CTGTATGAGT ATTTAAGAT TATTNGAGTA AAGTAAGTTT TAAAAAGCAG TCCCTAATCA 120
 TCAAAAGTAA AAAACTCTTG ATGTAGTCAT ATAACCACAC TAAGAACTCT TCCAGGTGAC 180
 TTCAAAACAT AGGACAGTAC ATCTCTAGTA GANTNTGCC TGAGAATGAA AAGAATGTAA 240
 40 CAGTGTTAGT ATTTGAATA AACATGTTAT TACTN 275

45

SEQ ID NO:188

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00202

SEQUENCE DESCRIPTION:

GATCACTTTT TTTAGAGTGA AGAAAGAACA ANCTTGTTTT TTGTGTTTTT TAAAGGAATA 60
 TAAATAATG AAGGATGTAT AATTGATGCC AAATAAGCTT GTNCTTTAGT CACACCGACG 120

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TCTTATTTTT CCCTTTAGGC CAGTTCTGTT TTAAAGGTGT ACATGGNCAA TGTACAGTG 180
 TAAGAAATC CATATCCATA TGTNCCCATT CGCATTTTGT ATTGGTTCAT GTATACCATT 240
 TTTNCAAAAN ANANGGAANA ANNGGNAGTN CTN 273

SEQ ID NO:189
 SEQUENCE LENGTH:271
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00203
 SEQUENCE DESCRIPTION:

GATCTGAAAA GCTCACTTTA AACTCATACT ACATTCGTNA CGAGTATTN ACGTTAACAT 60
 AATTGAAAAG TACAAGGTCC AAGCTGGCTT TCAATNATG TCTAAACAGA AATGGGACAA 120
 ATAGACTTGA AAATAGAAGG GATTTATTCC ACCCCTGCAA GGGTAAGAGT CAGGTGAGAG 180
 TCCCTTGGTG AGTCATTGT ACATCAGTGT CATTCTTCT TAACCTCTGA AGAAAGATGG 240
 GCATCAGAAA TAAAGACAAA GCACTATCAA A 271

SEQ ID NO:190
 SEQUENCE LENGTH:270
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00204
 SEQUENCE DESCRIPTION:

GATCTGCCAC GAGGGCAGCA GCCAAGAGGA CTTGCTCTCT CCATGTGAAT GTACAGGGAC 60
 CTTGGGGACA ATTCATCGGA GCTGCCTGGA GCACTGGCTG TCATCCTCAA ACACCAGCTA 120
 CTGTGAACTC TGCCACTTCA GGTTCAGT CGAGCGAAAA CCCAGGCCGT TAGTGGAGTG 180
 CCTGGGAAAC CTTGGCCCC AGATTGGGAG GGGNCTTTT TTTGGNGANA TGGTNNNTT 240
 TGGGTTNTAA ATNCCNGGG NNCCATNTNN 270

SEQ ID NO:191
 SEQUENCE LENGTH:166
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00205
 SEQUENCE DESCRIPTION:

GATCTCTGAG CTGCCAGCA TAGTCCAAGA CCTAGCCAAT GGCAACATCA CATGGGCTGA 60
 TGTGGAGGCC AGGTATCCTC TGTTTGAAGG GCAAGAGACT GGTAAAAAAG AGACAATCGA 120
 GGAATGAGGA CAATTTTGAC AACTTTTGAC CACTTGCGCT AATAAA 166

SEQ ID NO:192
 SEQUENCE LENGTH:276
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00206
 SEQUENCE DESCRIPTION:

GATCTACATG AGAAGTATAG TGGCTCTACC CCCTGAAAGA GGGTGGATGC AGCTGCTTGT 60

EP 0 679 716 A1

5 GTTCTTGGG GTGACTGTCA TTGGAATAC GGACACAGTG ACCCATCCTC CATCCTATTT 120
 ATAGTGAAG GGCCTTCAAT TGTATCAGTA CTTTNTTTTA AGCTCTGGCA CATTGACCTC 180
 TATGTGTTAC CAGTCATTAA TGAGCTGCTG CAGAGGTGAC TATTGTTTT ACTTCTTGG 240
 ATGTTAACAT TACTACTCTC ACTACTCAAT CTCAA 276

10 SEQ ID NO:193
 SEQUENCE LENGTH:273
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00207
 SEQUENCE DESCRIPTION:
 15 GATCTGACAT TTGACATGAA CACAAAGTTG CTAGATGCTC TTGTTGACTT CCAGCAGATG 60
 GGATGGGGGA AACACAGCAG TTCTTGGTAA AGTCCTTTGT AATAATAGTT TGATTTTTTT 120
 ATTTGAGAG AATCTTTCAT TTTCTATGT ATGCTTTTNN CCTTTTTTGC CCAGTTTCCT 180
 TATCACTTGC TGATAGTGGC TTATNTNGCA TTCATGCAGA CTATGTTGCA AGTCTGTTTC 240
 ATCTAGTAAA CTGAAAATNA TTGCTTAATC AAA 273

20 SEQ ID NO:194
 SEQUENCE LENGTH:267
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00209
 SEQUENCE DESCRIPTION:
 25 GATCCCAGAG AGGGAAGAGA ACCAGGGGCC CTTTCTCTT TNAGAAATTN CTTTAAATCA 60
 GCCCACCTTT TGACTCCCGG CCCGCCCAA TCCATTATNT TTTTCTGCCT TCCGGGTCCC 120
 ATCCTTAGAG CTCGAGTCGT TCCTTCCCCT CCTGGATTCC GGGTAGCAGA GGCAGCGCCG 180
 CAGGAGGCGG GTGCCCGTTT GTCCAGGNC TGGCGGTGGT GGAGNNAGGG GTGCTGGAAC 240
 AATAACGGC ACNNNNCAA TGTCAA 267

35 SEQ ID NO:195
 SEQUENCE LENGTH:384
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00210
 SEQUENCE DESCRIPTION:
 40 GATCCAAAAC ACTACTCAGC TCTCTGCAC TGAGGAAATT TTTCCCCCTA CATTGACTCC 60
 TGGCTACAT CAGCCAACT TAACCTTGGT GGGGTTTGA TTTGATAGCC AATTAGTTCT 120
 GTGCTGTTG CAAAGAATTG ATATTTAGAT GGTTTTAACT ACTCAGCAGA TTGTCTTCCT 180
 TTATATTGTG TCTTTTTTAT GTNGCATGTN GCTTTTGTTA TCAGCCTGAT TTTTGTCTCA 240
 GTATATGATA GTNCTGCTGA TGTTTTGTG ATTGGGCAGA CATATCTTCA TTAAGAGTTT 300
 TTGGAAACT CATCAAATC GATGAATACA TTTCTTCAT AACCCATTG GAATTATTCC 360
 TAATAAATG ATAAATACG TAAA 384

50 SEQ ID NO:196
 SEQUENCE LENGTH:277

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00211

SEQUENCE DESCRIPTION:

GATCTAAAAA AATTCAGAAG AAATATGATG AAAGGAAAAA GAATGCCAAA ATCAGCAGTC 60
 TCCTGGAGGA GCAGTTCAG CAGGGCAAGC TTCTTGGCTG CATCGCTTCA AGGCCGGGAC 120
 AGTGTGGCCG AGCAGATGGC TATGTGCTAG AGGGCAAAGA GTTGGAGTTC TATCTTAGGA 180
 AAATCAAGGC CCGCAAAGGC AAATAAATCC TTGTTTGTG TTCACCCATG TAATAAAGGT 240
 GTTTATTGTT TTGTTCCAC ATTTATGTTG CCTGAAA 277

SEQ ID NO:197

SEQUENCE LENGTH:271

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00212

SEQUENCE DESCRIPTION:

GATCGGCGGC GCGCAGNAAC CGCTCCTACA GCAAGCTGCT GTGCGGCCTG CTGGCCGAGG 60
 CGCTGCGCA TCAGCCCGGA CAGGGTCTAC ATCAACTATT ACGACATGAA CGCGCCAAT 120
 GTGGGCTGGA ACAACTCCAC CTTGCGCTAA GAGCCGAGG ACCCAGCTG TCTGCGCTGG 180
 CTCCACCCGG GAACCCGCCG CACGCTGTGT TCTAGGCCCG NCCACCCCAA CCTTCTGGTG 240
 GGGAGAAATA AACGGTTTAG AGACTAGGAA A 271

SEQ ID NO:198

SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00213

SEQUENCE DESCRIPTION:

GATCCTGTAG TGTTCTGGA GAAGCTAGAG CCTGATTGTA GGCTACTACT CATCAATTAA 60
 CTTCTACAGT GGAGACTACT TCTGGGACTG GAATATAAAA AAGAATCAAA GGTTCGTATT 120
 TTNAGTTGCA ATAAAGGGAA AGACCATGCT CATAGCAGTG CCAACATCTG AAGTGTGGAG 180
 CCTTACCCAT TTCATCACCT ACAACGGAAG TAGTTAACTG GAAGAGATTA CCAAGAGAAT 240
 AAAAAGAGAC TCATTCAAGT GAAA 264

SEQ ID NO:199

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00215

SEQUENCE DESCRIPTION:

GATCTGCCTT AAAGAAAAGA AAATTTTAGA AAGAAATATT GTTGCTCAGT GTTGTTAATA 60
 TAGCTCAAGA ATTGAGTTTA TATTTGCAGT ATGCTATAAA TGATACCCCC CTACCACACC 120
 CACACACACA GTTTTTGTCT AATGAAAATG TTGCTGTGAT TATTTATAAT TGGTAGTATT 180
 TCTTCCAGAA GAAGCTAAAA TAAGACTGGC ACTTACCCTG AAGTGCATTA ATAAAACCAC 240
 ACTTTAAAT TAANAAA 257

SEQ ID NO:200

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

5

TOPOLOGY:linear

CLONE:HUMGS00216

SEQUENCE DESCRIPTION:

GATCAACCTG AGCNTGGAGA ATGCCCTGGGG CATTTAACGC TCGTCATTG ACATCTGCAT 60
 10 GAAGCTGGAG GAGGGCAAAT ACCTCATCCT CAAGGACCCC AACAAGCAGG TCATCCGTNT 120
 CTACAGCCTC CCTGATGGCA CCTTCAGCTC TGATGAAGAT GAGGAGGAAG AGGAGGAGGA 180
 AGAAGNGGAA GAAGATGNGG ANGAACTTA AACCAGTGAT GTGGAGCTGG AGTTTNTCCT 240
 TCCACCGAGA CTACGNGGGC CTTTATGCT TAGTGGAATG TNTGTCTAAC TTTGCTCTCT 300
 15 TGACATTTTA GCAGTTGAAA TTAAATTATA TANTCTGTTT TNNGTCTTTT NAAATAAANA 360
 AAANNANATT NTGN 374

SEQ ID NO:201

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

20

TOPOLOGY:linear

CLONE:HUMGS00217

SEQUENCE DESCRIPTION:

GATCTGAACT ATTTGCTTC TCTCAAGAT AAGTTGTATT TTACCATGGA AAAATACAGT 60
 25 ATCTAACATT ACCATTACAG TTAATGAAG TTTCTCATA ACATTATCT TTAGTTTTAT 120
 GAAGTCATCG TGACCAATGT TACAGTAATT TCTGTTAGCT GATTGTGGTA AACAATGTTT 180
 AATGNGAAAA GAAATAAAA CTTCTTCAT CTGTTGTAGA ATATTTCTCT TCTTAAAAAT 240
 GGCTTCTATT CATAAA 256

30

SEQ ID NO:202

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35

CLONE:HUMGS00218

SEQUENCE DESCRIPTION:

GATCCCCACT GGAGCAGCCT CTGCAAAAGG GAGCCCATGT AGTGGCCAGG GGCTGTCCAA 60
 ACTCCAGCTT CTTCCCTGG GAAAAACCC AAAGAACCAA AAACAAACCA CCCCAAGGAT 120
 40 AATAATAGCT ACACTGCTAG CTTCTCAAGT TCTGTGAAA AACAATTAC ATAATGACAC 180
 AGTAGATGTG GAACACCTAG CCAGTGCCTG GGCAGGTCCC TATTATCATA AATGAACATA 240
 AAGTGCTCTA AAAACN 256

SEQ ID NO:203

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00219

50

SEQUENCE DESCRIPTION:

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EP 0 679 716 A1

5 GATCCAAATC AGGAAAAGAC GGCGCCACTA CAATGGAGAA GCATATNAGG ATGATGAACA 60
 TCATCCCAGA GGTGGTGTTC AGTGTGAGAC CTCTTAATGG GCCAGTGAAT AACACTCACT 120
 GCTGGCATT T AATGTGCAGT AGTGAATGAG TGAAGGACTG TAATCATAAT ATGCTCACTA 180
 CTTGCTCTTG TTTTGTGTTT AATAAACTAT AGTAGTGTTA TAANNNGTTA AATGAAGAAT 240
 AAACGCAAAT ATAANAGCTC TGAAA 265

10 SEQ ID NO:204
 SEQUENCE LENGTH:253
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00220
 SEQUENCE DESCRIPTION:
 15 GATCTAAAGA GACACTTAGA GACTCTTGGG GACCTCAGAT TTCCACCNCT CCACAGCATT 60
 CTGCCTACAC AGTTCCTCCTC ATTTTNCCTA GTTACTCGGA AGAGCGCTGG ACTTGAAATC 120
 AAAATAATTG CGTATGTCT TTGGTTATGT CGCTTCATCA TAGCACTTTC TAAAACTATT 180
 TGACAAACAT GTATTGCATA CCTACNGCAT TCCAGTTCTN GTACANGTAA TTAAATGCTC 240
 GACTAACGNN AAA 253

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 25 SEQ ID NO:205
 SEQUENCE LENGTH:253
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00221
 SEQUENCE DESCRIPTION:
 30 GATCTGGAAT TGGACATTTC TCTGTCAGAG CACAGAGGAG GCTCATATCA CCTCTTCCT 60
 CTCCTACTTG GCCCAGCTGC TTGGAGGACC GACCCCATGG CTGAGAATAT NACGGCAAGA 120
 GGAACAGAGN TTGCTCCAAG TGGGAAAAGG TCCAAGCAG TCCAGAGAAG ATGTCTGTGT 180
 GGCTTTCCT CCCTGCCTCC CCCAGCTCCC AACTGGCCT TTGTAAATAA ATGGCGTGGT 240
 CTTTGTGTG AAA 253

35 SEQ ID NO:206
 SEQUENCE LENGTH:253
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 40 CLONE:HUMGS00222
 SEQUENCE DESCRIPTION:
 GATCTGCCGT CTGTCACCTC TCTCCAAGTT GAGACAGGGG CCTGGATTTC AGCCCTTCCT 60
 GCCGAGAAAT CTTNTAAATT TCAACCTACC TTTAAAAATA AAGTCTCCCT ACTTAAAAATC 120
 CAGTAGATAT CATGGCACTA ATGCTAACAC CCCTTTCCTT AAATTAATAA AACAAAAATA 180
 45 AAAAAAAGAA AAAANTGCAG GCATGCAAGC TTGGCGTANT CATGGNNTNA GCTGTTTCCC 240
 NGTCACGGCG TGN 253

50 SEQ ID NO:207
 SEQUENCE LENGTH:251
 SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS00223

SEQUENCE DESCRIPTION:

5 GATCGAGACA CGTGATGGGA AGCTGGTGTC TGAGTCCATN ACGTCCTNCC AAGTGAACAG 60
 CTGCGGCAGC CCTCCCAGCC TACCCCTCCT GCGCTGACCC AGAGCCTGGG AAGGAGGCCG 120
 CTATGAGGGT AGCACTGGGA ACAGGAGACC CACCTNAGNC TCAGCCTNGC CTCAGTNTAC 180
 TGGGGAGTTT ACTACCTGGG GCCCANTTGA CATGCTCCAG CTACANACAN TTANTTGCTT 240
 10 TTTTNTTGGN N 251

SEQ ID NO:208

SEQUENCE LENGTH:243

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS00224

SEQUENCE DESCRIPTION:

20 GATCGATTCT TGTATATTNA TTTTATCTCT TTCTGTATCT ATAGGTAAAT CTCAAGGGTA 60
 AAATGTTAGG TGTTGACATT GAGAACCCTG AAACCCCATC CCCTGCTCAG AGGAACAGTG 120
 TGAAAAAAA TCTCTTGAGA GATTAGAAT ATCTTTTCTT TTGCTCATCT TAGACCACAG 180
 ACTGACTTTG AAATTATGTT AAGTGAATA TCAATGAAAA TAAAGTTTAC TATAAATAAT 240
 AAA 243

25 SEQ ID NO:209

SEQUENCE LENGTH:249

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS00225

SEQUENCE DESCRIPTION:

35 GATCACANTT AATGATTCAG TATAATGTTT GAGGCCAGAC AAGATATATA TTGTGCCTCT 60
 TACAGCCTTT GGNNCNNTTG TTTCCATTTT TTAAATATCT TCTATATCCA TATAGTATTC 120
 AAATNATTAA TGCTCATGTA CCAAGGTTTT GCTATAAAAG TTTTGNCTGT ATGAATAATG 180
 TGGCTTTAGT AAATAATCAT TTTTCAACTG TAAACTTATT CTGAAATAAA GTAAATTTCT 240
 AATTGTTTN 249

40 SEQ ID NO:210

SEQUENCE LENGTH:248

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00226

SEQUENCE DESCRIPTION:

45 GATCATAGAA ATATATGTAA AGTATTCAAT TTTCAATCAT TTTCAAATNA CTGTTATAAA 60
 TTGTTTTTGC TGAGTTGTAA TACTTTTNAG ATACAATGTA TTCCTTGTAC TGAAAGAATG 120
 AAAAAAGGACT TTTTCAGCAT TTGAGGTAAG TNCTTTAACG TTTCAITAAA ANCATTTTTT 180
 ACAAATATTT TGTACATGCA CTTGCAGTAT TGAGGTAAAT CATTTTAATA AATNCGGAAA 240
 50 TTAACACN 248

55

SEQ ID NO:211
 SEQUENCE LENGTH:247
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00227
 SEQUENCE DESCRIPTION:
 GATCTCAGCN TTGCAAAACAC ANTTNCTACA TAGATAGTAC TAGGTATNNT TTAGATATGT 60
 AAAGAAAGAA ATCACACCAT TAATAATGGT AAGATTGGTT TATGTGATTT TAGTGGTATT 120
 TTTGGCACCC TTATATATGT TTTCCAAACT TTCAGCAGTG ATATTATTTC CATAACTTAA 180
 AAAGTGAGTT TGA AAAAGAA AATCTCCAGC AAGCATCTCA TTAAATAAA GGTGTGTCAT 240
 CTTTAAA 247

SEQ ID NO:212
 SEQUENCE LENGTH:256
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00228
 SEQUENCE DESCRIPTION:
 GATCAAAACA AACAAATCCAG ATGTATAAGT ACTAGGCAGA AGCCAATTTT AAAATTCCT 60
 TGAATAATCC ATGAAAGGAA TAATTCAAAT ACAGATAAAC AGAGTTGGCA GTATATTATA 120
 GTGATAATTT TGTATTTTCA CAAAAAAAAA NGTTAACTC TTCTTTTCTT TTTATTATAA 180
 TGNCCAGCTT TNGGTATTTC ATTGTTACCA NGTCTATTT TTNGANTAAA ATTGTTCTCC 240
 TTCTAAANGT TTAAA 256

SEQ ID NO:213
 SEQUENCE LENGTH:244
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00230
 SEQUENCE DESCRIPTION:
 GATCGGCAAG CCCCACTG TCCCTTGCAA GCCAAGGCCA CCTTNTATGC CATTTCTAAG 60
 ACCTACAGCT ACCTGACCCC CGACCTCTGG AAGGAGACTG TATTCACCAA GTNTCCCTAT 120
 CAGGAGTTCA CTGACCACCT NGTCAAGACC CACACCAGAG TCTCCGTGCA GCGGACTCAG 180
 GCTCCAGCTG TGGCTACAAC ATAGGGTTTT TATACAAGAA AAATAAAGTG AATTAAGCGT 240
 GAAA 244

SEQ ID NO:214
 SEQUENCE LENGTH:243
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00231
 SEQUENCE DESCRIPTION:
 GATCAGATTG GGTCTGCTC CTCTCAACCT TGAAGTCCCC ACGTATGAGT TCACCAGTGA 60
 CGATATGGTG ATTGTTGGTT AAGAGACTTG GACTCAAGTC ATAGGCTTCT TTCAGTCTTT 120
 ATGTCACCTC AGGAGACTTA TTTGAGAGGA AGCCTTCTGT ACTTGAAGTT GATTTGAAAT 180

ATGTAAGANT TGATGATGTA TTGGCAAACA TTAATGTGAA GTAAATNGAA TTNAATGTNG 240
AAA 243

5 SEQ ID NO:215
SEQUENCE LENGTH:243
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
10 CLONE:HUMGS00232
SEQUENCE DESCRIPTION:
GATCGCCAGT GGAAGAAGAT TAGTGCAATC ATTGAGAAGA GGAAGAAGAT GGAAGCTGAT 60
GGGGTTGAAG TCAAAAGACC AAAATACTAA TCACTAGTTA CAACCAGAGA TGCTCCACAA 120
GGATATGCTC CCCACGGTTT TCTTTCTACA ATTTCCAAAG GTTGCAAGAT GTTTTTTTGT 180
15 GGATGAATAT AAAATTTTAT TGTGTAATTA CTTGGTTCCA TTAATATTGG TTAAGTTGCT 240
AAA 243

20 SEQ ID NO:216
SEQUENCE LENGTH:243
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00233
SEQUENCE DESCRIPTION:
25 GATCGTAGAT GTTAACCAAA TCTACAAAAT CCACTACTCC CCCGTTATCA ACGGGATACG 60
TTCCAAGACC CCCAGTGGAT GCCTGAAACT GGCTAATGCT GAACCCTACA TATACTATGT 120
TTTTNCTGTA CATATATATG ATAAAGTTTA AATNATAAAT NAGGTACAGT AACAACAATA 180
ACAGTAAAC AACAGTTATA ACAATATACT GTAATAAAAG TCATGTGAAT GTGGTGTTC 240
30 TCN 243

SEQ ID NO:217
SEQUENCE LENGTH:242
SEQUENCE TYPE:nucleic acid
35 TOPOLOGY:linear
CLONE:HUMGS00234
SEQUENCE DESCRIPTION:
GATCTTCTCC AGATTGGCAG AAAGTTGATA TAGGTGGACT TTTTACAGG TCAGTTGAGG 60
40 CAAAAACTA TGGGTTTTT CAGGTGAACC TCCCCATTT AAATACTCAG AAGATAAGGT 120
GTGAATGTAT GTATTATTAG AGTCCTAAAG TATTTTATAA GTACTGTTT CACCACGCTT 180
TGTGGGAGAG AAATCATTCA AATCATTTT TTTGTCCGTA CAATAAAGTT TACTAAAAAC 240
CN 242

45 SEQ ID NO:218
SEQUENCE LENGTH:238
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
50 CLONE:HUMGS00235
SEQUENCE DESCRIPTION:

55

5 GATCTTCGTG ATACTGTACA TAGCTGTTG AAATGCCAGA ATGACTTCTG ACATNCCAAG 60
TTTTTCACAA AATATATTN ATCTGTGATT AGCCATTGA CTAATAATAC TGGCTAACAG 120
ATGTTGAAAA AAATTGTCTG TTTTCTCATT AATTTTGGTC TAAACATGT TTGCACITGT 180
NTTTGACTTG TGTTTTATTA ACATTGATTG GCATATTAAA AGTCACTCNG AGCTTAAA 238

10 SEQ ID NO:219
SEQUENCE LENGTH:239
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00236
SEQUENCE DESCRIPTION:
15 GATCCAAANN ATGACTTCAG AAAAACTTG AAAGTAACAG CAGTGCCTAC ACTACTTAAG 60
TATGGAACAC CTCAAAAACT GGTAGAATCT GAGTGTCTTC AGGCCAACCT GGTGGAAATN 120
TTGTTCTCTG AAGATTAAGA TNGGTAGGAT GGCAATCATG TCTTGATGTC CTGATTTGTT 180
CTAGTATCAA TAAACTGTAT ACTTGCTTTG AATTCATGTT AGCAATAAAT GATGTTAAA 239

20 SEQ ID NO:220
SEQUENCE LENGTH:250
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00237
25 SEQUENCE DESCRIPTION:
GATCAGAGGT GAAGGGACAG AGAGAGGAGA GGAGGAAGAT TGAGCTGGGG GCAACAGCCA 60
AGCTCACCTG GGCAGGTCTC TGCCACCTCC TTGCTCTGTG AGCTGTCACT CTAGGTTATT 120
CTCTTTTTTT GTGGCTATTT TTAATTGCTT TGGATTTGTT AAATGTTTTT TGTCTTCTGT 180
30 TAAGTGTGTT TTCTCTGGAG ATAGAATGTA AACCATATTA AAAGGAAAAA GTTTCAGACA 240
AGCAATTAAA 250

35 SEQ ID NO:221
SEQUENCE LENGTH:237
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00238
SEQUENCE DESCRIPTION:
40 GATCAGCTTT GCTCCTGAAA TTGCATCCGA AGAAGAAAGA AAGGGGATGG TGGCTGCGTG 60
GTCCCAGAGG CTGCAGACCA TCTGGAAGGA AGAGCCCATC CCCTGCACAG CCCACTGGCA 120
CTTCGGGCAA TAACTCTGTG GCACGTGGGC ATCACGTAAG CAGCACACTA CGAGGCCAG 180
GCGCAGGCAA AGAGAAGATG GTGCTGTCAT GAAATAAAAT TACAACATAG CTACAAA 237

45 SEQ ID NO:222
SEQUENCE LENGTH:243
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
50 CLONE:HUMGS00239
SEQUENCE DESCRIPTION:

55

EP 0 679 716 A1

5 GATCAGTGTA GAACTGGTCA TAGAGGAAGA GCTAGAAATC CAGTAGCATG ATTTTAAAT 60
AACCTGTCTT TGTTTTGGAT GTTAAACAGT AAATGCCAGT AGTGACCAAG AACACAGTGA 120
TTATATACAC TATACTGGAG GGATTTTCATT TTTAATTCAT CTTTATGANG ATTTAGAAGT 180
CATTCCCTGT GTTTAAAGGG AATGTTTAAT TGAGAAATAA ACATTTGTGT ACAAATGCT 240
AAA 243

10 SEQ ID NO:223
SEQUENCE LENGTH:232
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00240
SEQUENCE DESCRIPTION:
15 GATCTAATAA CAGGTTGACA TAAGAAATAT TTGTCTCAA AATCAATGTA TTTAATAGTT 60
GACAGTTACA AATCTCATCA TTGAAAGATT TAATTTTAGT TACCTTTTGT TGATTTANN 120
NNNATTGCAT TTGTATATTG CTAAGTATA AGACAAATTG AGTTATTGAG CTATTAANTG 180
CACATTTTAA TATAANTGCA GAAATCCCA ATAAATGCT AACATACTGA AA 232

20 SEQ ID NO:224
SEQUENCE LENGTH:237
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
25 CLONE:HUMGS00241
SEQUENCE DESCRIPTION:
GATCACCCTG ACATCCGAGG TGCCTTTCTC CAAAAGGTAT TTGAAATATC TCACCAAAAA 60
ATATTGAAG AAGAATAATC TACGTGACTG GTTGCGCGTA GTTGCTAACA GCAAAGAGAG 120
TTACGAATTA CGTTACTTCC AGATTAACCA GGACGAAGAA GAGGAGGAAG ACGAGGATTA 180
30 AATTTCATTT ATCTGGAAAA TTTTGTATGA GTTCTTGAAT AAAACTTGGG AACCAAA 237

35 SEQ ID NO:225
SEQUENCE LENGTH:236
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00242
SEQUENCE DESCRIPTION:
40 GATCTTCACT TAANCTAAGT CTGTGAATTA CTTTATATT ATTTTGAAAN ACTCCTTGCA 60
GTATATTGGC ATGATACAGT AAAAGCANTT TCCACAGATT GTTATCACCT TCTTTAAAG 120
AAGTCAAAAT TTAATAAATA CAATAGCACG TTGTTGGTGT CATATTCAAT AACATTTC 180
ATGCTACATA TAATTTTATA GACATAATAA AGAAGGTATT GAAAAAATA AATAAA 236

45 SEQ ID NO:226
SEQUENCE LENGTH:227
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
50 CLONE:HUMGS00243
SEQUENCE DESCRIPTION:

55

5 GATCGCCACC TACCGCCGCC TGCTGGAAGA TGGCGAGGAC TTTAATCTTG GTGATGCCTT 60
 GGACAGCAGC AACTCCATGC AAACCATCCA AAAGACCACC ACCCGCCGGA TAGTGGATGG 120
 CAAAGTGGTG TCTGAGACCA ATGACACCAA AGTTCTGAGG CATTAAAGCCA GCAGAAGCAG 180
 GGTACCCTTT GGGGAGCAGG AGGCCAATAA AAAGTTCAGA GTTCAAA 227

10 SEQ ID NO:227
 SEQUENCE LENGTH:205
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00244
 SEQUENCE DESCRIPTION:
 15 GATCAGCAAG CAGGAGTATG ACGAGTCCGG CCCCTCCATC GTCCACCGCA AATNCTTCTA 60
 GCGGACTAT GACTTAGTTG CGTTACACCC TTTCTTGACA AAACCTAACT TGCGCAGAAA 120
 ACAAGATGAG ATTGGCATGG CTTTATTTGT TTTTTTGTG TTGTTTGGT TTTTTTTTTT 180
 TTTTGGGT NNCCCCNGGT TTTAA 205

20 SEQ ID NO:228
 SEQUENCE LENGTH:226
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 25 CLONE:HUMGS00245
 SEQUENCE DESCRIPTION:
 GATCTGCCA AAGAGGTGTT GGCTGAGCTT NAGGCCCTGG AGAGACGTGT GCACAAAATG 60
 TNACCTGAGG CCCTAGTCTA GCAAGAGGAC ATAGCACCTT CATCTGGGAA TAGGGAAGGC 120
 ACCTTGAGA AAATATGAGC AATTTGATAT TAACTAACAT CTTCAATGTG CCATAGACCT 180
 30 TCCACAAAAG ACTGTCCAAT AATAAGAGAT GCTTATCTAT TTTAAA 226

35 SEQ ID NO:229
 SEQUENCE LENGTH:228
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00246
 SEQUENCE DESCRIPTION:
 40 GATCAGCCCC AGATTTGACG TGCAACTCAA AGACCTGGAA AAATGGCAGA ATAATCTGCT 60
 TCCATCCCGC CAGTTTGGTT TCATTGTACT GACAACCTCA GCTGGCATCA TGGACCATGA 120
 AGAAGCAAGA CGAAAACACA CAGGAGGGAA AATCCTGGGA TTCTTTTCT AGGGATGTAA 180
 TACATATATT TNCAAATAAA ATGCCTCATG GACTCTGGTG CTTCCAAA 228

45 SEQ ID NO:230
 SEQUENCE LENGTH:308
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00247
 50 SEQUENCE DESCRIPTION:
 GATCTGCGAC CATTTCTGTA CAACACAAGC TGGCCTTGGC AGTTTCGGTG CATAGAAAAT 60

55

CAGGTGCTAC AGCTCGAGAG GGCAGAGCCA CAGTCCCTGG ACGGCGTGGA CTGAGGCCGG 120
 TTCCTTCCTG GAGGCCTCCT GTCCTCGGGG ACCCCAGCAC CTCATCATCA GCATTGCTGG 180
 AGCCAAGGGT AGGAGCCCTA CACTAGGAGC CCAGGATGGG ACGGNGNATN AGCCGAGAGG 240
 NAGGGAACTT TTNAGTNAAG TTCCTCAAAA AGAGGNTTAG AATAAANCCT TNGGCTTAAA 300
 AAGAGAAA 308

SEQ ID NO:231

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00248

SEQUENCE DESCRIPTION:

GATCCAAAGA CAGACCACAG ACTGGGAAAA GTTGGGAAGAT GAACACTTGA GGACTTCAGC 60
 TTCTCACCTA CTTAGTACAG TTGGGAACCA TACACTTCTG GCATGTTTGG AAATCAAAAT 120
 GTCACATTCT CGGGGGAGGA AGCCAGAAAA ATTGGGTATG TTCTAGAGAT TTACCACCAT 180
 TGCTTATTGC TTTTNTCTTT TAATAAAGTT TAGGAAAGTA GAATTTTAAA 230

SEQ ID NO:232

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00249

SEQUENCE DESCRIPTION:

GATCTAAAGA TTTCTCTATC CAATGAATCT AACAAAGTCA ATGGAAATTG AACTCTAGAA 60
 TTGTCTCTAG AAAACATAGC TTCTTACTGA ACTTGAACAT TTTTACAACA TTCACTGGTT 120
 TTTGTTTTGT TAGCTAATAA TCTATAATAG TTGAGTATCT CTGGGAATGG GGAGGGAAAT 180
 TATATGTAAT AGAGCTTAAA AATAAAGTGT CAATTCCAA GGNCTAAA 228

SEQ ID NO:233

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00250

SEQUENCE DESCRIPTION:

GATCAATAAG CATGTCAGAC TGATTAATGT CTAATGTGAA AATTTGGTAG TAAATTTNCA 60
 TTTGATATTA GATATAAATA TCTGAATATA AATAATTTNA ATATACTAGT CATGATGTGT 120
 GTTGATATTN AAAAATTATC TGCAACCTTA ATTCAGCTGA AGTNCTTTAT ATTTCAAAAG 180
 AATGAATAAC ATTGATAATA AAATCGCTAC TTTAAGGGAA A 221

SEQ ID NO:234

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00251

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

5 GATCTCTATG AATGTCAGAG CCCTAAGTTT CAGGCTTTGC ATTTTGTATA TGGGAAGAAA 60
TATGACAATC CTAGGTAATT AAACCATAGA CCCAAAGCCC TTACGTTTGA TGCAATTTAT 120
TTTTAAAATA GGCCTTGTTT TTCAGCTTCA TCTGCAGTTC TATGTGAAGA TTGATAAATC 180
AGTTTTTACT TGTTTTATTA ATAAAACGTA ATTNGGAAA 219

10 SEQ ID NO:235
SEQUENCE LENGTH:287
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00252
SEQUENCE DESCRIPTION:
15 GATCTCCGTT CCGCTCCCAG CGGCTCCAGT GTAAATTCCT CTCCTCCCTG GGGAAATGCA 60
CTACCTTGTT TTGGGGGGTT TAGGGGTGTT TTTGTTTTTC AGTTGTTTGT TTTTTTTGTT 120
TTTTTTTTTN CCTTGCCTTT TTNCCCTTT NATTTGGNGG GAATGGGAGG AAGTGGGANC 180
AGGGAGGTGG GAGGTGGATT TTGTNATTT TTTAAGCTCA TTTCCAGGGG TGGGANTTTT 240
TTTTNAANAT GNGNCATGAA NAAAGTTTGT TTTTGAAANT AACCAAA 287

20 SEQ ID NO:236
SEQUENCE LENGTH:222
SEQUENCE TYPE:nucleic acid
25 TOPOLOGY:linear
CLONE:HUMGS00253
SEQUENCE DESCRIPTION:
GATCAGAAAT GGCAGCACAA AGAAAACGCC CTCTCCTGAC TTGTATTGTG GCAGTCTGAA 60
CGNCCCAGAA AAATTGTGCC AAAGAGTTTA GAAAAATAAA TATACAATAA AAGTAAACAC 120
30 ATACACACAA AACAGCAAAC TTCAGGTAAC TATTTTGGAT TGCAAACAGG ATAAATTTAA 180
TGTTCAAACA ATCTGATAAA ATAACCATTT GGGNCTTNA AA 222

35 SEQ ID NO:237
SEQUENCE LENGTH:221
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00254
SEQUENCE DESCRIPTION:
40 GATCATCTTT CCTNTCCAG AGAAGTGGGC TGGATGTCTC CATCTCTGTC TCAACTTTAC 60
GTGTAAGTGA CTGCAACNTC TTACTTCCCT ACTGAAAATA AGAATCTGAA TATAAATTG 120
TTTTCTCAA TATTTGCTAT GAGAGGTTGA TGGATTAATT AAATAAGTCA ATTCCTGGAA 180
GTTGAGAGAG CAAATAANGT CCTGAGAACC TTCCAGACAA A 221

45 SEQ ID NO:238
SEQUENCE LENGTH:217
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
50 CLONE:HUMGS00255
SEQUENCE DESCRIPTION:

55

EP 0 679 716 A1

5 GATCAGACGT TTTACAAATN CATGAAGCGA ATTGCTGCTT GTAAGGAGCA GATTTTAAGG 60
TATTCCTGGA GTGGAGAGCC ACTCTTTTAA ACCTGCCCTA CATCAGANGT CACCGAGCTC 120
CCAGCCTGCA GCCAGTNTGG AGGCCAAAGG ATATTNNATT TTCANCTTAT GCCAGCNCTG 180
GTCAGCATGC TCAANAGTGC TANTTTAGGT CTTNCTN 217

10 SEQ ID NO:239
SEQUENCE LENGTH:217
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00256
SEQUENCE DESCRIPTION:
15 GATCTCTCTG AGTCCTGGCA ACATCCAGCA AAATACTGC TTATTCTCCA AAGAATATTG 60
GGAGCTCTCA ATCCTCGGTG ATATGGGAAA GAGAACTGAG TATTGCCCCT ATGACTGAGC 120
TTTCTATAGG AATTTTATTA AAGAATGTTT AATTNGTTG TCCTNCTNAA TGTTCTCAGT 180
CAAATAAATG AGTGAGCTGG TTTGGGCTGC TCTTGGN 217

20 SEQ ID NO:240
SEQUENCE LENGTH:216
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00257
25 SEQUENCE DESCRIPTION:
GATCCCATGG ACATTTGGGG AAAGGGCTCC TTGGGCTGCT GGTGAAGTTC TGTGGCCACC 60
ACCTCCTGCT CTTGACCTCC CTGGGAGGTG CTATCAGTCT GTCCTGGCCT TTCAGTTTAA 120
TAACTNGNTT CCAGCCCCAG TGTCTGACT TCTNCTGCAN AATAGGAGGG AGGCCTCCTT 180
30 TTGGGANGGN NGTACTTTGG GNGATAGTGN GGCCTN 216

35 SEQ ID NO:241
SEQUENCE LENGTH:220
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00258
SEQUENCE DESCRIPTION:
40 GATCTTTTAA GTTTCCTTCC CTACCCAGTC CCCATTTTCT GGTAAGGTTT CTAGGAGGTC 60
TGTTAGGTGT ACATCCTGCA GCTTATTGGC TTAATAATGA CTCTCCTTTT ATNTGGTCTC 120
TTTGGGGCCG ATTNNGNGAA AGCGAAATCA NTAGTGCAAC TGTTTTGATA CTGAATATTG 180
ACAAGTGTCT NTTTNAATA AAGACCCANT CCCTTCCAAA 220

45 SEQ ID NO:242
SEQUENCE LENGTH:223
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00259
50 SEQUENCE DESCRIPTION:
GATCACTAAT CAATAATCTG ATATTTAACA AAATATGGAC AGGCCACTTA TGCTCAGTTT 60

55

TACCTTAGTT ATTCCTTGGT ATCCACAGGC CCAAGTCCCT TAAATAAAA TACCCTCATA 120
 TTTCCATATA ATCTACATAC ATTCTCCCAT ATACTTTAAA TCATCTCTAG ATTACTNATA 180
 ATGTCTAATN CAAAATAAAT GCTATGTAAA TGTAATTATT AAA 223

5

SEQ ID NO:243

SEQUENCE LENGTH:216

SEQUENCE TYPE:nucleic acid

10

TOPOLOGY:linear

CLONE:HUMGS00260

SEQUENCE DESCRIPTION:

15

GATCAACTTA ATTCCTTTTC TTTATCTTCC NTCCCTCACT TCCCTTTTCT CCCACCCTCT 60
 TTTCCAAGCT GTTTCGCTTT GCAATATATT ACTGNNTAAT NAGTTGCAGG ATAATGCAGT 120
 CATAACTTGT TTTCTCCNAA GTATTGAGT TCAAAACGCC NGTATCTAAA GAAATACGGT 180
 TGGGGTCATT AATAAAGAAA ATCTTTCTAT CTAAAA 216

SEQ ID NO:244

20

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00261

SEQUENCE DESCRIPTION:

25

GATCTCAGAA CAATCAGATG CAAAGCTGAA AGAGATTGTA ACAAATTCT NTGGCTGGAT 60
 TTGAAGCTTA AACTCCTGTG GATTCACATC ANATACCAGT TCAGTTTGT CATTGTTCTA 120
 GTAAATTAGT TCCATTGTGA AAAGGGTTAC TCTCATACTC CTTATGTACA GAAATCACAT 180
 GAAAAATAAA GGTTCATAA TGCATAGTTA AA 212

30

SEQ ID NO:245

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35

CLONE:HUMGS00262

SEQUENCE DESCRIPTION:

40

GATCCATCTG CCTTTGTGGC TGCTGCCCT GTGGCTGCTG CCACCAACAG CTGCTCCTGC 60
 TGCTGCTGCA GCCCAGCTAA GGTGGAAGCC AAGAAAGAGT CGGAGGAGTC GGACGAGGAT 120
 ATGGGATTTG GTCTCTTTGA CTAATCACC AAAAGCAACC AACTTAGCCA GTTTTATTTG 180
 CAAAACAAGG AAATAAAGGC TTACTTCTTT AAAAAGTCAA A 221

SEQ ID NO:246

45

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00263

SEQUENCE DESCRIPTION:

50

GATCCCATG GAAGGAATGC TCTACCTCAC AGAACTCTGA ACCCTACAGA AATATGGGCC 60
 TGCTGCCATT TCCTGAAGAC CGGGGCATCG GGGTGGGGTG ATAAAGGATA CAACCTGCAC 120

55

AGGGGGAAGT TATTAAAGAG GCTGCAAAGT CCAGCCACCC TGAAGATACT CCCCAGTGCT 180
 CCCCTCCTGC TAAAGAACCA GTTACCCAG GAAA 214

5

SEQ ID NO:247
 SEQUENCE LENGTH:208
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

10

CLONE:HUMGS00264

SEQUENCE DESCRIPTION:

15

GATCCTCAAC TATTGAAAT NATGGACTGG TGGCCCTGGT ACAGAACCAT GACTGGCTGC 60
 TGAATTCTGA AAACCAGGAC TTGGTTCAAC ATTTAAATTT GATAGTTGCC CTGATTCCCA 120
 TTTTGGGTTT GTGAAAAGTG TATGTATTTA AATTGCTGT AAAACATAAT CACTAATAAT 180
 ATGCAATAAA TATTCCTTG AAGGGAAA 208

20

SEQ ID NO:248
 SEQUENCE LENGTH:208
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00265

25

SEQUENCE DESCRIPTION:

GATCTGTGGG AGGAATGGCA AGAGAAGCAA CCGGACCCTG AGAGAAGAGT GTTAAGGAAC 60
 CTGCGCATGT GGTTAGCTTG ACCTTTCTGT TGGGCATGAC ATGGGGTTTT GCATTCTTTG 120
 CCTGGGGACC NTTAAATATC CCCTTCATGT ACCTCTTCTC CATCTCCAN TTCATTACAA 180
 GGTAAGATAA ATTGTACATG AATAGTCN 208

30

SEQ ID NO:249
 SEQUENCE LENGTH:201
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00266

35

SEQUENCE DESCRIPTION:

40

GATCAAATAT CACTAAATAC TTAAATTGT TTTACTTAAG AGTCTAATCT GGAAGTTTT 60
 CAAATCATAC TATTAATGTG TAATCTAAGC TCTTCAGATG TATCCATGAA TAATCCTGGA 120
 ACAATATTGC TTGTATTCCT GTCATAGAAC AGGTTTTGTA ATCTTTAAAA GAAATGAAAA 180
 TTTATATAAT AAAGTTTCAA A 201

45

SEQ ID NO:250
 SEQUENCE LENGTH:211
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00267

50

SEQUENCE DESCRIPTION:

GATCACCTTG GTGTTCTTG TTTGGAAGAT TATTCCTCT GAATTTCTGG GCTTGGTCTT 60
 CCAGTTGGCA TTGCCTGAA GTTGATTGA AACAATTAN TGAAATATT AAATATTGG 120
 TTCAAAAGG CAGATTATC TTCTCCCAAC ATTCTGTTAT TTCTGATACT TTTGAAAAAC 180

55

TAATAAAAAAT TAATAAAAGA CATGAACTAA A

211

SEQ ID NO:251

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00268

SEQUENCE DESCRIPTION:

GATCCAAGAA AACGCCTCAC TGCCTTAACC TTAAGTGTTC TTCCTGGCGC TAAAAAGAGC 60
 TGTATTTTTT AAAGTGCTGG GGCAACAAA GNANCCCCAA AAGAGTTGAT GTGTGTTTAA 120
 AAAGNAAAAA CCAATGAGG AACAATTGGA GATTTTATG CAGAACTAA ATAATCCTTA 180
 ATAAATAAAT CTCTATTTTG GAATCAAA 208

SEQ ID NO:252

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00269

SEQUENCE DESCRIPTION:

GATCTTCTAA AAAAGGAACA GAAATGGTG TGAATGGAAC ATTAAGTCA AATGTAGCAG 60
 ACTCTCCCCG GAATAAAAAA GAGAAATCTT CATAATGAAT TATAAGCTAA TTGATTAATG 120
 TCCCCAAGA AATCTGCTTT CTACTATATC TTTCAGCATT AGAGATTTTC CTGTTCTNGA 180
 AAATNCAGTC TGTGCTCTTT GATTN 205

SEQ ID NO:253

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00270

SEQUENCE DESCRIPTION:

GATCTAGGCA AAGAAGAATA CAAATNAAAC CCCNTTCTTT CTCGTTTCCN GTCCAACAAC 60
 TCTGTAGAGC TCTCTGCACC CGTTACCCCT TTCCACCTTT TGTATTTAAT TTTAAAGTCA 120
 NGTGTACNTG CAAGGAATGC TGGATGCAAG ATAGATACTA TATTAACTG TACTGTTATT 180
 TAAGATGTAA TAAAGCAGTT TGACATGAGA AA 212

SEQ ID NO:254

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00271

SEQUENCE DESCRIPTION:

GATCTAAGAT GATTATTTTG TAAAGACTT TCTAGTGTAC AAGACACCAT TGTGTCCAAC 60
 TGTATATAGC TGCCAATTAG TTTTCTTTGT TTTTACTTTG TCCTTTGCTA TCTGTGTTAT 120
 GACTCAATGT GGATTTGTTT ATACACATTT TATTTGTATC ATTTATGTT AAACCTCAAA 180
 TAAATGCTTC CTTATGTGAA AAAACAAA 209

SEQ ID NO:255

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00272

SEQUENCE DESCRIPTION:

GATCTGCCAG CAGTGTCTT GCAATATGAG GAAGACAGTT ACAGCCACAT TATGGCTCTC 60
ATTGAACAGT ACGCAGCACC CTGCCCCCA GCCGTCTTTC TGGGGCTTGC GCGCAAAATC 120
TACAAGCGGA GAAAGTGACC TAGAGATTGC AAGGGCGGGG AGAGGAGGCT CTCAATAAAT 180
AATCGTGTA CCTTAAA 197

SEQ ID NO:256

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00273

SEQUENCE DESCRIPTION:

GATCTATCAC CTGTAATCAT AACTGGCTTC TGCTTGAAT CCACACAACA CCAGGACTTA 60
AGACAAATGG GACTNATGTC ATCTTGAGCT CTTCAATTAT NTTAACTGTA ATTTATTTGG 120
AGTGGAGGCA TTGTTTNA GAAAAACATG TCATGTAGGT TGTCTAAAA TAAATGCAT 180
TTAACTCAT TTGAAA 196

SEQ ID NO:257

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00274

SEQUENCE DESCRIPTION:

GATCTACCA GGAGAAATGA ATATGTGAGG TGATGGATGT AACTAGCTTG ATTGTGGTAA 60
TCAATTCGC AATGTGTACA TATATCAAAA CATCACATTG TACAAAATAC ATACAGTTTT 120
TGTCAATTTA AAGATATCAG AATTCTAGAA TATGATAAAG TTGTGTTTC AAGCAAGTAA 180
AGATAGNTTA CTAAA 196

SEQ ID NO:258

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00275

SEQUENCE DESCRIPTION:

GATCAGATTT TNCATTTTIN AATGTTCCGT GTTTTCTTAA GTAGCATGTA TGACATTTAT 60
AATNTAAAA AATNTTTTAA AATATGTGTA TGATACATAT TTTNATTGT CTTAGGGCAG 120
GCTTTTGAAA ATNTCAGCCT GTAGCCAAAT GCAAGATTTT CTCCATCCTT TAATAAAAAG 180
CACACTGAGA AATCCTN 197

SEQ ID NO:259

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00276

SEQUENCE DESCRIPTION:

GATCTCTGTC TTGAGTTTCT CCTTCCCCAT CAGCTGAAGC ACTCTTCAGA GACTACGTCC 60
ACAGACACTG ATGCTGAGGC CTCCTGGAG GAAGGAGGGT TAGGGGTGCC TATCCTCAAG 120
TATTGGAAGA GCAGAATTGA GGGAGAGACC TTTCTTCCTT GTTGAGGGTG AAAAATAAAT 180
ANGAATTACA TGTCTTAA 199

SEQ ID NO:260

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00277

SEQUENCE DESCRIPTION:

GATCAAGAAG GCTGGAACGG AACTGGTTAA CTTCTTGAGC TATTTCGTGG AACTTGAAC 60
ACAGCCTGCC ACCCAGTGAA GTGTCCAGAC CATTGTCTTC CAACCCACAG TGGCCTCTAG 120
AACACCCACT GGCCAGTCCT AGAGCTCCTG TCCCTACCCA CTCTTTGCTA CAATAAATGC 180
TGAATGAATC CNNNAAA 197

SEQ ID NO:261

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00278

SEQUENCE DESCRIPTION:

GATCTGAGTC AGTCGGAATT TGTGAAACAG GGTAGCAAAC AAGATATTTT ACTTCCATGT 60
ATACAATAAT TTTTTTAAAN NNTGCAATTT GCGTTGCAGC AATCAGTGTT AAATCATTTG 120
CATAAGATTT AACAGCATTT TTTATAATGA ATGTAAACAT TTAACTTAA TGGTACTTAA 180
AATAATTTAA AAGGN 195

SEQ ID NO:262

SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00279

SEQUENCE DESCRIPTION:

GATCTAGTGT AATGGAAGAC CTTTGAGAAC CTGGGTGTAT TAACTTTGTG TATATAGTGT 60
AAATATCCCC ACTGTACTGT TAGAGGCCAA CAATTCTAGT ATGGCTTGTT GGCAAAGAGT 120
GCTACACCGT TTCAATGAAA CAATGTATGT TTGTTTAAAC TGAACAAAA TAAATACATG 180
CTTAATCCTG AAA 193

SEQ ID NO:263

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

5 CLONE:HUMGS00280

SEQUENCE DESCRIPTION:

GATCCCTGGG ACCAACCGCA TCCTCAGCTT CTTCCTCGAG AAATGCTGGA GCAGGCTGTT 60
 CAGACCGACG TTGCCATCAA AACACATACA CCCAGAAAGA AACAAACAGAA ACCAAAACTC 120
 10 ACAAGGCGCA TGATTACTTG TTTTATATTT CATGTTGGGT TTTCCCTCCC ACTATTAAAC 180
 AGTCTGTTTC CGTAAA 196

SEQ ID NO:264

SEQUENCE LENGTH:192

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00281

SEQUENCE DESCRIPTION:

GATCTGTGTTAA AAAAGAAATC TGTTTCAACA GATGACCGTG TACAATACCG TGTGGTGAAA 60
 20 ATGAATTCAG ACTTATTAAA TGATGAACCT GTTAAATCTN CTCAGTGTCT ATTTATCAGC 120
 ACAATACACA CAGGAGANCT GTTGATGGCA TATTGAATAG ATTTNCCTGA ATAANTTGCT 180
 CTGGAAACCA AA 192

25 SEQ ID NO:265

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS00282

SEQUENCE DESCRIPTION:

GATCCTCGTC TTACAGCGAA TGGTTTCAAG ATAAAAATTGA TACCAGGAGT TTCAATTACT 60
 GAAAATTACT TGGAAATAGA AGGAATGGCT AATTGTNTCC CATTCTATGG AGTAGCAGAT 120
 TTTAAAGAAA TNCTTAATGC TATATTAANC AGAAATGCAA AGGNNGTTTA TGANTGTNGA 180
 35 CCTCGCANN 189

SEQ ID NO:266

SEQUENCE LENGTH:188

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00283

SEQUENCE DESCRIPTION:

GATCTTTTGT ACTTTAGGAC ATTAAATTGT ACAACTTTTG TATATATAAA AGCTTAGGAA 60
 45 CTTTCTGTTT AGCAGGAAGG CAACACATTC CTACACTTTT AATGTATATG TTTGTTATAA 120
 TGTCCATGTA AACATGCCCT ATGTTTGTGC CTTTAAATTA GTTTGTCTCA ATAAACAAAA 180
 TGTAGAGN 188

50 SEQ ID NO:267

SEQUENCE LENGTH:206

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00284

SEQUENCE DESCRIPTION:

GATCCTGAGA ACTTGAATT CCTTGTAAT GGAGCTCGGA GCTGCACCGA GGGCAACCAG 60
 GACAGCTGTG TGTGCAGACC TCATGTGTTG GGTTCCTCTCC CCTCCTTCCT GTTCCTCTTA 120
 TATACCAGTT TATCCCCATT CTTTTTTTTT TCTTACTCCA AAATAAATCA NGGCTGCAAT 180
 GCAGCTGGTG CTGTTGAGAT TCTAAA 206

SEQ ID NO:268

SEQUENCE LENGTH:190

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00285

SEQUENCE DESCRIPTION:

GATCAGAAAA AGAAAGAAGC CAAAGAGAAA GGTACCTGGG TTCAACTAAA GCGCCANCCT 60
 GCTCCACCCA GAGAAGCACA CTTTGTGAGA ACCAATGGGA AGGAGCCTGA GCTGCTGGAA 120
 CCTATTCCCT ATGAATTCAT GGCATAATAG GTGTTAAAAA AAAAANTAAA GGGCCCTCTG 180
 GGGCTACAAA 190

SEQ ID NO:269

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00286

SEQUENCE DESCRIPTION:

GATCAAGATA TAAAAATNTC GGATTATCT TTCCCATAT CCAAGTACCA ATNCTGTTGT 60
 AAACAACGTG TATAGTGCCT AAAATTGTAT GAAAATCCTT TTAACCATTT TAACCTAGAT 120
 GTTTAACAAA TCTAATCTCT TATTCTAATA AATATACTAT GAAATAAAAA AAANNGNTTG 180
 AAAGCTAAA 189

SEQ ID NO:270

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00287

SEQUENCE DESCRIPTION:

GATCTTGTGT ATTGAGCTTA TTGTTGAAAG GGATTTTGA AGGACAGAAC AATTACTGCA 60
 TGATGAATCT TCCTNTCTCT GCCTTCTGAG CACCGNCTTT AATTTCATA TCTTCAAGTC 120
 TTGAAGAAGT TGATGTTAAT TGAAGAATTC ACTTGTCTGG TTGAAATAAA GCCTGTTTCT 180
 GTTGTGAAA 189

SEQ ID NO:271

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00288

SEQUENCE DESCRIPTION:

GATCTGATTT GCTAGTTCTT CCTTGTGAGA GTTATAAACT GAGAGTGACG TCACTTCAGC 60
CAGAACATAT TCTCCATACT CTGCATATAA TTTGTGGCTG CAGAATATTG TAATTTGTTG 120
CACACTATGT AACAAAACAA CTGAAGATAT GTTTAATAAA TATTGTACTT ATTGGAAGTA 180
ATATCN 186

SEQ ID NO:272

SEQUENCE LENGTH:185

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00289

SEQUENCE DESCRIPTION:

GATCTAAAT GTCAGCATCA TGCAAAGTGC ACGATATATA GTGAATTTNG CTCTAAAAGA 60
GCATGAACAA GTCTTTCTAA TGTTTTGTAC AGTGCCTGGC ACTCTGTGGG TGCTCAATAA 120
ATGGATAGGA GTTTTCATT GAAGGATATT TGAATTTTAA AAATAAAGTG TTTTATTCCC 180
NTAAA 185

SEQ ID NO:273

SEQUENCE LENGTH:184

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00290

SEQUENCE DESCRIPTION:

GATCTGGTCA CTGTGGTTCC TGCATGAAGA CAGTGGCTGG CGGTGCCTGG ACGTACAATA 60
CCACTTCCGC TGTACGGTA AAGTCCGCCA TCAGAAGACT GAAGGAGTTG AAAGACCAGT 120
AGACGCTCCT CTACTCTTTG AGACATCACT GGCCTATAAT AAATGGGTTA ATTTATGTAA 180
CAAA 184

SEQ ID NO:274

SEQUENCE LENGTH:185

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00291

SEQUENCE DESCRIPTION:

GATCTGATTT GCTAGTTCTT CCTTGTAGAG TTATAAATGG AAANATTACA CTATCTGATT 60
AATAGTTTCT TNATACTCTG CATATAATTT NTGGCTGCAG AATATTGTAA TTTGTTGCAC 120
ACTATGTAAC AAAACAAC TG AAGATATGTT TAATNNATAT TGTACTTATT GGAAGTAATA 180
TCAAA 185

SEQ ID NO:275

SEQUENCE LENGTH:188

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00292

SEQUENCE DESCRIPTION:

5 GATCAAAGAC ATCCTCATCC AGTATGACCG GACCCTGCTG GTAGCTGACC CTCGTCGCTG 60
 CGAGTCCAAA AAGTTTGGAG GCCCTGGTGC CCGCGCTCGC TACCAGAAAT CCTACCGATA 120
 AGCCCATCGT GACTCAAAAC TCACTTGAT AATAAACAGT TTTGAGGGA TTTTAAAGTT 180
 TCAAGAAA 188

SEQ ID NO:276

10

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00293

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SEQUENCE DESCRIPTION:

GATCGGGNTA CTACAAAGTT CTGGGAAAGG GAAAGCTCCC AAAGCAGCCT NGTCATCGTG 60
 AAGGCCAAAT NCTTCAGCAG AAGAGCTGAG GAGAAGATTA AGAGTGTGG GGGGGCCTGT 120
 NTCCTGGTGG CTTGAAGCCA CATGGAGGGN GTTCATTAA ATGCTAACTA CTTTNCCTA 180
 AA 182

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SEQ ID NO:277

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

25

TOPOLOGY:linear

CLONE:HUMGS00294

SEQUENCE DESCRIPTION:

30 GATCCAGCCA GAGGATGCCA CGCCAGCCCA GCGCTACCAG GCTGCCAAG GGGGGCGGGC 60
 CTGGGAAGAG CCCTACACGG GGCAGCACCT AGGATGGGGC AGAGACTTGT TGCATCTTTG 120
 TCCCCAGCAA AGGCTACATG TTACCTCCTT CAATTGATAA TAAACCTTC TGAGATGCAG 180
 AGGGTCCAGG TCAAA 195

SEQ ID NO:278

35

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00295

SEQUENCE DESCRIPTION:

40 GATCCCATTA ACTCGATGCT GAGTATCTAC ATGGATACAT TAAATATATT TATGCGAGTT 60
 GCAACTATGC TGGCAACTGG AGGCAACAGA AAGAAATNAA GTGACTCAGC TTCTGGCTTC 120
 TCTGCTACAT CAAATATCTT GTTTAATGGG GCAGATATGC ATTAAATAGT TTGTACAAGC 180
 AGCTTTTCGT GAAGTTTAGA AGATAAGAAA CATGTCATCA TATTTAAATG TTCCGGTAAT 240
 45 GTGATGCCTC AGNTCTGCCT TTTTCTCTGG AGAATAAATG CAGTAATCCT CTCCCAAAAA 300
 AAAAAAAAAA NNNTNNNTNN NNNTNNN 327

SEQ ID NO:279

50

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS00296

SEQUENCE DESCRIPTION:

GATCCAAATC CTCATCTTAC TTTCCTGACC TTAAGGATGT AGCTGCTGCT TGTCTGTTC 60
 AAGTTGCTGG AGCAGGGGTC ATGTGAGGCC AGGCCTGTAG CTCCTACCTG GGGCCTATTT 120
 CTACTTTCAT TTTGTATTTC TGGTCTGTGA AAATGATTTA ATAAAGGGAA CTGACTTTGG 180
 AAA 183

SEQ ID NO:280

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00297

SEQUENCE DESCRIPTION:

GATCAAAGTG GCTGCAGCAG AGTTAGCTGT CTAGCGCCTA GCAAGGTGCC TTTGTACCTC 60
 AGGTGTTTTA GGTGTGAGAT GTTTCAGTGA ACCAAAGTTC TGATACCTTG TTTACATGTT 120
 TGTTTTTATG GCATTCTAT CTATTGTGGC TTTACCAAAA AATAAAATGT CCCTACCAGN 180

SEQ ID NO:281

SEQUENCE LENGTH:180

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00298

SEQUENCE DESCRIPTION:

GATCACATGA TTTTGTCTCT CAGTTCTATT AATGTTCTTG GATTCTGTTT AATGTTCTGT 60
 TCACATTGCA GAAAAAGCAT TTGACAAAAA AATTTAGTA GCTGCTGAAA AAGCATTGTA 120
 TAAAATTCAG CATACTTTTA TGATACAAAA AACCTTCAAT AAAGTGGGTA TATATGNACN 180

SEQ ID NO:282

SEQUENCE LENGTH:178

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00299

SEQUENCE DESCRIPTION:

GATCTTGAAT TATTTATAAA CTGGAAAGTG GTTGATTAT TGTGAGTCAA AACTCTAAGT 60
 GGTAAAAAAT TAGTATGAAT TTTTAGCTT CTTAATGAAT ATGGATTAA AACTCTCCAG 120
 TTCTTATTTT ATGAAATGAC TTGCCTTTCT GGTAATACAA TGCTGATTTT TTAGTAAA 178

SEQ ID NO:283

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00300

SEQUENCE DESCRIPTION:

GATCCCAAT ATGAAGTCAT CGAAAAACCC CAGGCCTGAA GAAATAAAGT AAAAATNAAT 60

CTGGTAATTT GTCACGGATT AGTTGTACAA CTAGTTAGAA GTTTCAGAAT AACATGCAT 120
 TTCATAACTG TCAAAATGTTT TTTTAATTCT GAGTCCAAAT AAATTATTTG GTGATGTTGA 180
 AA 182

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SEQ ID NO:284
 SEQUENCE LENGTH:179
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00301
 SEQUENCE DESCRIPTION:

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GATCTCTGAG TGAGAGGGAA ANAGGTCAGA TTTATACAAC TGAGCGCCAG AGGGGAAAAT 60
 GCACCTTGTT GGAGTGAGAA ATGTTCTGAA ACTGAATTAC TTCTTGACA GCTGAGATAG 120
 CTTCTTCTGA ACTATTATTA AATAAGTGAA TACAAAGGCC CTATGATGGG AAATCCAGN 179

20

SEQ ID NO:285
 SEQUENCE LENGTH:201
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00302
 SEQUENCE DESCRIPTION:

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GATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG CTGTGGACCG GGATGCAGTN 60
 TCAGGCATGG GAGTCATTGT CCACATCATC GAGAAGGACA AAATCACCAC CAGGACACTG 120
 AAGGCCCGAA TGGACTAACC CTGTTCCAG AGNCCACTTT TTTTCTNTT TTTGANATAA 180
 AATAGCCTGT CTTTCAANAA A 201

30

SEQ ID NO:286
 SEQUENCE LENGTH:176
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00303

35

SEQUENCE DESCRIPTION:
 GATCGGAGAT GCTTTGTAAT CTACTGTCCA GCTGGAACA GCTCATGTTA CGCGGAAAAA 60
 ACTACAAGTA ATGTTCAAAT CTATTTTGGG TCATTTTAT GTACCTTTGG GTTCAGGCAT 120
 TATTTGGGGG GTTTTGTTTC CAAAGGAAC AAATAAAGTC ATATTGCTTA TAGAAA 176

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SEQ ID NO:287
 SEQUENCE LENGTH:176
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

45

CLONE:HUMGS00304
 SEQUENCE DESCRIPTION:
 GATCTTTGCT GGGAAACAGC TGTGAAGATG GACGCACCCT GTCTGACTAC AACATCCAGA 60
 AAGAGTCCAC TCTGCACTTG GTCCTGCGCT TGAGGGGGGG TGTCTAAGTT TCCCTTTTA 120
 AGGTTTCAAC AAATTCATT GCACTTTCCT TTCAATAAAG TTGTTGCATT CCCAAA 176

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SEQ ID NO:288

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00305

SEQUENCE DESCRIPTION:

GATCCGCAAG ACCAAGTACC GCCCGACCT GCGCATGGCA GCCATCCGCA GGCCAGCNTC 60
 ATCCTGCGCA NCAGAAGCCT GTAATNGTGA AGAGGAAGCG GACCCGACCC ACCAAGAGCT 120
 CCTGAGCCCC CTGCCCCCAG AGCAATAAAG TCAGCTGGCT TTCTNACCTG AAGAAA 176

SEQ ID NO:289

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00306

SEQUENCE DESCRIPTION:

GATCTCAAAA CACAGTGAGA GGTCTGAAGG CTGGCTTCTG AAGAATCCCT GATGTCTTAT 60
 TGAACAACC ACTGAGCTAC GGAGAGCTCT GCTGTGATGG GCTAGGCACT TTATATCTGT 120
 GTGAATACAG ATTTATAAAA CAGGTAAATA AACTTATCCA AGGTCACATT TCAAA 175

SEQ ID NO:290

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00307

SEQUENCE DESCRIPTION:

GATCTGAATT CTTTATGTAT ATTTGTAGCT ATATTTTATA CAAAGTGCTT TAAGTGTGGA 60
 GAGTCAATTA AACACCTTTA CTCTTAGAAA TACGGATTCTG GCAGCCTTCA GTGAATATTG 120
 GTTCTCTTT GGTATGTCAA TAAAAGTTA TCCGTATGTC AGAAA 165

SEQ ID NO:291

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00308

SEQUENCE DESCRIPTION:

GATCATTCTT TCTGTAGCTC AGGAGAGCAC CCCTCCACCC CATTTGCTCG CAGTATCCTA 60
 GAATCTTTGT GCTCTCGCTG CAGTTCCCTT TGGGTTCAT GTTTTCCTTG TTCCCTNCCA 120
 TGCCTAGCTG GNTTGACAG TTAAGTTTAT GATTATGAAA TAAAAACTA ACTGACAATT 180
 NTCAA 186

SEQ ID NO:292

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00309

SEQUENCE DESCRIPTION:

5 GATCTTGTAG AAAATTTTGA TGAGGCATCA AAGAATGAAG CTAACATAAA GTTGGTTTT 60
 TGGAAGCTGG CATGGACTAG ATTTAACAAA TCAGCTATGT GGTTCCAAAG TTTTACAGAC 120
 ATGGAGAACA TCACCTGTGA CTAGTTCAGT AATATAAATA TTTTGTATAT TAATN 175

SEQ ID NO:293

10 SEQUENCE LENGTH:406

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00310

15 SEQUENCE DESCRIPTION:

GATCAGATTA CCAGGAACAT CAGGAGTGGG TTCCTGCCCC AACCAAACCG CATTTCGTGTG 60
 GATTTTTTTA TTCAACTTAA TTGGCTATTC CAAAGATTTT TTTTTCCTA TTTTGTACGA 120
 TTGGNGCCCT TAAGATGCAC GATGGAATTG TGTTCCTTNCGT TTTTNGGTAA AAGGAGCAAA 180
 GCGNGGNCTT GGAGATAAAC GCTGGAGCAA TCTCCTTGGG AGGATTCAGC ACGAGTAGAT 240
 20 GGTAACATT TAAAGGGGAA AGGGGGGTTT GTTTAAAAA GTAAATCAGT AAGTCACTTC 300
 TAAATTTAAA GAAACCAAAA TTGGGAGTTG AAGAATAAGT AGGGTTTCCA ATTGGGCTAT 360
 TGCCGNTTTN CTTTGNAAAA ATTAACCACAT TTTTAAAAA CCTAAA 406

25 SEQ ID NO:294

SEQUENCE LENGTH:218

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00311

30 SEQUENCE DESCRIPTION:

GATCCCATAG ACCAGAGCCC ACCTTTTNN TAAACTTAGT AAAGTCTTNG AGACTAGAAG 60
 CAAGATAGTT TGTGACACAT AAGCTTCCCA AAAACTNGAA TAGATTTTNA CTGAATAGTG 120
 GTCTATCTGA TGGTATATGT TTCTTAAAGG TCCAANTGTA ATAAAAAANA TTGAAAAANA 180
 35 GGTCTCAGTG TTTTNAATGC ACTNCATATT TGTNTGCN 218

SEQ ID NO:295

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS00312

SEQUENCE DESCRIPTION:

GATCCACCAA GCACGCCTAT NAATACAAAG TAAACTATNA TTTTNTATTGT GAAATTTTCA 60
 45 TAGATGGAAT ATTGAATATN CTGTCCATTT CATTTTACAA TNATCTTACC ACTTATTTT 120
 GTACCATGTA TTTCAATTGC CTGTTTAGTG AAAAATAAAA ATTAATAAAA CCTAAA 176

SEQ ID NO:296

SEQUENCE LENGTH:172

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

55

CLONE:HUMGS00313

SEQUENCE DESCRIPTION:

5 GATCCCAGCA AGATAATGTC CTGTCTTCTA AGATGTGCAT CAAGCCTGGT ACATACTGAA 60
 AACCCCTATAA GGTCTCTGGAT AATTTTTGTT TGATTATTCA TTGAAGAAAC ATTTATTTTC 120
 CAATTGTGTG AAGTTTTTGA CTGTTAATAA AAGAATCTGT CAACCATCTA AA 172

SEQ ID NO:297

10 SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00314

15 SEQUENCE DESCRIPTION:

GATCGGTGAC ATCGTCAAGA TGGGCGAGTG CCGGCCTCTG AGCAAGACAG TCGGCTTCAA 60
 CGTGCTCAAG GTCACCAAGG CTGCCGGCAC CAAGAAGCAG TTCCAGAAGT TCTGAGGCTG 120
 GACATCGGCC CGCTCCCCAC AATGAAATAA AGTTATTTTC TCATTCCCAG AAA 173

20 SEQ ID NO:298

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00315

25 SEQUENCE DESCRIPTION:

30 GATCGTTTCC AGATGAGAAT TCACAAGCGA CTCATTGACT TGCACAGTCC TTCTGAGATN 60
 TGTTAAGCAG ATTACTTCCA TCAGTATTGA GCCAGGAGTT GAGGTGGAAG TCACCATTGC 120
 AGATGCTTAA GTCAACTATT TTAATAAATT GATGACCAGT TGTTAAA 167

SEQ ID NO:299

SEQUENCE LENGTH:171

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00316

35 SEQUENCE DESCRIPTION:

40 GATCTGGTGG TGGAAGTGGT GGATATGGTA GCAGAAGGTT CTAAAAACAG CAGAAAAGGG 60
 TTGAATGAGA ACCCTACTTG CCTAAATNAG GAATGTCTTT CCTACCATCT AAAATACGAA 120
 GGTTTCTGGC TGGGTAAGGT TTGTAGTTGA CAGTAAAACC TGATGACACC N 171

SEQ ID NO:300

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00317

SEQUENCE DESCRIPTION:

50 GATCCGAGTG TGATTGGAAT TCTGTGATAT TTTCACACTG GTAAATGTTA CCTCTATTTT 60
 ACTTACTGCT ATAAATAGGT TTATATTATT GATTCACCTA CTGACTTTGC ATTTTCGTTT 120
 TTAAAGGAT GTATAAATTT TTACCTGTTT AAATAAAATT TAATTTCAAA TGTAAG 176

55

SEQ ID NO:301
 SEQUENCE LENGTH:169
 SEQUENCE TYPE:nucleic acid
 5 TOPOLOGY:linear
 CLONE:HUMGS00320
 SEQUENCE DESCRIPTION:
 GATCTTTGTT TTGTGTTTAA CCATAATGGT TGTGTACTGA ACCACTTCAT ATTTGTAATA 60
 10 TATAATATAT ATATATNNGN TNCCCTNAAG ACTCAGCCTC CTGGTTTACC CCCCCGGCCT 120
 GGGCATCTNA CCTCCCCAC CCCAGTGTGA TTAAACATCC NGGNACTGN 169

SEQ ID NO:302
 SEQUENCE LENGTH:174
 15 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00322
 SEQUENCE DESCRIPTION:
 20 GATCTAGCTC TGAATGTATG TTTCCTGACG TTTTACATTT CCACTTTCCT ATTCCATTCA 60
 TTAAGCTAGC CAACAATCCA CCATCCTTTA AAGATTGTTT TCATAACTGA ACAAAAACCA 120
 CATAATCTAA ATAGAGCAA GCTACAAGAA ATAAATTTAT TTAAACGCAA GAAA 174

SEQ ID NO:303
 25 SEQUENCE LENGTH:177
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00323
 SEQUENCE DESCRIPTION:
 30 GATCCTAGCA TATGTTAAAA TTCAAATTAA TGTAACACAG ATTAACAACA ACAAAGAAAC 60
 TGTCTATTG AGTGAAGTCA TGCTTTCTAT TATAATAACT TGGCTTCGGT TATCCATCAA 120
 ATGCACACNN ATACTGTTAT CTGATTGTTT ATAATAAAGA ATACTGTACC TNNTAAA 177

35 SEQ ID NO:304
 SEQUENCE LENGTH:167
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 40 CLONE:HUMGS00325
 SEQUENCE DESCRIPTION:
 GATCAGATGG TTTTAGTATT GTGGCAGAAG CGAGAAAAC TGTGTTATTG AAAAAAAAG 60
 AAAAAAGAAAG CAAGAAAAAA AGATACTATG GGGTCAAGTG TAACTCCATG GAAATGCCAC 120
 GTCTGCTCTT CAGTGAAGAA GCTGGTTTAG AGTCTCACAG AAAACTN 167

45 SEQ ID NO:305
 SEQUENCE LENGTH:170
 SEQUENCE TYPE:nucleic acid
 50 TOPOLOGY:linear

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EP 0 679 716 A1

CLONE:HUMGS00327
SEQUENCE DESCRIPTION:
5 GATCGCTCAC AATNTTTCCT CCAAGAACCG CAAAGCCATC GTGGAAAGAG CTGCCCAACT 60
GGCCATCANA GTCACCAACC CCAATNCCAG GCTGCGCAGT GAAGAAAATA AGTAGGCAGC 120
TCATGTGCAC ATTTTCTGTT TAAATAAATG TAAAACTGC CATCTGGAAA 170

SEQ ID NO:306
10 SEQUENCE LENGTH:171
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00328
SEQUENCE DESCRIPTION:
15 GATCGGGAAT GGTCTGTGTG TTATCAGCTG CGACTGGTTC ACTGCGNCTT AGACAAGCCT 60
CATGGGGACT GGGGATTCTG GCCAGTGTA TTTCTGTCAA CCACGGACGT TTGCCTTCAT 120
GTGTAGAATT TACTGTTGTT ATGCAAATTA TATTTTCAAT TATAAATGAA A 171

SEQ ID NO:307
20 SEQUENCE LENGTH:164
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00329
25 SEQUENCE DESCRIPTION:
GATCAGACAG AATAATATTT NCTAGTTATT ATGTGTAAGA TGAGTTGCTA TTTTCCTAAT 60
GCTCATTCTG ATACAACTAT TTTCCGTGTC AAATATCTAC TGTGCCCAAA TGTACTCAAT 120
TTAAATCATT ACTCTGTAAA ATAAATAAGC AGATGATTCT TAAA 164

SEQ ID NO:308
30 SEQUENCE LENGTH:261
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
35 CLONE:HUMGS00330
SEQUENCE DESCRIPTION:
GATCCCCGCC CTGGGGTCTG GTCCTCGCCC ATCCTGCAGG GATTGCCAC CGTCTTCCAG 60
ACACCCACCC TGAGGGGGGC ACCAGGTTTA GTGCTGCTGC TTTCAGTNT GCACCCGCGC 120
CCTCGGGCGG CCCCCGAGC AGCCTTTGTA CTCTGCTTGC GGAGGGCTGG GAGACCTCC 180
40 AGGACATTCC CACNNTCNC CATGCTGCCA AGTTNNNNCT ATAGCTACAA ATAAAAAAA 240
ACCTTGTTTT CAAGAAATAA A 261

SEQ ID NO:309
45 SEQUENCE LENGTH:163
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00331
50 SEQUENCE DESCRIPTION:
GATCGAGTCA AGATGAGTTA GTGGAGCTGG GCTTGCCAG GGAGTCTGGG GACAAGGAAG 60

55

CAGATTTTCC TGATTCTGGC TCTAGCTTCC CTGCCAAGAT TTTGGTTTTN ATTTTTTTAT 120
TTGAACTTTA GTCGTGTAAT AAACCTACCA GTGGCAAACC AAA 163

5 SEQ ID NO:310
SEQUENCE LENGTH:165
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00332
10 SEQUENCE DESCRIPTION:
GATCATGCTG CTGTGATACT GAGTTTTCTA AACAGCATAA GGAAGACTTG CTCCCCTGTC 60
CTATGAAAGA GTATAGTTTT GGAGGGGAGA AGTGGGACAA AAAAGATGCA GTTTTCCTTT 120
GTATTGGGAA ATGTGAAAAT AAAATTNTCA ACTCTTTCAG TTAAG 165

15 SEQ ID NO:311
SEQUENCE LENGTH:164
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
20 CLONE:HUMGS00333
SEQUENCE DESCRIPTION:
GATCTCAGTT TCCTGGCTTT TCCTCCCTCA GCGCCTTCTC ACCCCTTTGC TGTCTGTGT 60
AGTGATTGG TGAGAAATCG TTGCTGCACC CTTCCTCCAG CACCATTAT GAGTCTCAAG 120
25 TTTTATTATT GCAATAAAG TGCTTTATGC CGGCTTTTCT CAAA 164

SEQ ID NO:312
SEQUENCE LENGTH:337
SEQUENCE TYPE:nucleic acid
30 TOPOLOGY:linear
CLONE:HUMGS00334
SEQUENCE DESCRIPTION:
GATCATTGAA TGTGAGACCC TTCTAACATG ATTTGAGAAG CTGTACAAGT ATAGGCAGAG 60
35 TTATTTTCTT GTTTACATTT TTTTTTTGTT TTGGGGAAAA AATTGGTAGG TGTCTAATNA 120
CTGTTTACTT CATTGTTATA TTGCAGTAAA AGTTTAAAN CANCCATTGC ATGTTNGCTT 180
TTGATGTATC CCTTTGNGAA ATTAGCACTT TTGGGGCCAN TGGNGAAATG CAGCATTAC 240
TCTCCCTGTC TTTTCCCTT CCCTCAGCAG AAACGTGTTT ATCAGCANGT CGTGAGTCAA 300
40 ACTGCTGCCT TTTAAAAANC CCACAAANTT GNTNNGN 337

SEQ ID NO:313
SEQUENCE LENGTH:176
SEQUENCE TYPE:nucleic acid
45 TOPOLOGY:linear
CLONE:HUMGS00335
SEQUENCE DESCRIPTION:
GATCCGCCGT CACTGGGGTG GCAATGTCCT GGGTCCTAAG TCTGTGGCTC GTATCGCCAA 60
GCTCGAAAAG GCAAAGGCTA AAGAACTTGC CACTAACTG GGTTAAATGT AACTGTGTTA 120
50 GTTTTCTGTA CATAAAAAATA ATTGAAATAA TACAAATTTT CCTTCAGCCA GTGAAA 176

55

SEQ ID NO:314

SEQUENCE LENGTH:176

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS00336

SEQUENCE DESCRIPTION:

10 GATCACCTCT GAGACCCACC TTGCTCATAA AAAAAATGCC CATGTTGGTC CTCTGCCCTG 60
GACCTGTGAC ATTCTGGACT ATTNNTGTGT TTATTTGTGG CCGAGTGTA CAACCATATA 120
ATAAATCACC TCTCCGCTG TTTTAGCTGA AGNATTANGN CATCTTGTCT ATTAAA 176

SEQ ID NO:315

SEQUENCE LENGTH:258

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00337

SEQUENCE DESCRIPTION:

20 GATCATATTT AATGAATTAT AGTATAATGC TTGCAGGCC AGTACAAGCA TATATATNGT 60
GCCTCTTACA GCCTTTGGAA TACATTGTTT CCATTTTITA AATATCTTCT ATATCCNNNT 120
AGTATTCAAA TTATTAATGC TCATGTACCA AGGTNTTGCT ATAAAAGTTT TGTCTGTATG 180
AATAATGTGG CTTAGTAAA TAATCATTTN TCAACTGTAA ACTNATTCTG AAATAAAGTA 240
AAATNCTAAT TGTTTAAA 258

25

SEQ ID NO:316

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS00338

SEQUENCE DESCRIPTION:

GATCTTGGAC ACTTACAGAT TGAGCTGTAT GAATTCAGCG GGTCTCACTC CAGAGGGTCA 60
GAACGTTTGC TTTAGTTTTT TCATCTGTTT TGTTCTTGA GTCAGTGCTG TTGATGATGA 120
35 GTTGTCTTGA ATAAATNATG TGTTCTTTGC AAA 153

SEQ ID NO:317

SEQUENCE LENGTH:157

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00339

SEQUENCE DESCRIPTION:

45 GATCAAAGCT AGAAAATGNA GATTCCTTAG CCTGGATTTC CTTCTAACAT GTTATCAAAT 60
CTGGGTATCT TTCCAGGCTT CCCTGACTTG CTTAGTTTTT TAAGATTGTG GTTTNCTNT 120
NTCCACAAGG AATAAATGAG AGGGAATCGA CTGTAAA 157

SEQ ID NO:318

50 SEQUENCE LENGTH:161

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00340

SEQUENCE DESCRIPTION:

GATCTCCTTA TATAGCAGCC AAAATCAATG AAGCTAAAGA TTTACTAGAA GGTCAGCTA 60
AAAAATGAAG TAAATGTATG ATGAATTTTA AGTTCGTATT AGTTTATGTA TATGAGTACT 120
AAGNNTTTTA TAATAAAATG CCTCAGAGCT ACAATTTTAA A 161

SEQ ID NO:319

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00341

SEQUENCE DESCRIPTION:

GATCTGAAAA CATGTAGAGA AGATGAGTTG AGGACAGCTT TTCTAAGGCA ATGTNATGTC 60
TTTCCTTTCT NATTTCTNTT TCTCTGCGTT GTTAGTTTTN AAGAGTGGAG GAGCTAGGGG 120
CTCCAGAAAG AATCTTACAC ATGTTTTGAA GACATTGATG TCATAGGGAG CGGGGAGCTG 180
CATTCCCTTC TGGGCTGTTA CTGCTAAATC TCAGTATGAA CAGACCAGGC GGAAAGCTTG 240
GTGGCCAAGC AGTCTGTGTG CTCCCCGCT GATGGAGAAC GTTGCCTTGT TCACAATAGG 300
GCCTCATGGG TGN 313

SEQ ID NO:320

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00342

SEQUENCE DESCRIPTION:

GATCTTGTTT ACAAGTAATC TGTGACAGT GCCAATAAAT NATAAAAAAA AAATTAACAT 60
GTCACAATGT AACGGATGAC CATATGCACA ATTCCATGAA TTAAATCTGT TTCCTGTGTT 120
AGTCAGTATT CTAAATAAA ATTTATAATT GAAACATGAA A 161

SEQ ID NO:321

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00343

SEQUENCE DESCRIPTION:

GATCTATTGA NAGCCCTCTC TCNCATTCTG TAATGAGTAC AGCAGAGACC TTCCTGCTTT 60
TAACTGGGGA CTCCAGATTT TCCCCAAACT TGCTTCTGTT GAGATTTTTC CCTCACCTTG 120
CCTCTCAGGC ACAATAAATA TAGTTATACC ACTGCCCATC AAA 163

SEQ ID NO:322

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00344

SEQUENCE DESCRIPTION:

5 GATCATCCTA ACAATGTGGG GCTGTTAGGT TTTACCTTTG ANCTTTCATA GCACTGCAGA 60
 AACCTTTAAA AAAAAAATGN TNNATGAATT TTTCTTTCC TACAGTTGGG TAGGGTAGGG 120
 GAAGGNGGNT AAGCTTTTTT TTTTNAATG ACTGAN 156

SEQ ID NO:323

10

SEQUENCE LENGTH:255

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00346

15

SEQUENCE DESCRIPTION:

GATCATGCTG CCCTGGGACC CAACTGGTAA GATTGGCCCT AAGAAGCCCC TGCCTGACCA 60
 CGTGAGCATT GTGGAACCCA AAGATGAGAT ACTGCCACC ACCCCCATCT CAGAACAGAA 120
 GGGTGGGAAG CCAGAGCCGN CTGCCATGCC CCAGCCAGTC CCCACAGCAT AACAGGGTCT 180
 CCTTGGCAGC TGTATTCTGG AGTCTGGATG TTGCTCTCTA AAGACCTTTA ATAAATTTT 240
 20 GTACAAAGGC AAAAA 255

SEQ ID NO:324

25

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00347

SEQUENCE DESCRIPTION:

30 GATCTCTAGT ATAACACTCA GGCTACTGAG GTATTTTAGA GCAACAAGCT GGGTTACTTT 60
 CAGAGCAACC AGCTTGACTG GAACTGAGAG TAAATTGGGA ATGTATGACC AATCTTAGAC 120
 CCTGAAAAAT GGCAGAAAAT ACATGGAAAT TTGN 154

SEQ ID NO:325

35

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00348

SEQUENCE DESCRIPTION:

40 GATCTAGGGA AGACAACGTA GTCACCCTCG GTGCTTCCTC TGTCTCCTCT TTCTCCCTGG 60
 CCTGTGGTTG TCCCCAGGCC TCTGCCACCC TCCACCTCCT CGGTCAGCCC CAGCCCCAGG 120
 TTGATAAATC TATTGATTGA TTGTGATAGT AAA 153

SEQ ID NO:326

45

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00349

SEQUENCE DESCRIPTION:

50 GATCTCTAAT ATTTTAAAGC CCAAGCCCCT TGGACACTGC AGCTCTTTTC AGTTTTTGCT 60

55

TATACACAAT TCATTCTTTG CAGCTAATTA AGCCGAAGAA GCCTGGGAAT CAAGTTTGAA 120
 ACAAAGATTA ATAAAGTTCT TTGCCTAGTA TAAA 154

5

SEQ ID NO:327

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10

CLONE:HUMGS00350

SEQUENCE DESCRIPTION:

GATCAAATTC TAATGGAATT GAGCCGGTTT CTTATCCTAA ATGTTTCCTC CCTTTTACA 60

ATCTCTGTCC AGCACCTCTT GGTAAATAA TGTATGCTGT GAGACATGNA ATTAAACAG 120

15

GCCTATGGAA TAAATTATTT TAAACCAGN AGGTAAA 158

SEQ ID NO:328

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

20

TOPOLOGY:linear

CLONE:HUMGS00351

SEQUENCE DESCRIPTION:

GATCTTAAAG CAGAATGCCN TTTNCTTTT TTGCTTCAGT TGTAAGAAG AGGGAATACA 60

25

TGATAAGTA ACTGGTTTGA TTTCTCGTTC ATTGTACACT GCCTCTGAAC ANCTAATTGT 120

TTTGTAGTTGT CTAATAAAA TGCCTCTAAA ACAA 155

SEQ ID NO:329

SEQUENCE LENGTH:165

30

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00352

SEQUENCE DESCRIPTION:

35

GATCCAAGAG GAAGAATCCA GCTGCCTATG AAAATAACAA ATNAGCAACG CATCCGGATG 60

ACGGTTCCCT GTCTCTGAAA GACCTTCTC TGGAAGAGGA GTCTGCATTG TAGTGTCTCA 120

AAGACACAAT AAACCTCCTA TGGTCTGCAC TGTGTGATA TTAAA 165

SEQ ID NO:330

40

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00353

SEQUENCE DESCRIPTION:

45

GATCTACTTT GTTTGAGCAA AACAGCATT TTTGTTATGT TAATNATGGT TAATTTCCAT 60

TTTATTGGTT TTATGTTTAT TTAAATTTGT AAATGTTTGA GCATTTATNA TTGTATGTNA 120

NCTATATTN CCTATTTNAT GTTGATAAA 149

50

SEQ ID NO:331

SEQUENCE LENGTH:151

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00354

SEQUENCE DESCRIPTION:

GATCAAAATG CTAAACATG ATGATTAAGT GCACACCGTG TGCCATAGAA TGGCACATGT 60
 CATTGCCAC TTCTGTGTAG ACATGGTTCT GGTTAACATA ATATTTGTCT GTGTGCTACT 120
 AACAGATTAT AATAAATTGT CATCAGTGAA A 151

SEQ ID NO:332

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00355

SEQUENCE DESCRIPTION:

GATCTTTGTT CTAGGCAGCT GGAATAGAC ATGGTACTTA CCTTAGAGTT TTCCAATTTA 60
 TCTCAATTTT ATATGGCTTG TGATTCATT NCTTAATCCA AATATATATA ANCGTGTGTG 120
 GTCTNATTCT NCCCCCGCA ANANNAN 147

SEQ ID NO:333

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00356

SEQUENCE DESCRIPTION:

GATCCTTACG GAAAAGGAAC AGATTGTNCC TAAACCAGAN GAGGAGGTTG CCCAGANGAA 60
 AAAGATATCC CAGANGAAAC TGAAGAAACA AAAACTTATG GCACGGGAGT AAATTCAGCA 120
 TTAATAATAA TGTAATTAAG AGGAAAAGAA A 151

SEQ ID NO:334

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00357

SEQUENCE DESCRIPTION:

GATCTTTGCA GTAATTTCTA GGAGCTGTTT ATGTTTGGAG GTAATTGGTC CTTTGTCCAT 60
 ATATATGAGA TGTAAGTNTT ATTTTCCAGT TTATCTTTT GCTTATTTT TTTGACTTTT 120
 TATTGTAAAA TAAACATCA AACTGCACAG AACAGTTGAA TAGCTTAATG AATAACTACA 180
 GTAAAAGCTA TGGTAACCAC TAAA 204

SEQ ID NO:335

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00358

SEQUENCE DESCRIPTION:

GATCCAATTA ACATGTGGGG TTCTTGGTNT GGGTCTGGGG AGCTGAAGGA TTNATGGAG 60
CTGGTGCTTT GGAGGAATCT TAAGGGAAAAG NAGTAGAAGC TCAGGCCTTT AAAGGATTTC 120
ANCTCCTCCT CTCTGTAATT NNTNCN 146

SEQ ID NO:336

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00359

SEQUENCE DESCRIPTION:

GATCGCATCT NTTAAACAGG TACAAGTTGA CATGAGGTTA GTTTAATTGT ACACCATGAT 60
ATTGGTGGTA TTTATGCTGT TAAGTCCAAA CCTTTATCTG TCTGTNATTC TTAATGTTGA 120
ATAANCTTTG ANTTTTTTCC TTAAAA 146

SEQ ID NO:337

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00360

SEQUENCE DESCRIPTION:

GATCAGTGTT GAAGAAAGTG CAAAAGGAAC TTTTATATAT TTAACAGTGT AGGAAATTGT 60
CTATTCCTGA TATAATTACT GTAGTACTCT TGCTTAAGGC AAGNGTTCA NATTTACNGT 120
TGAAATAAAC CCAACTCTTC NTGNAAA 147

SEQ ID NO:338

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00361

SEQUENCE DESCRIPTION:

GATCTNGAAA ATNATCATTG AACATATTAA TGGTTATTTC TTTTCTTGG ATTTCCAGAA 60
AAGCCTCTTA ATTTATGCT TTCTCATCGA AGTAATGTAC CCTTTTTTTC TGAAACTGAA 120
TTAAATACTC ATTNATCANN NTGNAAA 147

SEQ ID NO:339

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00362

SEQUENCE DESCRIPTION:

GATCAGTTTT TTCACCTGGA AGCATTGTT TCTACTTTGA TATGACTGTT TTTCGGACAG 60
TTTATTTGTT GAGAGTGTGA CCAAAAGTTA CATGTTTGCA CCTTTCTAGT TGAAAATAAA 120
GTGTATATTT TTCCTATAAA 140

SEQ ID NO:340

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00363

SEQUENCE DESCRIPTION:

GATCTGAACT TTTCATCTGC AGAGGCAAGA AAAATATTTA ACATTGTGAC TTGACTGTGG 60
AAGATGATGG TTGCATGTTT CTAGTTTGTG TATGTTTCCA TCTTTGTAAT AAGATGATTT 120
AATAAATCTC TTAAATACT TAAA 144

SEQ ID NO:341

SEQUENCE LENGTH:291

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00364

SEQUENCE DESCRIPTION:

GATCAAAAGC TTATTATCT GTTTTNCCTT TTCGTTGGTG TAAAGCCAAC ACCCTGTCTA 60
AAAAACATAA ATTTCTTTAA TCATTTTGCC TCTTTTCTCT GTGCTTCAAT TAATAAAAAA 120
TGGAAAGAAT CTAATAGAGT GGTACAGCAC TGTATTTTT CAAAGATGTG TTGCTATCCT 180
GAAAATTCTG TAGGTTCTGT GGAAGTTCCA GTGTTCTCTC TTATTCCACT TCGGTAGAGG 240
ATTTCTAGTT TCTGTGGGC TAATTAAATA AATCATTAACT ACTCTTCTAA A 291

SEQ ID NO:342

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00365

SEQUENCE DESCRIPTION:

GATCTTAAAC CTATGATTCA GTAACCTCTT ACCATATAAA AAGGATAATT GCTTTATTTG 60
GAAAAGAATT TAGGAATACT AAGGACAATT ATTTTATAG ACAAAGTAAA AAGACAGATA 120
TTTAAGAGGC ATAACCAA 139

SEQ ID NO:343

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00366

SEQUENCE DESCRIPTION:

GATCCGTGGC AGGGCTGCTG AGGCCTGTGG GTGGGACACC ANNTGCGAAA CCCTCATCCA 60
GTTTCTCTC CATCTCTTT CTTTGTACAA TCCCATTTC TATTACCATT CTNTGCAATA 120
AACTCAAATC ACATGTCTGC AAA 143

SEQ ID NO:344

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS00367

SEQUENCE DESCRIPTION:

5 GATCCAGTGA CATTGTGAGT GAAGACGCAA ACAGGTTTTG ACTCCTGCAT GGCCGATGAC 60
CTTTTCTGTA GGCTTACCAG AAAAGTACAT NCAACAGTTC TTTGAGGTTT AACTAGAGCA 120
GCAAATAAAG CAAAAGTTN 139

SEQ ID NO:345

10 SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00368

15 SEQUENCE DESCRIPTION:

GATCAAGAAT CTTTGTGAA ATTATAGAAA TTTACTATGT AAATGCTTGA TGGAATTTTT 60
TCCTGCTAGT GTAGCTTCTG AAAGGTGCTT TCTCCATTTA TTTAAACTA CCCATGCAAT 120
TAAAAGGTAC AATGCAGAAA 140

20 SEQ ID NO:346

SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS00369

SEQUENCE DESCRIPTION:

30 GATCCAGCTT GCCAGGGACT TAGGTTTATC CTGTTTGTGTT TGCTACTGGT TACAAATTCT 60
ATTTTCTGTA CAATTAGTCA GACTAAAGTT TTCCTGTGT TTGTTTGGCA AAACAAATTA 120
AACAAAAAGT AAGGTTTTTA AA 142

35 SEQ ID NO:347

SEQUENCE LENGTH:156

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS00370

SEQUENCE DESCRIPTION:

GATCTCCGTN AACACATTT TTNTTCTTAG TCTATCTCTT GTACAAACGA TGTGCTTTGA 60
AGATGTTAGT GTATAACAAT TGATGTTTGT TTTCTNTTGT ATTTTAAACA GAGAAAAAAT 120
45 AAAAGGGGGT AATAGCTCCT TTTTCTTCT TTCAAA 156

50 SEQ ID NO:348

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS00372

SEQUENCE DESCRIPTION:

55 GATCTACAAT NGGAGTTGTG AGTNGCAATC TTACATGGCT ACGNCTTTCG TTTGATAGCC 60
AGTCATGGTN ACCACATGAG AACCATATGC TGAGATGCAA TAAAGTAAGA GAATGTTTTC 120
TGACAAAAAA ATCTN 135

SEQ ID NO:349

SEQUENCE LENGTH:133

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00373

SEQUENCE DESCRIPTION:

GATCTTAAGC GTGTCTTGAG TTCCATGCAA ATTCAATTCT GTTGATAATG TGTCCATAAT 60
CAAATCATCA TCTTGCAATG CAAGGGGTAC CCCATAATTA TCAGACATTA AAATAGTTTA 120
TTTCTTTTTC AAA 133

SEQ ID NO:350

SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00374

SEQUENCE DESCRIPTION:

GATCTCGTTC CGCCGGTTCC CCTTGGCCGC CAGTTCCGTT CTCCTCACGG GCCGAACGGA 60
ACAAGGGGTC CAGCTTGCGG GGGACCCTCC CCAGCCCATT CCTGCTGTCA AACAAACAAA 120
ACCTTGCAAA GCGCAAA 137

SEQ ID NO:351

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00375

SEQUENCE DESCRIPTION:

GATCAAGCGT GCTTTCCTTA TCCGAGGAGC AGAAAATCGT TGTGAAAGTG TTGAAGGCAC 60
AAGCAGAGAG TCAGAAAGCT AAATAAAAAA ATGAAACTTT TTTGAGTAAT AAAAATGAAA 120
AGACGCTGTA AA 132

SEQ ID NO:352

SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00376

SEQUENCE DESCRIPTION:

GATCAAGTTC CCGCTGCCCC ACCGGGTNCT GCGCCGTCAG CACAAGCCAC GNTTCACCAC 60
CAAGAGGCCC AACACCTTCT TCTAGGTGCA GGGCCCTCTT CCGNGTTTTG CCCCATAAA 120
ACTCANGAAC GNCCCGGTTA AA 142

SEQ ID NO:353

SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00377

SEQUENCE DESCRIPTION:

5 GATCAAGGAT ATTTGAAATC ACTACTGTGT TTTNCTGCGT ATCTGGGGCG GGGGCAGGTT 60
 GGGGGGCACA AAGTTAACAT ATTCTTGTTT AACCATGGTT AAATATGCTA TTTTAATAAA 120
 AATATTGAAA CTCACCAGTA AA 142

SEQ ID NO:354

10 SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00378

SEQUENCE DESCRIPTION:

15 GATCTCTAAT GAAAAAGGGA TGTCTTTTGT TTTATAGTCA TGTGGCAAGA TGAGAGTAAA 60
 ACCAGAGAGC AAACCTCTAT AAGTNTTGAG TATATGTATA CATTTGAAAT AAACCAGAAA 120
 TTTGTTACCT TAAA 134

20 SEQ ID NO:355

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00379

SEQUENCE DESCRIPTION:

25 GATCAGCTCT GAGGTGCACT TCTTCACATA CTGTACATAC CTGTGACCAC TCTTGGGAGT 60
 GCTGCAGTCT TTAATCATGC TGTTTAAACT GTTGTGGCAC AAGTTCTCTT GTCCAAATAA 120
 AATTTATTAA TN 132

30 SEQ ID NO:356

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00380

SEQUENCE DESCRIPTION:

35 GATCNGGGCT GGATTGACGG ATGTCACCCC CNATCCCCTC GTGACATGCA CGTCNGCAGG 60
 AATGGGGGGT CTGCNGTGGT CGCCNGTCGT GTGAACAAGA TTCCGTCAA ATATTTTCTG 120
 40 TTAATAAATT GCCTTCATGT AAA 143

SEQ ID NO:357

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00381

SEQUENCE DESCRIPTION:

45 GATCTAGAAG ATGATGTTCA AACTATGAAA CTGCTTGTTGA ATTGTGAAAT GACTTTGTTC 60
 50 TTTGCTTGTT TTTTNAATT TCCTATAATG NACATACTAA CTTTAAAAA ATAAAGGTTA 120
 TTTTAAAGC CTGAAA 136

55

5 SEQ ID NO:358
 SEQUENCE LENGTH:133
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00382
 SEQUENCE DESCRIPTION:
 10 GATCTTCTAT GTAACAGTTG AAATNTGGAA GTGACGTCAC TTACCTGTCT AACGTGGTGT 60
 GGGNGAGAAT TTACAAGTCC TTTATTGNAA GAATAATTGT TGCAAAATAT ATTGCTTCTA 120
 CTTTGCCTGG AAA 133

15 SEQ ID NO:359
 SEQUENCE LENGTH:130
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00383
 SEQUENCE DESCRIPTION:
 20 GATCAAGAAAT TTGGGTGGGA GAAAAGAAAG TGGGTTATCA AGGGTGATNN GAAATTTTCT 60
 GCAGCATTAA AGCTGGCGCT TAATAAGAAT AAGTAATAAT AAAGAAATTT CTAACATTCC 120
 ATGTCAGAAA 130

25 SEQ ID NO:360
 SEQUENCE LENGTH:157
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00384
 30 SEQUENCE DESCRIPTION:
 GATCTGAAAC TAATAGTAGG AGTTTCCCCA GAAGTCATTT TCAGCCTTAA TTCTCATCAT 60
 GTATAATTA CCATAAATNA TGCATGTNTG TTTACTTTAG TGACGTTCCA CAGAATAAAA 120
 GGAAACAAGT TTGCCATCTT GGTGTTGCAA TATGAAA 157

35 SEQ ID NO:361
 SEQUENCE LENGTH:132
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 40 CLONE:HUMGS00385
 SEQUENCE DESCRIPTION:
 GATCTGAAAA GGCGTCTNCA CTGCTTTATC TCATGATGCT TGCTTGTAAG ACTTGATTN 60
 AGTTTTTCAT NNCTCAAATA GGAATACTAC CTTTGAATTC AATAAAATTC ACTGCAGGAT 120
 45 AGACCAGTTA AA 132

50 SEQ ID NO:362
 SEQUENCE LENGTH:197
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

55

CLONE:HUMGS00386

SEQUENCE DESCRIPTION:

5 GATCTGCCAG GNTGGGTGGT TCTACTGCTT TCTCAATTC TAAGAACCTT TTTTTTCT 60
 NAAAGAGTTC TGCTGAATTA TTTGACAATA TTTGNAAGTA CCATGTTTCC TNGNGGGGTA 120
 TGCTCTGTNC TGGTTTCTGT TTTNAAATCA AATGCCTGTT TGGGAGGAGA TGAACGNATT 180
 NAGTCTATTA GATTTGN 197

10 SEQ ID NO:363

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15 CLONE:HUMGS00387

SEQUENCE DESCRIPTION:

GATCACAGTG TCAGAGACGC GTCCTCTTTC TTGGGGAAGT TGAGGAGTGC CCTTCAGAGC 60
 CAGTAGCAGG CAGGGGTGGG TAGGCACCCT CCTTCCTGTT TTTATCTAAT AAAATGCTAA 120
 CCTGCAAA 128

20

SEQ ID NO:364

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25

CLONE:HUMGS00388

SEQUENCE DESCRIPTION:

GATCCCAGGA GACACCAGGG CCAGAGTGAC CACAGCAGGG CAGGCATCAT CGTGTGTGTG 60
 TGTGTGTGGA TGTGTGTGTG TGGGTTTNT AAAGAATTCT TGACCAATAA AAGCAAAAAC 120
 30 TGTCAAA 127

SEQ ID NO:365

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

35

TOPOLOGY:linear

CLONE:HUMGS00389

SEQUENCE DESCRIPTION:

GATCTACAAA TGGGAAGCTT GTGAGTGGCC CATCTTTGTT GGCCTACGAA CTTTGGTTTG 60
 40 ATGCCAGTCA GGTGCCACAT GAGAACCTTT GCTGAGATGC AAATAAAGTA AGAGAATGTT 120
 TTCCTGAAA 129

SEQ ID NO:366

SEQUENCE LENGTH:125

45

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00390

SEQUENCE DESCRIPTION:

50 GATCAGCTAT TAAATTTATA TAAACATAG GCATGTTTGT ACTAATGAAA CGTACTGTCA 60
 ACCTCTATCA CATTGTAAAA TTAACACTTT TGGTGGTAAC TCAATAAAAT TGAGAAAAAT 120

55

GGAAA

125

5 SEQ ID NO:367
 SEQUENCE LENGTH:246
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00391
 10 SEQUENCE DESCRIPTION:
 GATCTTTTTA ATTATAATTT TGTTGTATTT GTTCCTAGG AGCAAGTGTT CCTGCTGCCA 60
 GTTCTTTTCT CTTTAGGCGT GGTTGAGAAA AAGCAGAAAC TTTACATAAA GCTGTATTTC 120
 TTAATCATCT TTAATTTGAA ACTTAAGNAA ATGAATTTAT TCTGTNATAT TTATGTAAC 180
 15 NATTTCTGG NAGTNATATC TACTAGTNTT GNTTGATAAT AATAAAATTN GGCTATACCT 240
 TGNAAA 246

20 SEQ ID NO:368
 SEQUENCE LENGTH:132
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00392
 SEQUENCE DESCRIPTION:
 25 GATCTAAAT TTATTGTGGT GATGTTTGCA TAACAGTGCA AATATACTGA AAACCACTGA 60
 ATTTTACACT TTAAATCAGT GGCTTCTGTG GTATGTTATC AATATTTCTC AATAAAACTT 120
 CAAAAAATA AA 132

30 SEQ ID NO:369
 SEQUENCE LENGTH:131
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00393
 35 SEQUENCE DESCRIPTION:
 GATCTGGTAT TAGGAAATTA CTTTCACAGT AAATATCAAA GAAAAAAGAT TAAGGGTCTC 60
 TTTGCCATGC TTTTCATCAT ATGCACCAAA TGTAATTTT GTACAATAAA ATTTTATTTT 120
 CTAAGTAGAA A 131

40 SEQ ID NO:370
 SEQUENCE LENGTH:123
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00394
 45 SEQUENCE DESCRIPTION:
 GATCTGAAAA AGAACACTGT GCGAGATTGT ATTCCTGCTT ATCCTTTCCA AGTTAGTAGG 60
 CAGATTGGAA CTATAGAATT TATCCGTGAT AATAATAAAG TCCGCATAAC TTTTGTCTTG 120
 AAA 123

50 SEQ ID NO:371

55

EP 0 679 716 A1

5 SEQUENCE LENGTH:123
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00395
SEQUENCE DESCRIPTION:
GATCTAAAGA GAAACTGTAG ATTGTTTTCC TGACAGCAAA AGACTAATGT GACAAAATGA 60
AGTCATTGTA AAGAAGCGAT GCAACTTGTC AAATATTTAA TAAAGAATTA TGGAAGCTGG 120
10 AAA 123

15 SEQ ID NO:372
SEQUENCE LENGTH:124
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00396
SEQUENCE DESCRIPTION:
GATCACAAC GNAAGATAAC AAGAGATTTA AGTTTAAAGG GCATTTAATC AGGAGGAAAG 60
20 GTTTGGAAAA CTAATCAGG TGTATTTNTT GTTAAAGCAG AAATAAAGTT TAATTTTNC 120
TTGN 124

25 SEQ ID NO:373
SEQUENCE LENGTH:122
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00397
SEQUENCE DESCRIPTION:
30 GATCTGTGTT AGAATGAGTG CTTCCCTTC CTACTGATGT GATTGTGGAT TAGGAATTCG 60
TGACCGAGTG ATTTTGGCC AGTGGTTGGG TTTAAATTC TATTAAATTT TGTAGTTTGG 120
GN 122

35 SEQ ID NO:374
SEQUENCE LENGTH:121
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00398
40 SEQUENCE DESCRIPTION:
GATCGCCGCC CTGCTGGCCA CCTGCGNTGG NGCTGGCNCT CGTGGTCGTC GCGCTGAGAA 60
AGTTTTCTCC CTCCTGAAGC GAATAAAGGG GCCGCNGCCG GCCGCGGCGC GACTCGGCAA 120
A 121

45 SEQ ID NO:375
SEQUENCE LENGTH:120
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
50 CLONE:HUMGS00399
SEQUENCE DESCRIPTION:

55

EP 0 679 716 A1

GATCAGGCC GGTGCCTGCA GACCTGGTGC TCCCTCGGGC AGGGCTGGGT GCCGCACCGC 60
CTGCTGGCTT TTCTGGCAGC TCCTCTGTAT CAGAACCAAT AAAGTGCAC TGTTCCTCGGN 120

5

SEQ ID NO:376
SEQUENCE LENGTH:119
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00400

10

SEQUENCE DESCRIPTION:
GATCAGGCAG TCCTTNAGGA TAGACAGATA TACACACCAC ACACACACAC CACATACACC 60
ACACACACAC GTCCCATCC ACTNACCAC ACACTACACA GNCTGNTNCC TTATAGCTN 119

15

SEQ ID NO:377
SEQUENCE LENGTH:225
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00401

20

SEQUENCE DESCRIPTION:
GATCTNATTT GTAACCCACT GAGAGGACAG AGAGAAATAA GTGCCCTCTC CCACCCCTCN 60
CCTACTGGTC TCTCTATGCC TCTCTACAGT CTCGTCTCTT NTACCCTGGC CCCTCTCCCT 120
TGGGCTGTGA TGAAAAATTG CTGACTGTAG CTTTGGGAG TTTAGCTCTG AGAACCGTAG 180
ATGGATTNCA GTTCTGGGAA AATAAAACCC GTTGATTACT NNAAA 225

25

SEQ ID NO:378
SEQUENCE LENGTH:125
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00402

30

SEQUENCE DESCRIPTION:
GATCTTAATA TATTGAAAA AAACCTCATT CTCGTGAGTC ATTTAAATGT GTACAATGTA 60
CACACTGGTA CTTAGAGTTT CNGTTTGATT CTTTTTAAT AAACCTACTCT TTGATTAAAA 120
GCAAA 125

35

SEQ ID NO:379
SEQUENCE LENGTH:147
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00403

40

SEQUENCE DESCRIPTION:
GATCTCAGTT CTGCGTTTAT TGTAAGTTGA TAAAAACATC TGGAAGAAAA TAACTAAAAAC 60
TGTTTGCATC TTTGTATGTA TTTATTACTT GATGTAATAA AGCTTATTTT CATTACAAAT 120
TTGTATTAAA ATNTGGGTTC CTTGAAA 147

45

SEQ ID NO:380
SEQUENCE LENGTH:116

50

55

EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 5 CLONE:HUMGS00404
 SEQUENCE DESCRIPTION:
 GATCACCTTT TCAGAAATTT AGATGTGAAC ACCAAAAGAA GCATTTTCTC AACAAAAATT 60
 AATAGCTGGT TCTATTTTTT TTAAACCTAG AAAAAATAAA GTTGATTTTT TTCAA 116

10 SEQ ID NO:381
 SEQUENCE LENGTH:119
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 15 CLONE:HUMGS00405
 SEQUENCE DESCRIPTION:
 GATCAATAGG GAGAGAAAAT CCACATTCTT GGGCTGAACG CGGGCCTCTG AACTGCTTA 60
 CACTGCACTC TGACCCTGTA GTACAGCAAT AACCGTCTAA TAAAGAGCCT ACCCCCAA 119

20 SEQ ID NO:382
 SEQUENCE LENGTH:115
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 25 CLONE:HUMGS00406
 SEQUENCE DESCRIPTION:
 GATCTTTATT ATGGAAANCA TTTCAAGTTT ACTCCTTCTG TTTAAGTTT TGTAGCAGTG 60
 TACCCACGCT GGGTATTACN NCCNAAATAA TCTGTNAGTG AAAGTTGCCA TTATN 115

30 SEQ ID NO:383
 SEQUENCE LENGTH:115
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 35 CLONE:HUMGS00407
 SEQUENCE DESCRIPTION:
 GATCGANCTG CGCAANTGNG NAAGCTGCAG AGGACATCGC GTACCANCTC TCACGCTCTC 60
 GGAACATCAC CTACCTGCCA GCGGGGCAGT CCGTGCTCCT CCAGCTGCCC CAGTN 115

40 SEQ ID NO:384
 SEQUENCE LENGTH:113
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 45 CLONE:HUMGS00408
 SEQUENCE DESCRIPTION:
 GATCTCTCAA AAAACAAAGA ATTACATGAG TTAGTACATG AAAAAATTAT GGGAAACTAC 60
 ATGAAATATA CTGTTACGTT CAATAACAT TAGCTTCTGT ATATAATANT AAA 113

50 SEQ ID NO:385
 SEQUENCE LENGTH:116

55

SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00409
 SEQUENCE DESCRIPTION:
 GATCTCTTCC CCCAACTTCC TAACACTTAT TAATTTATGA AACTGTTTT CTCAGCGCAG 60
 TTTTGTTTTG TGTGTCCATT GGATTACAAA CTTTATTAAA AAATATAAAA CACAAA 116

SEQ ID NO:386
 SEQUENCE LENGTH:118
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00410
 SEQUENCE DESCRIPTION:
 GATCTCTCTC TTCTCGCGCG CGCACTCTCT CTTCAACACT CCCCTGCGTA CCCCAGTTCT 60
 AGCAAACACC AATTGATTGA CTGAGAATCT GATAAAGCAA CAAAAGATT GTCCCAA 118

SEQ ID NO:387
 SEQUENCE LENGTH:247
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00411
 SEQUENCE DESCRIPTION:
 GATCTATAAA AAGTCAGCAA CTGATGTGTT TGAAAAGCAT CCTTGCTNT ATATCCTAAT 60
 GTTTGGATGT GTCTTTNCTA AAGTCTCACA AAAATTAGTG GTAGCTCACA TGACCAAAAG 120
 TGAACATAT CTNCAAGACA CTGTCTNNGG GGGGCCAGGT CTTTGTTTT TAGGNCCAGT 180
 ACTTNATAA TTTNTAGAC GGATATGGTT GTCCTATGGA TGGCAATGGG TGNTTNTCTC 240
 ATTTGNN 247

SEQ ID NO:388
 SEQUENCE LENGTH:112
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00412
 SEQUENCE DESCRIPTION:
 GATCCTAGGA AGAGAGAACA GAGTGGCTCA CAAGCCCCAA CACAGTNAGC AGCAGATGAC 60
 AGGCACNCTN AGACCACACT NTAGGCCACC CATGGGNCCA AAAGGAACA GN 112

SEQ ID NO:389
 SEQUENCE LENGTH:111
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00413
 SEQUENCE DESCRIPTION:
 GATCACCACN TAAGTCAGAA AAATGTATTT TTAAATGTTT CTTGAAGTGC CTTTGAACA 60
 TTTTAAACA GCGGATTAA ATAATGCATA AANTAAATTG CCATGNTCAA A 111

SEQ ID NO:390
SEQUENCE LENGTH:109
SEQUENCE TYPE:nucleic acid
5 TOPOLOGY:linear
CLONE:HUMGS00414
SEQUENCE DESCRIPTION:
GATCACCTTA GTTTGATTCT ATTTTTCAGC TTGCAAAAAG TGACTTATAT TCCAAAGAAA 60
10 TTAAATGTT GAAATCCAAA TCCTAGAAAT AAAATGAGTT AACTTCAA 109

SEQ ID NO:391
SEQUENCE LENGTH:111
SEQUENCE TYPE:nucleic acid
15 TOPOLOGY:linear
CLONE:HUMGS00415
SEQUENCE DESCRIPTION:
GATCGTNACG CTCGACATCTA TAGATAACGG CTCTCCAGAC CTGAGCTTTC CGCGTCANAA 60
20 TGTAGGAATN GTTTTCCTG CAGAGAATAA AAGGACCACG TGNAATACTT N 111

SEQ ID NO:392
SEQUENCE LENGTH:109
SEQUENCE TYPE:nucleic acid
25 TOPOLOGY:linear
CLONE:HUMGS00416
SEQUENCE DESCRIPTION:
GATCTTATTG AAGGACATCT TACAGCTTCC CAATGAGAGG CCAGGAAGTG TGAACATACT 60
30 GATAGAAAAA GACTATATTT TATCCCTCAT AAAATGTTTT AAATGTAAA 109

SEQ ID NO:393
SEQUENCE LENGTH:116
SEQUENCE TYPE:nucleic acid
35 TOPOLOGY:linear
CLONE:HUMGS00417
SEQUENCE DESCRIPTION:
GATCACTGAG TGTACAGAAG AGAGAAATTC AAACAAAATA TTGCTGTTCT TCAGTTTTGT 60
40 TTGTGGAATT TAAATNACT CAAATTTAAA ATAAATNACT GGACTGTGGA AATAAA 116

SEQ ID NO:394
SEQUENCE LENGTH:115
SEQUENCE TYPE:nucleic acid
45 TOPOLOGY:linear
CLONE:HUMGS00418
SEQUENCE DESCRIPTION:
GATCTCAAGA GTTCACCTGG CTNACAGAAA GAAGATGCCA GATGACACTT AAGACCTACT 60
50 TGTGATATTT AAATGATGCA ATAAAAGACC TATTGATTG GACCTTCTTC TTAAA 115

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10
SEQ ID NO:395
SEQUENCE LENGTH:114
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00419
SEQUENCE DESCRIPTION:
GATCATTCTG AACTGTACAT ATTTATGTNG CGAGAGGCAA AGGGCAAGTT TTGGATTTTC 60
CTTCTTCCAA GTTTGTTTTT AAACGACAAA TAAAAAAGA ACATTTTAAA TAAA 114

15
20
SEQ ID NO:396
SEQUENCE LENGTH:106
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00420
SEQUENCE DESCRIPTION:
GATCTGAATC TNTGACTTAT TGATTATGGA ACCTGTCAAG TAGTTTTNAA CTCTCCCAGT 60
GAGGATAATT AAACATGCTC AGCCTGAGCC ACCTCTAAGT NTCAAA 106

25
30
SEQ ID NO:397
SEQUENCE LENGTH:107
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00421
SEQUENCE DESCRIPTION:
GATCGTTCCT CATGGGGGTA AGAAAAGCTG GTCTGGAGTT GCTGAATGTT GCATTAATTG 60
TGCTGTTTGC TTGTAGTTGA ATAAAAATAG AAACCTGAAT GAAGAAA 107

35
40
SEQ ID NO:398
SEQUENCE LENGTH:112
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00422
SEQUENCE DESCRIPTION:
GATCCCCCTCA AAAGGCAGGA NTGCTGCCCT CTNCCATGGT GCGCGTNCCT CTTTGCTGTN 60
TATGTNAACC ACCCATGTAA GGAATAAAC CTGGCACTAG GTCTTAAATA AA 112

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50
55
SEQ ID NO:399
SEQUENCE LENGTH:105
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00423
SEQUENCE DESCRIPTION:
GATCANCTCT AAGGTGCAAC TNCCTCCACA TACTGTACAT ACCTGTNACC ACTCTTGGA 60
GTCTGCAAGT CTTAATCAT NCTGTTTAAAN CTGTTGTGGC ACAAN 105

5 SEQ ID NO:400
 SEQUENCE LENGTH:104
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00424
 SEQUENCE DESCRIPTION:
 10 GATCTGGAAC TTGAAGATGC CATTCATACA GCCACTTAAC CTAAAGGGAA AGCTTTGAAG 60
 GGCAAATGAC AGAGGGTAAC ATAGGAGGTN GGATNCTNAA TNNN 104

15 SEQ ID NO:401
 SEQUENCE LENGTH:104
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00425
 SEQUENCE DESCRIPTION:
 20 GATCTTTGAT ATATCATAGT CATTAAAAGA CTTTTTCGTA TTTGTATTGA TAATGTATTA 60
 AAAGTNGTTT GTNCTTAATA AAAGACTTCT TTAANCATCT NAAA 104

25 SEQ ID NO:402
 SEQUENCE LENGTH:109
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00426
 SEQUENCE DESCRIPTION:
 30 GATCCCCGGC CTCAGTCCCT ACTCTGCTTT GGGATAGTGT GAGCTTCATT TTGTACACGT 60
 GTGACTTCGT CCAGTTACAA ACCCAATAAA CTCTGTAGAG TGGAACAAA 109

35 SEQ ID NO:403
 SEQUENCE LENGTH:110
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00427
 SEQUENCE DESCRIPTION:
 40 GATCACCTGC AGCTGGCCAC ACCACAGGCC CCCGNTGCCT GCAGCACTAC TCNGTNCCTN 60
 AAACACCTGG CCTGCTAGGA GGCTCCAATA AAGCTAACCC GGACCAGAAA 110

45 SEQ ID NO:404
 SEQUENCE LENGTH:157
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00428
 SEQUENCE DESCRIPTION:
 50 GATCCTCAGA ACTTCTCTGG GACAATTTCA GTTCTAATAA TGTCTTAAA TTTTATTTC 60
 AGCTCCTGTT CCTTGAAAA TNTCCATTGT ATGTGCATT TTTAAATGAT GTCTGTACAT 120

55

AAAGGCAGTT CTGAAATAAA GAAAATTTTA AAATAAA

157

SEQ ID NO:405

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00429

SEQUENCE DESCRIPTION:

GATCAGCAAC ATTTGCTGAG CCTGTTTTN AAGCTAATGT GTATTCTNAC TAATNTNCCT 60
 ATCAAGAATG GATTGTAAAT ATATNCTGTC TATTCTAAT GTN 103

SEQ ID NO:406

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00430

SEQUENCE DESCRIPTION:

GATCTGTAAG CACAGTCTTA TTTNCTTTTG TTGTCCAGAA TACTTATAAT TCTTGAGCCT 60
 CCCAGAAATT GGAAGCTAAA TAAAGCAACT CAAGTTTCCT TTAAA 105

SEQ ID NO:407

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00431

SEQUENCE DESCRIPTION:

GATCAGCATC ATTGGAACAT GGGGACGAGT GACGGCAGGA GGACCACGAG GAAATACCCT 60
 CAAAACAACT TTGTTTACAA CAAAATAAAG TATTCCTAC CAAA 104

SEQ ID NO:408

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00433

SEQUENCE DESCRIPTION:

GATCTATCAC TCTCGTNCTT GTAGCTCCCA GCCGAGGACG TCGGATGTAA TCGTCCTTNC 60
 TGCTTTGCCA CCCCATTCCC GTCAATAAAG TGGTTTGAAC CAAA 105

SEQ ID NO:409

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00434

SEQUENCE DESCRIPTION:

GATCAAACCT TTCTGGCCTG TTATGATTCT NAACATTTGA CTTGAACCAC AAGTGAATCT 60

TTCTCCTGGT GACTCAAATA AAAGTATAAT TTNACCTGC GGAAA

105

SEQ ID NO:410

SEQUENCE LENGTH:101

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00435

SEQUENCE DESCRIPTION:

GATCAACACA AAGCACAATG NATTAACNCGN AATTCAGTAT TTTCAAATTT ACATATTTAA 60

AGTCATGCAA GCTGTAACCT CCCNGTCAAA ATTACTNGCT N 101

SEQ ID NO:411

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00436

SEQUENCE DESCRIPTION:

GATCATAAAG NNCTATCAAG GAGTTCTATC AAGGCATCCA TGTCAGTGGT GCTATGCTGG 60

TTACAACCTTG AGATTTTTGA AATAAAAAAT TTGTCATAAA 100

SEQ ID NO:412

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00437

SEQUENCE DESCRIPTION:

GATCAACAGG CTTATTAGAA GAATGAACTA AGGTGTCTAC CATGATTATN TTTCTAAGCT 60

GGTTGGTTAA TAAACAGTAC CTGCTCTCAA ATTGAAAAAG AAA 103

SEQ ID NO:413

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00438

SEQUENCE DESCRIPTION:

GATCTGTGTC TGTGTCAAAG TAACAGACTA GAACCTTCTT TCAAGTACCT GAATTGAAAT 60

NAAACTCATT TTGAATAATA AAAACTCTAG AAACCTCAA 99

SEQ ID NO:414

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00439

SEQUENCE DESCRIPTION:

GATCTGTAAT AGCATATTGT AGATGCACTT TGCAGCAGTT GGAAAAGAAA GTGTTGTGTG 60

ATTTGATTGA AATAAACTA AATGTGTTGT CCTCCTAAA

99

5 SEQ ID NO:415
SEQUENCE LENGTH:96
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00440
10 SEQUENCE DESCRIPTION:
GATCCCTGTG CCAGGAGCCA ACCTGGTCTT CCCGAGGGTC AGTGCCCCAG TGAAGACAGA 60
AGCGAGAGAA TAAAGTTCCC TGTAAGTCCT CTGTCN 96

15 SEQ ID NO:416
SEQUENCE LENGTH:97
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00441
20 SEQUENCE DESCRIPTION:
GATCCTCCCA TCCGTGTTGT GAGCACAGGC ATTTGTGTNT GGNCTGTCCT CCCTGTTGAT 60
TGGTCTGGCA TTTCCGGTAT TAAATGATA ANATAAA 97

25 SEQ ID NO:417
SEQUENCE LENGTH:93
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00442
30 SEQUENCE DESCRIPTION:
GATCCTGCAT ATCTCAAGGA CCCTAAAGTT TGTAACATCA GATATCGGGA ATAAATTCTA 60
TCACGTTACC ACTAATAAAC TTATTTTACA GTN 93

35 SEQ ID NO:418
SEQUENCE LENGTH:97
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00443
40 SEQUENCE DESCRIPTION:
GATCTGTATT TTGCAATAT TTTCTTCAAT ATGTGGCTTG TCTTTTGGTT CTCTTAACAA 60
GGTCTCTTCC AGAGTATAAN CTGTAATAT TAAGAAA 97

45 SEQ ID NO:419
SEQUENCE LENGTH:98
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00444
50 SEQUENCE DESCRIPTION:
GATCTGGACA GAATCGCCGG ACAGGTGGCA GCTGCAACAA GAAGCATTAG AACAAACCAT 60

55

GCTGGGTAA TAAATTGCCT CATTGTAAT CCTGGAAA

98

SEQ ID NO:420

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00445

SEQUENCE DESCRIPTION:

GATCTATTCT GAGTATTTT TAGAGAGTTA ATATTTATAT TTTTAGTAAT TTTCTGGTAG 60

AAGGAAATTG CACAATAAAA TNATTTGGTT TGGTTTGAAA 100

SEQ ID NO:421

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00446

SEQUENCE DESCRIPTION:

GATCGTTGGC ACCATAGCCT TATGGCCAAC AGGTGGTNTG TGGTGAAAGG GCGGTGGAGT 60

TTCAATATCA ATAAACCACC TGATATCAAT AAA 93

SEQ ID NO:422

SEQUENCE LENGTH:94

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00447

SEQUENCE DESCRIPTION:

GATCTGTGTT TNCCTGACG AATGGAATTT ATCCTCACAA ATTGGTGTTT TAAATGTNTT 60

AAGAACCTAA TTAAATAGCT GACTACAAAA CAAA 94

SEQ ID NO:423

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00448

SEQUENCE DESCRIPTION:

GATCCCAAAC CTTACGGCCA AGTTTCTTCT AGTATGATGG AAAGTTTCTT TTTTCTTTGC 60

TCTGAATAAA ACTGAACTGT GGGTTCTCTA TAAGTGGCAT TTGGGGCTTT CCTCTTTTT 120

TGTAAGCAA TGTCTGCCTA GTTTATTGTC CAGTTAACTT TAGTGACCTT TAAAAAGTTG 180

GCATTGTAAA TAAAACAACT TGCAAA 206

SEQ ID NO:424

SEQUENCE LENGTH:481

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00450

SEQUENCE DESCRIPTION:

5 GATCTCACCA CTGCACTCCA GCCTGGGCAA CAGAGCGAGA CTCTGTCTCA ACAACAACAA 60
 CAAAAAGTCC TGAACATGAT TGTGGAAGTG TGTGCTCTT TCAAGTTCTA TCACTTTTTG 120
 TTTGCAAAGT TCAAAGCTGT ATTGTTTGGT ACATATACAT GTAGGTTTGC CAAGTCTTTG 180
 TGGTGAATTG ACTCTTCTGT CATTATGTGA TGTCAATTTT TTGCCTTTTA ATAGTCTTGT 240
 CAATACTTTA CCTGATGTTT TCATAGTGAC TCCTGCATAT TTTGATTAAT GTTTGCATGG 300
 TTAATATTTT TTCATTTTAT TTTAAAGCTT ACCTGTATCA TTACTTATGA AGTCAGTTTC 360
 10 TTTGAACAGC ATATACTCAG GCCATGCTTT TTTNATTCA TTCCTGCATA TGGCTCTCCT 420
 TAAATTGGGA ATGGTGAAA ATGGNTTTAC CATTAANAAT AAATTAATTG GTATTTTAA 480
 A 481

SEQ ID NO:425

15 SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00451

20 SEQUENCE DESCRIPTION:

GATCTGGTCC ATGAGGCTGC CCAGAGAAAG CACTGCTTCT NTATGTCTCT TGTGGTATTG 60
 GAACAATAAA CCCGTACAAC CTGCAAA 87

25 SEQ ID NO:426

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00453

30 SEQUENCE DESCRIPTION:

GATCATACTT GAAAGTGAAC TTAAACATTG AAAAATCGTA CAGTCATTTT AAGAATAAGA 60
 AAATAAAATT TTCTCTTTGT CTGAACCTGC AAA 93

35 SEQ ID NO:427

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00454

40 SEQUENCE DESCRIPTION:

GATCCCATGT GCTCTCACAC CATGTTTTTG TACAGAACTG ATGGTTGAAT CTTTGTTCCT 60
 TTGAAATAAA CAGAAGAAAA TGAAA 85

45 SEQ ID NO:428

SEQUENCE LENGTH:87

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00455

50 SEQUENCE DESCRIPTION:

GATCTATTAA AGAAGTAATT GGCCTTTCTG AGCTGATTTT TCCATCTTTT GTAATTATCT 60

55

TTATTAATAA ATTGTACTTG GATTAAA

87

SEQ ID NO:429

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00456

SEQUENCE DESCRIPTION:

GATCTCATTG CATGGGAAAA AAAAAATCC TGTCTTNTTC ANAAATTGAC AATGTAAATA 60

AATTNAAATA TGGTTCCTG TTAATCTTAA A 91

SEQ ID NO:430

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00457

SEQUENCE DESCRIPTION:

GATCTGAGAA ACAGGTGTGA CAAGAGCATG AACCANAGGT GCACCTGGGG CAGTTCCTTA 60

ATAAACTGG TTTGTACAGT CAAA 84

SEQ ID NO:431

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00458

SEQUENCE DESCRIPTION:

GATCATGAGA GTGCCTGTCC CTTGTGAGCA CTATGAAAGT GTTAGCTGTT CTTTACCAGA 60

ATAAATGCAT TTCTATATCT TCN 83

SEQ ID NO:432

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00459

SEQUENCE DESCRIPTION:

GATCACCAGC TGAATAATTT GTTTTACAAT AGTTCTGTGG GGCTGTTTTT TTGTTATNAA 60

ACAAATAATT TAGATGGTGG TAAA 84

SEQ ID NO:433

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00460

SEQUENCE DESCRIPTION:

GATCTTGATG GATTTNCATA CGATTGTAAA TGNAGCTATA TTAAAGTCTA TTAAAGGAAG 60

CCCTTCTTGT TTGAGGGAGN

80

5

SEQ ID NO:434

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00461

10

SEQUENCE DESCRIPTION:

GATCTATGCT TGTTGTTTT TGTAATCCAT ATCATAGTTG CTTTCTTTAA TTGTTCC TTC 60

TGAATAAACA GTTATTAA GATAAA 86

15

SEQ ID NO:435

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00462

20

SEQUENCE DESCRIPTION:

GATCCAGTCA CTGACTCTGT CTGGTGTGA CAGAGGATTT ATTTAAGCTA TTATTTAAT 60

AAAGNACTTT GTACATTTT AAA 83

25

SEQ ID NO:436

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00463

30

SEQUENCE DESCRIPTION:

GATCTACATA CAAACAAATG CAACCAACTA TCCAAGTCGT TATACCAACG TAAAACCCCC 60

AATAAACCGT TGAACATGTG ACAA 85

35

SEQ ID NO:437

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00464

40

SEQUENCE DESCRIPTION:

GATCTGCTTT TACTTTGTAA TTTGTAGTTC TCAAAGACT TTTTTTAA AAAATAAAGN 60

CCATACTTAC ACTTAGGCTT TATAAA 86

45

SEQ ID NO:438

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00465

50

SEQUENCE DESCRIPTION:

GATCATTCTG AGTGTGCGAG TGTGTGTGCA CATGTTACAA AGGCANCTGC CATGTTAATA 60

55

AAATATTCAA TTTGAAATCC AAA

83

5

SEQ ID NO:439

SEQUENCE LENGTH:78

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00466

10

SEQUENCE DESCRIPTION:

GATCCAAACT GTCTTTTTT TGTATCTGTT ATTTAAAGCC CAGTGGATAT TTCAATNAAA 60

AAAAAATCT AAAGATGN 78

15

SEQ ID NO:440

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00467

20

SEQUENCE DESCRIPTION:

GATCTGACCA CCTCTGCCCT GTCCACCAGG ATAAGTGACA CCTAGGACCC AGGAAATAAA 60

TGCCGATGAT TTGTGTGAAA 80

25

SEQ ID NO:441

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00468

30

SEQUENCE DESCRIPTION:

GATCTTACAG GGAGAGAGAT TGGGTGCAAT TTGCCTCTTT CTTTGAATAA AAAGCTCTTT 60

GCTCACCTC AAA 73

35

SEQ ID NO:442

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00469

40

SEQUENCE DESCRIPTION:

GATCAAAAGT CTACATAACT AATACTCACA GCTGAGCTAT GTAGTATGCT ATGATTAAAT 60

TTACTTATGT AACTTTTATT GTCTTTGGCA TTAACAGTGT TTCAAAAAAT TTCCTGTGTA 120

TACCCATCAG TGATTCATTC CCAAATCTNC TAGAAGCATA AGTGTCTCAA TATATTAAAA 180

CATATTGAAT AATCAAA 197

45

SEQ ID NO:443

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00470

50

55

SEQUENCE DESCRIPTION:

GATCCAGGCG CCACGCTGGC GGTTCTGTGAG TGTCGAGGCA CCACTAAATA TAGCTGTCTG 60
CCGTCCACTC ATAAA 75

5

SEQ ID NO:444

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10

CLONE:HUMGS00471

SEQUENCE DESCRIPTION:

GATCANATTG TAAGCTTTTC TGTTTNATT CTTTTAAGAA CCTTTGAATA AAAAACATCT 60
GAAATTTTAA NAAA 74

15

SEQ ID NO:445

SEQUENCE LENGTH:73

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20

CLONE:HUMGS00473

SEQUENCE DESCRIPTION:

GATCTCTTTG TAGCCATCCT GTTAAATTG TAAACAATCT AATTAAATGG CATCAGCACT 60
TTAACCAATG AAA 73

25

SEQ ID NO:446

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30

CLONE:HUMGS00474

SEQUENCE DESCRIPTION:

GATCATGTCT GAATTATGTA TGAAAATTAT TCTATGTTT TATAATAAAA ATAATATATC 60
AGACATCGAA A 71

35

SEQ ID NO:447

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40

CLONE:HUMGS00475

SEQUENCE DESCRIPTION:

GATCTCTACC CACCCCATGC CTCTCCCNAG TCTTGATAC TAATAAAATG ATAAGCATTC 60
TGGTTCTCN 69

45

SEQ ID NO:448

SEQUENCE LENGTH:68

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50

CLONE:HUMGS00477

55

EP 0 679 716 A1

SEQUENCE DESCRIPTION:

GATCGTAATG TAAATTCTT TTACCATGTA CAAGAATTAT TAAATACAG GTACTTGACC 60
ACATTCTN 68

5

SEQ ID NO:449

SEQUENCE LENGTH:72

SEQUENCE TYPE:nucleic acid

10

TOPOLOGY:linear

CLONE:HUMGS00478

SEQUENCE DESCRIPTION:

GATCGGGCCC CGGGGGCCTG AGCCTGGGAC CCCACCCNGT GTTAATGAAA AATGAGTTT 60
GGCAGCGCCA AA 72

15

SEQ ID NO:450

SEQUENCE LENGTH:64

SEQUENCE TYPE:nucleic acid

20

TOPOLOGY:linear

CLONE:HUMGS00479

SEQUENCE DESCRIPTION:

GATCCTTTTG TAATGACTTA CACTGGAAAT GCGAACATTT GCAGTAAAAA AATATATATA 60
TAAA 64

25

SEQ ID NO:451

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

30

TOPOLOGY:linear

CLONE:HUMGS00480

SEQUENCE DESCRIPTION:

GATCATGCAT TTAGATTTAT ATTTTNCCTA NAAAATACAA GGTTATAATA AACTAAGAN 60
CTACCN 66

35

SEQ ID NO:452

SEQUENCE LENGTH:70

SEQUENCE TYPE:nucleic acid

40

TOPOLOGY:linear

CLONE:HUMGS00481

SEQUENCE DESCRIPTION:

GATCTCTATT GTAATCTCTA TTGGAGATTA CAATGATTAA ATCAATAAAT AACTGAAACT 60
TGAANATAAA 70

45

SEQ ID NO:453

SEQUENCE LENGTH:65

SEQUENCE TYPE:nucleic acid

50

TOPOLOGY:linear

CLONE:HUMGS00482

55

SEQUENCE DESCRIPTION:

GATCACTAAT TTTGCATCAG TAAATGAAT TTTTAAAA CCAATAAATC ATCAATTATT 60
 AGAAA 65

SEQ ID NO:454

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00483

SEQUENCE DESCRIPTION:

GATCACAGTT GCGTCATTGT GTATTAAATA CTTGGAATAA ATCAAGCAGG TCTCAACGCC 60
 AAA 63

SEQ ID NO:455

SEQUENCE LENGTH:68

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00484

SEQUENCE DESCRIPTION:

GATCATTAAAT TGTAAGCGC TTTGTAAAT TCACATTAC AAAATAATAA AGTCAGTTCA 60
 AACCTAAA 68

SEQ ID NO:456

SEQUENCE LENGTH:63

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00485

SEQUENCE DESCRIPTION:

GATCTGTGTC TGAGTCATCT TTGTATCTTG CCTAGCACCT ATCAATAAAT ACTTCTTGAA 60
 TGN 63

SEQ ID NO:457

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00486

SEQUENCE DESCRIPTION:

GATCATGGGA ATATGCAGAA TTTCCAATGT ATTTTAAAT ACAAATAAAA TTGTAATTTA 60
 GN 62

SEQ ID NO:458

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00487

SEQUENCE DESCRIPTION:

GATCTAACAC TAACTGTATT GTTTTGTTC CATCAAATAA ACATCTTCTG TGGACCAGGA 60
AA 62

SEQ ID NO:459

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00488

SEQUENCE DESCRIPTION:

GATCTCGGCT CACTGCAATC TCTGCCTCCC GGGTTTCAAG CTTGTCCAGG NNNATCTCAA 60
A 61

SEQ ID NO:460

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00489

SEQUENCE DESCRIPTION:

GATCAACCTG AGTTTTAAAA TACCTTTAAT AAATATNAGT NGAAAAAATG TCTACTTNAA 60
A 61

SEQ ID NO:461

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00491

SEQUENCE DESCRIPTION:

GATCAAACAC CCCACCCTCA CAAAAATGGC CACGTTGCAA TAAAAATTGT GGCATATTAC 60
N 61

SEQ ID NO:462

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00493

SEQUENCE DESCRIPTION:

GATCTTTATT TTCCCTTTGT ATTCATTTTA AGCATCTAAA TAAATTGCTG TATTGTGCTT 60
AATGTAAATA TTTGCTTTAT TACAAA 86

SEQ ID NO:463

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00494

EP 0 679 716 A1

SEQUENCE DESCRIPTION:
 GATCTCTACT ACTGTTGATT TTGCCCTCGG AGCAAAGTGA ATAAAGCAAC AAGATGAAAA 60
 CTGAAA 66

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SEQ ID NO:464
 SEQUENCE LENGTH:70
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00495
 SEQUENCE DESCRIPTION:
 GATCAAACTA GAACTCATAT GCCATACTAG ATATGGTTGT CAATAAACTT ATGACGTGAA 60
 AAAAAAGAAA 70

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SEQ ID NO:465
 SEQUENCE LENGTH:57
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00496
 SEQUENCE DESCRIPTION:
 GATCCAAAA GTGCGCGATG CGAGTAGTCA AGTCGTACTC CGCCATCTTG CCAAAGN 57

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SEQ ID NO:466
 SEQUENCE LENGTH:65
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00497
 SEQUENCE DESCRIPTION:
 GATCTAAAGC TCTTTCGATT TTATACTGAT TAAATCAGTA CTGCAGTATT TGATTAACCA 60
 AGAAA 65

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SEQ ID NO:467
 SEQUENCE LENGTH:55
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00498
 SEQUENCE DESCRIPTION:
 GATCTAAGGC AAGAGTTTCA GATTTACTGT TGGAAATAGA CCAACTCTT CATGN 55

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SEQ ID NO:468
 SEQUENCE LENGTH:56
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00500
 SEQUENCE DESCRIPTION:
 GATCATAAAT ATTAATGGNG AAAACACTGT AGTAATAAAT TTCNATATGC CAGAAA 56

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SEQ ID NO:469
SEQUENCE LENGTH:52
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00503
SEQUENCE DESCRIPTION:
GATCTGTTCA GTGCTACTCT GTACCCTCAA CATATATCCC TTGTGCGATA AA 52

SEQ ID NO:470
SEQUENCE LENGTH:54
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00504
SEQUENCE DESCRIPTION:
GATCCCCGGT NGGTTTTGTG CTCAAAATAA AAAGCCTCAG TGACCCATGA GAAA 54

SEQ ID NO:471
SEQUENCE LENGTH:57
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00505
SEQUENCE DESCRIPTION:
GATCATCCGG TTATAGAGCA TAATTTGCCA ATAAAGCTTT TGGAAAGCGGG AAAGAAA 57

SEQ ID NO:472
SEQUENCE LENGTH:60
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00506
SEQUENCE DESCRIPTION:
GATCCAGTGT TGGNATTCTT TGGTGTAAT AAACGTTTGG TTTTATTAT NCAGGTAAAA 60

SEQ ID NO:473
SEQUENCE LENGTH:51
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00507
SEQUENCE DESCRIPTION:
GATCTCATTT ATTGCCACAG ATGCACAAAA TAAATAACCC AAAATCACAA A 51

SEQ ID NO:474
SEQUENCE LENGTH:80
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

CLONE:HUMGS00510

SEQUENCE DESCRIPTION:

5 GATCATATAT TTTGACAAAA TATATTTATA ACTACGTATT AAAAGAAAAA AATAAAATGA 60
 GTCATTATTT TAAAGGTAAA 80

SEQ ID NO:475

SEQUENCE LENGTH:77

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00511

SEQUENCE DESCRIPTION:

15 GATCCAAAAC TTTAATGTTG CACNTGTATT CCAAATAAAG GGTAAAAACA GAACCAAAGT 60
 TATAACTCCA ACACAAA 77

SEQ ID NO:476

SEQUENCE LENGTH:669

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00532

SEQUENCE DESCRIPTION:

25 GATCAAAAAG AAGGCTTAGA ATTCTGCAGT TAAGCTGAGG TTAAACTAA AAANTGTTTC 60
 CTTGGGTCAG TGGTTTTNAG GTCCAGTAGC TAGGCTTTTT TCTTTTGTCC TTCCTGTTGG 120
 AATGAAAACA TTTCGATTTT CCTTCATCTG TGAAGGTGC CATAGACACA GGTTCATAGT 180
 TTTAACTTAC AGTATTGTTT GAAATTTACC TGTTTTTNTT GTCAAACTG AGCACTCCTC 240
 CTGCTGAAGT TTCTTATTTA ATTCCAGAGT ACTGTCCTCT ACTCTAAGGC ATTACTTTTA 300
 30 AGTGATTAT TAAGGCAGTT TTCAAAGGAT ATGACCAGTT GGGGGTAATT CAAATTAATA 360
 AGGAAAAGAT TTGTTGGGA AGTAACTGGG TGTCTCTAAG AGGGAATTT TAGGATGTCC 420
 AGTTTGGGAG GCTCTTTCCC CCCTCAAAT GAGANGCTCC TTGGTTAATT CAGAGCTCCC 480
 ANGACTAGGC CCTGGGCTAA CCAANCATTN GGGNGGCCAA AGGTAGGGA ACCATTNGNT 540
 35 ACCAAGCTTT TGNANCAGGG GGNNTTNTNC CATTTGGGTA ATAGGGCCCT TTCANGCCT 600
 TTANGGGTAN GCTTTTTTAN CCCNGAAACC NTNTNTNNT TTGNAATTAA ACCGGAACCT 660
 TTTGNCAAA 669

SEQ ID NO:477

SEQUENCE LENGTH:651

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00533

SEQUENCE DESCRIPTION:

45 GATCAACCTG GAGCTCTACG CCTCCTACGT TTACCTGTCC ATGTCTTACT ACTTTNACCG 60
 CGATGATGTG GCTTTNAAGA ACTTTGCCAA ATACTTTCTT CACCAATCTC ATGAGGAGAG 120
 GGAACATGCT GAGAACTGA TGAAGCTGCA GAACCAACGA GGTGGCCGAA TCTTCCTTCA 180
 GGATATCAAG AAACCAGACT GTGATGACTG GGAGAGCGGG CTGAATGCAA TGGAGTGTGC 240
 50 ATTACATTTG GAAAAAATG TGAATCAGTC ACTACTGGAA CTGCACAAAC TGGCCACTGA 300
 CAAAATGAC CNCCATTGTG GTGACTTCAT TGAGACACAT TACCTGAATG AGCAGGTGAA 360

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AGCCATCAAA GAATTGGGTG ACCACGTGAC CAACTTGCGC AAGATGGGAG CGCCCGANTC 420
 TGGCTTNGGC GGAATATCTC TTTGACAAGC ACACCN TGGG AGACAGTGNT AATGGAAGCT 480
 5 TAAGCCTTGG GGNTAATTN CCCCATANGC NGTTGGGTG ACTTCNCTGG TCANCAGGGC 540
 AGTTCANTGA ATGTTNGGGG TTNCCTTTAC CTTTNCNTTA GGTNGTCCNA AACAATCCNT 600
 NAAAGTCTTT GNTTTGNACC NTTCCGNAA TAANGGATTN GGGCCCNAA A 651

SEQ ID NO:478

SEQUENCE LENGTH:617

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00534

SEQUENCE DESCRIPTION:

GATCAAGAAA GTGGGGGAA AAAAAACAAA CGTTAAAACC TCAATCCTCA GTAGGAAGGT 60
 AGATTACATT AGGTGAAATT ATAGGTAATC TATGTATGTN CTAATGGGGT TGGAAAGAAC 120
 CTTACAGAGC ATATTACCTG ATAAACTGGA GTGGGTTTGG GAGAACAAAC TAATAGGATT 180
 20 ATNGTNTCTC CTAGTTGGTA CCTGGGAGCA ATTGACATGC CCCCTTCAGA ACCTTAACTG 240
 TTAGTAGCAG TGGCTGTAAC AACACAAACC AGTGACCAGA GATAACAGCT TTTNGGCCAA 300
 GCTGGCCTGA CGGTATGGCT GCAGGANGTG ACTGAGCAGT AGCGGTACTC AGCCAGACCA 360
 AGACGGAGAG GGGAGAGTCC ACAGCTTTCT GGAGCTAAGG CATTCTGGTG GTAGAAAAGT 420
 GTGCCCNAA G CCTCATNGG CGGGTTATAN GGTCTNAAGA TAAGTCTCCT CTTGTNTGGG 480
 25 ATNCCATACT NTGCTAAATA ACCNNGGTAT TANC CGGGTT TTCNTGTAA CNGCCTCTNG 540
 GGAGGAANTG ACTNNGNAA NTGGCACAGG TNTTTAAGCN TNAATGGAAA GGGNNAATC 600
 CTNCTCAAAN TAGAACN 617

SEQ ID NO:479

SEQUENCE LENGTH:569

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00535

SEQUENCE DESCRIPTION:

GATCTGTGAG CTGCTTAATT AATTGAAACT TCTCTGTCAT TGATGTTGCA TTTCCAAGGA 60
 GATAATCTCC TTCTTGGTGC CTAATTTTCT AGATGATAAT AGGCTAGTTT TGATTCTTG 120
 CTCATTTTCA GAATAACTTT CCAGGAAGAG ATGGCATTTA GAACTTCAGC TTTGGTGCTC 180
 40 AGGTATAAAG CCAATTAAGG TACAATTGTA CCATAAAGGG AACAATCTGT TTCTGATTGC 240
 ACAGTTTCTA ATTTTAAAA CTGNNGTGGT TTGCATTTCA TAAAAGGCAA AGTTTACAGA 300
 NCCATAAACA TTCTCAATTT TCTTTATGCT AGACATATAA ATTTATTTT CCAAACGTGA 360
 ATAGGATTTG GGGTAAAAAG NTTGTCTCAG GTNCCTCTNC CCANTTTGCC AATGGGGNAA 420
 AAAAAAGGCT TAATTTTTC CATNNTACT TNAATTTTC TAAAACCCNT GGTAACCCCC 480
 45 CATTGGNACC CCNATTTTTC CANTTTAAG GGTCTNGCAT NGGCNGGCTT TTTNAATTNN 540
 CCCTGGGGGG GTTTTNCCTG GGAGGGCCN 569

SEQ ID NO:480

SEQUENCE LENGTH:556

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS00536

SEQUENCE DESCRIPTION:

5 GATCCTGAGC NTGGTGCTGT GCTGTGGCAT CCGGAACAGC TCCGTGTACT GAGGCCCCGC 60
 AGCTCTGGCC ACAGGGACCT CTGCAGTGCC CCCTAAGTGA CCCGGACACT TCCGAGGGGG 120
 CCATCACC GC CTGTNTATAT AACGTTTCCG GTATTACTCT GCTACACGTA GCCTTTTTTAC 180
 TTTTGGGGTT TTGTTTTGT TCTGAACTTT CCTGTTACCT TTTCAGGGCT GACGTACACAT 240
 GTAGGTGGCG TGTATGAGTG GAGACGGGCC TGGGTCTTGG GGACTIONAGG GCAAGGGGTC 300
 10 CTCTGCCCT GGGGTCCAG GGTGCTCTGC CTGCTCAGCC AGGCCTNTCC TGGGAGCCAA 360
 TNGNCCAAGA GACTCAGCTT GGNCAAAANTT GGGGGGGNTN TGTNCAACCA NGCCCGCINN 420
 TCCTNTTNGG GTTGAAAAGT TTAACCTTGT TTCCCTTTCT NGCCCCGGTT TTGGAGAACC 480
 CGANTTTTTT GGGGNAATTT TTIGCTTNA ATNAACTTNT NCCTTTTTTA AAAANGTGGG 540
 15 TTTAAACTN TNAATN 556

SEQ ID NO:481

SEQUENCE LENGTH:551

SEQUENCE TYPE:nucleic acid

20 TOPOLOGY:linear

CLONE:HUMGS00537

SEQUENCE DESCRIPTION:

25 GATCTACTGT CTTGTTCAG AGGTCAAATA AAAACCTAGT CTCCTTTTAT TCTACTTTCT 60
 ATTCTTAGCT AGAATGAAAC TCAGCATATA TACACTTCTG GACATAATAA TATTGAATAG 120
 TAATTACCTT TACTAGATGA AAGAAATTTT CATTACAAAC TTAAATCATG TAAAACTCAA 180
 CAACTCAGAT TCCTGGACCT GGTGTCTTGG NTGGGTCCAA GGTGATTTTA CAGAAGNAAA 240
 AANCAACTNA AGCATTCTGG TGGCAACATA GAGATTGTAG GCTGCTTCTA AGGAAGTNAT 300
 TAACAATTNG GAAATTCNA AGTAGGATGA GAGTTAGTAA CTGGATACGA GTGAAGTTTA 360
 30 TATCCAAGTT CAGNCTCAA GGCATNATTA TGATTNGCTT CTTCCTATGT CTNCCATGGN 420
 CCTGCTTCTC AAAGTTTTTC TNATCNATCA CACTGCTGCC TAACTGCTCT GAGNATGCAT 480
 GNGGTNTTCA ATTCAGCGTN NTNTNAATCN GGNNTANCTN TGGATTGGGA TGGGATACG 540
 GACNTTAAGG N 551

35 SEQ ID NO:482

SEQUENCE LENGTH:520

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS00538

SEQUENCE DESCRIPTION:

45 GATCTTAATT TTGAAATTGA CATGAAAGTG TCATATCAGT AATCTGTGAA CCACCAGTCC 60
 TTGGTACCTA TCAGAGGGTC AAAAATCACG ATTAATATA ACCAAAAAAC TTTATAGTGA 120
 CTGATTCAAA TTTGAATACT GGTTTTAGCT AATGTAGTAG TAATGAACTG GTTTGGGGGT 180
 AAGATTTTCC TGGTATCTTA TTGCTGTAGA AATTTTCCTT TAACAGTTAC AGTGTTTTCT 240
 TCCAAATCCT TCACTTCTCT GTCCTGGCTT GTAAAGAAAA CATCTGAGGA CTGAGGGGTC 300
 ATATTTGAAT TGCTCTNTAT AATACCATAG ACTACTCATT GCTTAGACTN TACTAAGCTA 360
 GAAATCACAA GAGCATAAGC NACTCTNAAA ATTNATATNA TGNGAATGTA AAAGGTACCT 420
 50 GNCTGCAAA ATCTNGANCN TCACTTTGGC TCAAGTNTCN NGTTAACCTG TNNNNTAATA 480
 CNGNNATGTG AATTNGGCCA CCAGGTCCAT GNTTGGCAAA 520

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EP 0 679 716 A1

SEQ ID NO:483
SEQUENCE LENGTH:517
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

CLONE:HUMGS00539

SEQUENCE DESCRIPTION:

GATCATGCTT TTNGTGCCTG TCACCAGGTC TCCCAAGTGC ACTCATCCAG GTCAGTGCTC 60
AGATGTGTTT AAGGAGACCC TATATTCAGG GAAGTTGCGT GAACACTGCA GTGGGGAGAA 120
TTGAGAATAG TCAGGCCTAT CAGTCTCACA GAATCACCCC TCTACCTTTG ATATTCCACT 180
TAGCTGTAGA GTCCATCTGT TTGTCCATCT GCTGAAATGA GAAAAGAAAA ATTTATGCAC 240
TGATTAAAA CAAACCAAAA AAAAAGAAAA AAACAAAAAA AAAAATCCNT CCTTCTNGC 300
TGACCAAAAN TGTGCAGTTA ATNCTGGNG CTTGAAANTG CAGTGGTGAA TNTGGACCAA 360
GCCTGTCTGT ATATCTGGTA GCTCTTTTCT GGCTTNGTTT TTNCTTACCA GTATTCNGGC 420
CTAACGTTTT GCTTCGGGNN TGGTAATATN NCCTNGNAAG NACANCNGTG GGTGTGGAA 480
ATGGGTNGG CAAAANGGAA NTTCCNGGG TNTTGGN 517

SEQ ID NO:484
SEQUENCE LENGTH:515
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00540

SEQUENCE DESCRIPTION:

GATCTTCTGG CTCTACCACC ACAAGATATT ATCCTTGCAT CTNATGTGT CTTGAACCA 60
GAAGATTTTA AAGACATTTT GGCTACAATA TATTTNTTAA TGCACAAGAA TCCCAAGGTC 120
CAATTGTGGT CTACTTATCA AGTTAGGAGT GCTGACTGGT CACTTGAAGC TTTACTCTAC 180
AAATGGGATA TGAATGTGT CCACANNNGT CTTGAGTCTT TTGATGCAGA CAAAGAAGAT 240
ATAGCAGAAT CTACCNTTCC AGGAAGACAT ACAGTTGAAA TGCTGGTCAT TTCCTTTGCA 300
AAGNACAGTC TCTGAATNAT ACCNACAACC NGTNCTGGGA CAGTATCAAT ACTGATGAGC 360
AACCNGGCAC ACAAATATG AGCAGACCAC TTCAGCTTGA GGAATGCAGT GGGTCTGAGG 420
ATGGTCAAGT CTGTTTGCCT TAGATTTTGN TGTCACTTGG CCACACTTGA AANCTNNTT 480
GGAACAAAAN TTAAATTCG GGTTCCAAG GTAAA 515

SEQ ID NO:485
SEQUENCE LENGTH:510
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00541

SEQUENCE DESCRIPTION:

GATCTGCAGC TCTCAGAGGA CGACTGAGGC AGCCCATCTG GGGGGCCTGT AGGGGCTGCC 60
GGGCTGGTGG CCAGTNTTTC CACCTCCCTG GCAGTCAGGC CTAGAGGCTG GCGTCTGTGC 120
AGTTGGGGGA GGCAGTAGAC ACGGGACAGG CTTATNATT TATTTTNAG CATGAAAGAC 180
CAAACGTATC GAGAGCTGGG CTGGGCTGGG CTGGTGTGGC TGCTGAAGCC CCACAGCTGT 240
GGGCTGCTGA AGTCAGCTCC GCGGGGAGC TGCCCTGACG TCAGCAGACC GAGACCAGTC 300
CCAGTTCCAG GGGGAGGCCT GCAGGCNCTG GCCCTTCCAC CACCTNTGCC CTNCGTCTGC 360

EP 0 679 716 A1

AGANCTTGGT NCATCTGCAC CAGGCTCTGC TTNACTCINN NANAGTNTTT GGAAATTTGT 420
TCTNNTCCTN TGAAAGTCAC ATTTGNTTNT AAAAATTTTG TGGNTTGAAT CGGAAACGGG 480
AAGNAATAAA GCGGTGGGNG GNAGGGCAAA 510

SEQ ID NO:486

SEQUENCE LENGTH:507

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00542

SEQUENCE DESCRIPTION:

GATCCTTACA TCTGCCATT CTGTGGTTAG TCAATGGCTT GCAATAAATG TGCAAACTGC 60
ATCTATAGGA AACATTTTGT TGATTACGGA ATACTTTAGT TGATTGCTGA AAATATTGAA 120
AGGTCTTCAT TTTACAGTGA TGAGTACATA TGCATGTTTC GGGGACTTGG CCCTTCTGAT 180
GAGGGGCCCT CGGTACTCTG GATAACGAAG CTTGTGCAGA GTGGTAACCA TGCTTACACA 240
CTAAACTATA ATATAAGGA AATGAAGCCA TGTTAATCTG AGAGCAGTGT CGCCATAGTT 300
GTGTTGTTTA CAATACTCTA TAAATGGGGT TCCTGTTGCC CTGTAATTAA CCTGCTGCCC 360
GTAGAGGCCT TTCCAGTTC TTTCTGTCC TTNCCCCTTT CTTAACACAA GCTCAAATTT 420
TCCTAACTNG GTTTNNATT TGGAGGNCTT TAAAANGGN CCATTTTCAA TACCATNAAA 480
ANTAACCAGG GCTTTATAAT ANTAAAA 507

SEQ ID NO:487

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00543

SEQUENCE DESCRIPTION:

GATCCACTAC CGGAAGAAGA AACAGCTCAT NAGGCTACGG AAACAGGCCG AGAAGAACGT 60
NGAGAAGAAA ATTGACAAAT ACACAGAGGT CCTCAAGACC CACGGACTCC TGGTCTTAGC 120
CCAATAAAGA CTGTTAATTC CTCAAAAAAA NGAAA 155

SEQ ID NO:488

SEQUENCE LENGTH:499

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00544

SEQUENCE DESCRIPTION:

GATCTTAAAA ACTAACTTCT AAGATGATTT CATCTTCTCA TAGTATAGAG TTTACTTTGT 60
ACACGTTTGA AACCAACTAC TGTAGAAGAT GAGGAATCTA TTGTAATTTT TTGCTTTATT 120
TTCATCTGCC AGTGGACTTA TTTGAAATTT TCACTTTAGT CAAATNATTT TTNGTATTAG 180
TTTTTGATGC AGACATAAAA ATAGCAATCA TTTTAAATNG TCAAAATTTT CAGATTACTG 240
GTAAAAATTA TTTGAAAACA AACTTATGGG TAATAAAGGC TAGTCAGAAC CNTATACCAT 300
AAAGTGTAGT TACCATACAG ATTAATATGT AGCAAAANTG TATGCTTGAT ATTNCTCACC 360
NGTGNTAATG TTNCTGCNGT ATTCAGCNG ACCAAACCAA TATTAAGNAT GCATCTGTAT 420
AAAAATGGNG CCTATNGGNT AATGGGAATN ATTNNGGTAA TNGGCCTNTA CCNGGNTGGT 480
NATAATGGNG CCCTNTGGN 499

EP 0 679 716 A1

SEQ ID NO:489

SEQUENCE LENGTH:516

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00545

SEQUENCE DESCRIPTION:

GATCTACCCC GGACACGGGA GGCCTACGC CAGGNCCGAC GGGAAGGTTT TCCAGTTTCT 60
 TAATGCGAAA TCGGAGTCGG CTTTCCTTTC CAAGAGGAAT CCTCGGCAGA TAACTGGAC 120
 TGTCTCTAC AGAAGGAAGC AAAAAAGGG ACAGTCGGAA GAAATTCAAA AGAAAAGAAC 180
 CCGCCGAGCA GTCAAATTCC AGAGGGCCAT TACTGGTGCA TCTTTTGCTG ATATAATGGC 240
 CAAGAGGAAT CAGAAACCTG AAGTTAGAAA GGCTCAACGA GAACAAGCTA TCAGGGCTGC 300
 TAAGGNAGCA AAANAGGGCT AAGCAAGCAT CTAAGAGGNC TTGCAAATGG CTGCTTGCTA 360
 AGGCACCTTC AAAGGGCAGC ACCTTAGGCN AAAAGGATTT GTNTAAGCCN TGTGAAAAG 420
 TTTCCAGCTT CCCCGTNTTT TGGTTGGGAA NNGGNTAAAC CTTGGCAGGG TTTGNTTTT 480
 TTTAATTAAN AGGTTTGGGG TTTAANCTN TTTAAA 516

SEQ ID NO:490

SEQUENCE LENGTH:497

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00546

SEQUENCE DESCRIPTION:

GATCAAGCTG ACAGACCCNN CTCTGCTCTG ACCTGGAGGT CTCCACTCTG GTCAGCAAGT 60
 ATCCAGACAT CAGGGATGAC CACATCGGTG CGCTNCTGGC TGTGCGTGGG GACGCCAGCC 120
 GTGACATGAA GCAGACCATC ATGGAGACCC TGGAGCAGGG CCCAGCACAG GCCAGCCCCA 180
 GCTACGTGCC CCTCTTCAAG GACATTGTGG TGCCCGAGTG AACGTGGCCA AGCTGCTCAA 240
 GTAGCCTCCG CGGNCTGCCT GCTCGCCCTC CACAGCTNGG TCCTGCTTTA GAACGCGGGC 300
 AGTNATTGTC TCTTGGCACA CGTGTCCTTT TAGTGACGGC TGTNTTITAG TGCANTGTNA 360
 TGACNNGGTG TCGCTCGAGT GANGTCNGAG GGCACGTGCG GAGGCNGTAN TTTGCTGTAA 420
 AGGCTGTGGG TTCAGNGTTT NCNGACAGCG TTNNTTGGGT GTTGTNTTTC AGNGGTGAAG 480
 TGTNNGGGAA AGNGNCN 497

SEQ ID NO:491

SEQUENCE LENGTH:494

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00547

SEQUENCE DESCRIPTION:

GATCCAAGAA ACAATTCTG ATAATTGTGT GGTGATTTN TCAAAAACAT CCTGTTCTTA 60
 CTGTACAATG GCAAAAAGC TTTTCCATGA CATGAATGTT AACTATAAAG TGGTGGAAGT 120
 GGACCTGCTT GAATATGGAA ACCAGTTCCA AGATGCTCTT TACAAAATGA CTGGTGAAAG 180
 ANCTGTTCCA AGANTATTG TCAATGGTAC TTTTATTGGA GGTGCAACTG AACTCATAG 240
 GCTTCACAAA GAAGGAAAAT TGCTCCCACT AGTTCATCAG TGTATTATA NNNNAAGTAA 300
 GAGGAAAGAA TTTCACTGAT GTTTATACTA ATAAGTTTGC TAGTACAGTG TCAGTTATTT 360

AAAGTGGTAA TGCCCGNTAA TGTCTTTTAA ATGTTTTGAG GGATGTTTAA AAATACATGC 420
 NATTTGCTTC ACGGAGGAGG GNTGTAAAAA TTANTGGGCC AATAAATTGC GGGTGGGAAN 480
 CCNTNTTCTT NAAA 494

SEQ ID NO:492
 SEQUENCE LENGTH:489
 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00548

SEQUENCE DESCRIPTION:

GATCTTGACG AGGCTGCGGT GTCTGCTGCT ATTCTCCGAG CTTCGCAATG CCGCCTAAGG 60
 ACGACAAGAA GAAGAAGGAC GCTGGAAAGT CGGCCAAGAA AGACAAAGAC CCAGTGAACA 120
 AATCCGGGGG CAAGGCCAAA AAGAAGAAGT GGTCCAAAGG CAAAGTTCGG GACAAGCTCA 180
 ATAACCTAGT CTTGTTTGAC AANGNTACCT ATGATAAACT CTTTAAGGAA GTTNCCAAC 240
 ATANACTTAT AACCNNAGCT GTGGTCTCTG AGAGACTGAA GATTGAGGC TCCCTGGCCA 300
 GGGCAGCCNT TCAGGAGCTC CTTANGTAAA GGNCTTATCA AACTGGTTTC AAAGCACTGA 360
 GCTCANGTAA TTTACACCAG AANTACCANG GGTNGAGATG CTCCAGCTTG CTTGTGAAGA 420
 TGCATGATTA GGTCCACCAG CTGTACATT GGAAGAANTA NANTTNTGT TAAATCAATG 480
 NGGTNAAA 489

SEQ ID NO:493
 SEQUENCE LENGTH:487
 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00549

SEQUENCE DESCRIPTION:

GATCCTCTGN CACGGGATAA ATTTNCAGGN GAAGAGTGAG GTTGTATGG CCTCAGCTAT 60
 GCTTCCNGGC TCTCCCTCAA GAGTGCAACC TTGGCTAGAG AACTCACAGC TCTGGGAAAA 120
 AGAGGAGCAG ACAGGGTTCC CTGGGCCAG TCTCAGCCCA GCCACTGATG CTGGATGACC 180
 TTGGCCTGAC CTTGGTCTGG TCTCANAATC ACTTTTCCCA TCTGTAAAT TGAGATGAAT 240
 TTTNGTGTG AAAGTNCITC CNNGAGCAGA TGTCTAGAA GGTTTATAGG ATAGTGACAG 300
 AGTCAGGNCA CCCNAAGGGC CATGGGGAGC CAGCTGACCT GCTTNGCCGA AGGATTCTG 360
 ACAGACTATC TTTGGGGATG TTTTCAAAGA AGGGATATAG GTTATTGACN TNNGGGCATT 420
 TAAAGNAAAT TNTNTCTCGG GGATTAANTT TTAGGANAA TNAAGCTTT NGTGTCTANN 480
 GGCAAGN 487

SEQ ID NO:494
 SEQUENCE LENGTH:481
 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00551

SEQUENCE DESCRIPTION:

GATCCCCAGC TGCCACTGAA TCTGGCTGCC CTTCAGGCC ACCTGGCCCA GGAGAACCCT 60
 GTGGTGGCCT TCTTCAGCCT GGCTCTACTG CTTGCCCCAC TGGTGGAGAC GCTTATTCTA 120
 CTGGACCGGC TGCTGTACCT TCAGGAACAG GGTTTCCATG CTGAGCTCCT GCCATCTTC 180

AGTCCTGAAC TCTCTCCCAG AACCTGGTT CTGGTGGCCA CCAAGATGCC CCTGGGTCAG 240
 GCTCTTTNTG TTCTGGAGAC TGAAGACAGC TGATGCAGCC TGAGGAGACA TCTCAGACCC 300
 CATCATCTGA AAGTGNCCAG AGAGCACAGT GGCAGAGTAC ATCTNATCCA GAGAAACAGC 360
 ATCCTGCATC CTCCAGAGTC CTGGTTCCTT CAAGTTTCAT CNCTTTTNTC TCCTTTCCAT 420
 GGGNTTATGT AAATACAATT GTAAAGTTT AATTAAATTA AAAAATTGGG TTATCTGGAA 480
 A 481

SEQ ID NO:495
 SEQUENCE LENGTH:472
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00552

SEQUENCE DESCRIPTION:
 GATCTAAGCT CCAGGCACGC CTGAAGATGT GTTGCTACTC TNACATCCCG AGTTTCTGTC 60
 CACACATTGC ATGCACAGCG CCCACACAT TGGATACTGT TGTTCACGAT AATTCTCTCC 120
 GTTTTCCAGA GCATTTAACA TAGCTTGGAG GCGTAAATG GCTCTGTATT TTAATAACAC 180
 AGAAACATTT GAGCATTGTA TTTCTCGCAT CCCTTCTCGT GAGCNCTTAG ACCTTTTNTC 240
 ATTTTAGTCG GATTTGTTT TGGAAATTTG CTTTNGTATG AACACTCAGC AGAAAAGTAC 300
 TTACTTCTNG CCAGTTATCT ATTAACCAAA ACCNTTGATT TGTAAGTTTA AAGNTTAACC 360
 GNCAAGTTC TNTNCATAAC TGCCTTGGCC AGTNNGGGGT NGTNCCGGTN CTGGTTAATN 420
 GCCTGTGGCN TTTTNGGTGG TTTGTGNTTG GTNTTACNT GNGCANTTAA GN 472

SEQ ID NO:496
 SEQUENCE LENGTH:461
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00553

SEQUENCE DESCRIPTION:
 GATCAACCAA TTTTNTAAA AGTTCAGTCG AAAGCTTTTA AGTATAGCTT CCTCCCTTGA 60
 AAAAAAATGT AAATATGAC TGCTGAGTGA TAAACACTG TGGTGTGAAA GTNTCATCTT 120
 CACTGCCAAT CAGGCAAGA CCGGAAAGAT TTGCATTTTA TTATGTCTGT CTTATCATGC 180
 AATGGAAATN ATGCTTTTNG TAAGTATGCA TCTTACCAAT GATGTAACGG TTTAATACCN 240
 TTGAATGTTT TAATAACCAA GTNGCTGCTG AACTTATACT AAATCAGGGG CAAAAAACT 300
 NGCTCTNATC NNCTCAAATN GTATNCNATA TCCATTAATG TATCAGTTAT NCCAAAGCCT 360
 TCAGGTGGAG GGGTTTACCA CCNTCCTAGG TCGTTCAACC AGGTTTTGTG AGGAATGCAT 420
 TCAAAGTGGC TNTATAAAG ANGATTTTCT TTAGCATGAA A 461

SEQ ID NO:497
 SEQUENCE LENGTH:459
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00554

SEQUENCE DESCRIPTION:
 GATCCCAAAA TTCCACTTTT CAACACAGAT GTGGACAACC TAGAAGGGAA GACACCACCA 60
 GTTTTTNCTT CTAAAGGCAA ATACAGGGCT CTGAAATGG ATTTTCCTCT ACCCCCTTCT 120

ACTTACGNCA CCATGGCCAT TCGAGAAGTG CTAAAAATGG ATACCAGTAT CAAGAACCAG 180
 ACGCAGCTGA ATACAACCTG GCTTCGCTGA GCAGTACCTT GTCCACAGAT TAGAAAACGT 240
 ACACAAGTGT TTGCTTCCTG GCTCCCTGTG CATTTTGTN TTAGTTCAGA CTCATATATG 300
 GATTTCAAAT CTTTGTAATA AAAATTATTT GTATTTTAA GTNTTTATTA GCTTAAAGAA 360
 ATAATTNGCA ATATTNGTAC ATGTACACAA AATNCNGGAG GTTCTTANTT TTAGCTCAGG 420
 NTATAAATNA GTCAAATNCN NNGGTNNNGG NTNNGTGN 459

SEQ ID NO:498
 SEQUENCE LENGTH:481
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00555

SEQUENCE DESCRIPTION:
 GATCCAGCAG AGAAGGATGA AAAGGGCATG CCTGTGACAG CTCGTGTGGT GTTTGTTTTT 60
 GGTCTTGATA AGAAGCTGAA GCTGTCTATC CTCTACCCAG CTACCACTGG CAGGAACTTT 120
 GATGAGATTC TCAGGGTAGT CATCTCTCTC CAGCTGACAG CAGAAAAAAG GGTGGCCACC 180
 CCAGTTGATT GGAAGGATGG GGATAGTGTG ATGGTCCTTC CAACCATCCC TGAAGAAGAA 240
 GCCAAAAAC TTTTCCCGAA AGGAGTCTTC ACCAAAGAGC TCCCATCTGG CAAGAAATAC 300
 CTCCGCTACA CACCCAGGCC TTAAGTCTCT TGGAGAAGCT GGTGCTGTNA GCCAGAGGAT 360
 GTCAGCTGCC AATTGTGTTT TCCTGCAGCA ATTCCATAAA CACATCCTGG GTGTCATCAC 420
 AGCCAAGTTT TTTANGGTTN CTATACCAAT GGGTTTATTT AAATGAAAAT GGGCACTTAA 480
 A 481

SEQ ID NO:499
 SEQUENCE LENGTH:453
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00556

SEQUENCE DESCRIPTION:
 GATCCAGATG CAGAGGCCAG GATGTGGGCC CAGCCCTGTG CCAGGAGGCT GGCTGGAATA 60
 AAGGTACAGA TAGAGGCCTC ACCCCCTCTG GGACCACTGG CACTCAGGGT GTTTGCAGCC 120
 TCAGAGCCCA CTGCCCCCA GGGCCACAGC TGCATCTCCT GCCCTGCTGT CATTACAGGG 180
 ATGGGCAGGC TGGCATGGGG GCACCCGCTG CCCCTGCCTG GNTGTTGCTG TGTATTCCTG 240
 CCGGCCAGGG GCACTGCCAG GACCAGCCT CCNTTTNAT ATCCNGATTG TTAAGTTCTG 300
 CTATTGTGGT ATTCTGGTGG AGAAAAAGA CCGNGTGGCT GTTTTGAAC TGCCTGGAAC 360
 CTAAGACCTT GAATTCCTTT CCCCCAAGG GAAAATCTAT ATGGAAACAT TTATTTAAAT 420
 ACAGGATGAA GTAATTAAAA GNTTTAATTC AAA 453

SEQ ID NO:500
 SEQUENCE LENGTH:446
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00557

SEQUENCE DESCRIPTION:
 GATCAAAGTT GGCAAGGTGC GGACTCGAGA CATGGGCGGC TACAGACCAC AACCGACTTC 60

ATCAAGTCTG TCATCGGTCA CCTGCAGACT AAAGGGAGCT AGAGCCCTTT ATTTCTTCCA 120
 ACCTTGCAAG GACCACACTN CCCATACNT TCAGTGCAGT GTACCAGGGA AGAGCCTTGT 180
 GCCTCTAAGC AGTGGACCAT GGTCACTTG CTGGGTAGAG CCTAGGTTGT CCTTGGGCCG 240
 GCTTCCTTAG GGGACAGACT NTTGGGTGGT GATGGGGATT GTAGGATGGA GCCAGGCACA 300
 TGGATGATGA TGATTCTCCC NCACAGGTTG GAACCTCTGA CATGGGTGGC TATGCTACTN 360
 GCNATGCTTA NTGAGGNTGT CATTGCTGCT TTCCNAACC ATAGGCCTGT CATACNNTGT 420
 AAGNGTCAA TAAGGACATG ACCAAA 446

SEQ ID NO:501
 SEQUENCE LENGTH:434
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00558

SEQUENCE DESCRIPTION:

GATCCAATTC AGTTAGGCT TGTGTGATT TTTTTCAG AAAATGTATT CCATAAAGTT 60
 TGTACTTAGA CCAGACGGGT GACTAAGAA TCATTCATGA GTAAATGTGT GTTGAATATC 120
 TACCCTTGAC CTTTTTTGA GAAATAGAGT AAACACAGTC CCTGTAGTCT GACAGCTAAT 180
 GGGGAGAGAG GGTAGACTTT TCATCGAATT AAATTTCTAC ATGCACCTTT CCCCAGAAA 240
 TCTTACTCAT GGTGGTCTC AAGTAAGTCT TTATTGAAA ATATNGACAT ATCTNCTTCC 300
 TCTTCCTTCT CCTCACTGTC TTCCTTTAG TAGTTAGGCA GAGTTAATAG GTAAGAAAA 360
 TTATCTGCAT TTATGTGTAG TTTGTAATCT ACTAAAGGGG TTCTAGAATA AATGTNGNCA 420
 TNTNGTAACN GAAA 434

SEQ ID NO:502
 SEQUENCE LENGTH:430
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00560

SEQUENCE DESCRIPTION:

GATCAAAACAG GTTCAAAGTA AAACGTAAAA TTTCACATTT NTTTTAAAGA ACTCTTAAAG 60
 TGTAAACAGTT ACGCCATACT TCATAAGTGG TAAAGAAAGG TATAAAATTT GGAAACATTT 120
 TGTGGGCAT AGTAGTGATT GGGTGAAAAG GATAAATTAT ATCAAAATGA GAATGTNCTG 180
 TAATTGGAAG TAGGGAGCTA AAGGATGTTT CTTTCAGTTT AGTAGAACTG GAACGTTTAA 240
 CTATTAAACA TGGCTTTTAT AAATNCATGG TCCAATAATT TTATCACTG TTAGTATTTA 300
 ATTCACTGTC AGCTTATTAA TGTTTCTGT ACCCATTAAT GAATTTTAAA TTACAAAAAA 360
 TTGTCTAGCA GCTTCCAGTT TAANAAATGG AACCTAGGCC ATTAAATTA AATTGGTAA 420
 ATTTTTTAAA 430

SEQ ID NO:503
 SEQUENCE LENGTH:428
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00561

SEQUENCE DESCRIPTION:

GATCCTAAAT GTGTTGCTGA AATCAGGCAG CCCGAGCCTC TGGTCTCTCC AGAGAGCCCG 60

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TTTTCACATT TGTNTATTCC TCAGCACTCA CCCGAACTG AACAGATGGG GAGTGGTCTT 120
 GATTGTCAAG ATAAACTGG TGAAGAAAGC TAAATGCTGA GAACTGAGC ATCTATTGTG 180
 GTGTTTAAGC TTAGCTGGGT CCTTTCTAGT TTGTTTTTAC AGCTTACTAG GTGAAGTAGT 240
 TTGCACTATT TTNGCAATAA ATTCATGGAA AACCTAACAG TTAGTNGTNT NGTTTCTNAC 300
 TGTGTGTATA TAANCTAATA CTAAANGTNT GGCATAGTGT TTNTGCACCT NCNTACATAA 360
 CCNCTAACAT GCACAGAATG CTGGTAAATN TGATAAANTA TGANGTGANT GATGATNNGA 420
 TANAGTGN 428

SEQ ID NO:504

SEQUENCE LENGTH:422

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00562

SEQUENCE DESCRIPTION:

GATCCTCACC CTCCTGAGGC CCAGTGGGGA AGAATGAACA TGGCTTCATC CAGGTAACT 60
 NATGCTGCCA TTTGCCCAGC CTCTTCCATC CCAGCCCTGT CAGTNAGCCC AGGTCTGGTG 120
 CAACTNCTGC AGGATGCCTG TAGTAGGGAA CTCTGGAAGT GTATTGGGCT GAGGTGGGAT 180
 TTTCCCTCCC CACAGTGCAC TGAGCAATGG AGGGTGGTGA GGGAGCCATG CTGCTGAATT 240
 CTGTTGGCA TTTCCCATTT ATGTAAATG GGGTGTGGG TAGGGCAGAC TCTGCTTGGG 300
 TTTGGTTGTA AGATAAACCT GGAGGAGAAG CACAGTTGTC CCATTGAATT ATTTGAGCAA 360
 AAACTACTGT AAATAACTTT TTTGGGCTNT TGTCAAATAA AATTTTTTTT TGTTTNTTTA 420
 AA 422

SEQ ID NO:505

SEQUENCE LENGTH:417

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00564

SEQUENCE DESCRIPTION:

GATCTGATTC AGAAGGGCGT CATCCAACAC AAAGAGAAAT GCAACCAATG AAGAATCAAG 60
 CCACTGAGGC AGGGCAGAGG GACCTTTGAT AGGCTACGAT ACTATTTTCC TGTGCATCAC 120
 ACTTAACTCA TCTAACTNNT TCCCCGGACA CCCTCCACCT CTAGTTGTTA CTAAGTAGCT 180
 GCAGTAGGCA TTGCTGGGGA AGAAACAAAC ACACACCAAA CAGTACTGCT ACTTAGTTTC 240
 TAAGGCTGCA CAGGGAAGGG AAAGACTGGG CTTTGGACAA TCTAGAGGTA ATTTATATCC 300
 GCCCCCAGGT GGAGCAACAT GCGATTNTGG AGGCACGGGG GTAAGTGAAA GTGAGTACAT 360
 ATAGNTTTC TGTTTCTGG GGATAACCCA TCAATAAAAG CTGCTTCCTC TNGTAAA 417

SEQ ID NO:506

SEQUENCE LENGTH:421

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00565

SEQUENCE DESCRIPTION:

GATCTTCTTT ATAATTCTAC TTTGAGTGCT GTCTCCATGT TTGATGTATC TNAGCAGGTT 60
 GCTCCACAGG TAGCTCTAGG AGGGCTGGCA ACTTAGAGGT GGGGAGCAGA GAATTCTCTT 120

ATCCAACATC AACATCTTGG TCAGATTTGA ACTCTTCAAT CTCTTGCACT CAAAGCTTGT 180
 TAAGATAGTT AAGCGTGCAT AAGTTAACTT CCAATTTACA TACTCTGCTT AGAATTGGG 240
 5 GGAAAATTTA GAAATATAAT TGACAGGATT ATTGGAAATT TGTATAATG AATGAAACAT 300
 TTTGTCATAT AAGATTCNNT ATTTACTTCT TATACATTG ATAAAGTAAG GCATGGTTGT 360
 GGGTAAANCT GGGTTATTT TTNGTCCAC AAGTTAAATA AAATCCATAA AACCTTGGA 420
 A 421

10 SEQ ID NO:507
 SEQUENCE LENGTH:413
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00567

15 SEQUENCE DESCRIPTION:
 GATCCCANAC TGGTCNTTGA ACAGACAGAA GGANGTAAAG GNTGGAAACT ACAGCCAGGT 60
 GTGTACTGAA ATNAGGGCAG GATTAGAGGA AGGGTGGAGG GTCCTAACAG AATTGGGCAT 120
 AGGAGGTCAG GGGATAAAC ATCCCTTGCC CCCTCCTCTG AATCCAGGNC CTAGCCAATG 180
 20 GNCTGGACAA CAAGCTCCGT GAAGACCTGG AGCGACTNAA GAAGATTCGG GCCCATAGAG 240
 GGCTGCGTCA CTTCTGGGGG TGAGTGGGGG GTCTCATCTC CCTGCCTACC TCGACTCAGC 300
 ATTCTCCTA CTCGNTCTTC TTNTTTTCCC AACCTTTTGG TTTCTTGCTT GTNCATGACC 360
 TNGTGACTTN TTCNTNTTTT TACCNTGCAN GCCTTNGTN GTCCTAGGGN CAN 413

25 SEQ ID NO:508
 SEQUENCE LENGTH:407
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00568

30 SEQUENCE DESCRIPTION:
 GATCTNAGGG TGAACCACTT CATTCTGCAG GGTCTCCCT CCCACCTTAA AGAAGTTCCC 60
 CTTATGTGGG TTGCCTGGTG AATGGCCTTC CTTCCGCCA NAGGGCTTGT AAACAGACCG 120
 GAGAGGACAG TGGATTGTTT ATACTCCAGT GTACATAGTG TAATGTAGCG TGTITACATG 180
 35 TGTAGCCTAT GTTGTGGTCC ATCAGCCCCT CACATTCCTA GGGGTTNAG ATGCTGTAGG 240
 TGGTATGTGA CACCAAAGCC ACCTCTGTNA TTTGTNGTGA TGTCTTNTCT TGGCAAAAGC 300
 CTTGTGTATA TTTGTATATT ACACATTTGT ACAGAATTN GGAAGATTTT CNAGTCTAGT 360
 TGCCAAATCT GGCTCCTTTA CAAAAGGAN ATTACCCTTG NGGNAAA 407

40 SEQ ID NO:509
 SEQUENCE LENGTH:402
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00569

45 SEQUENCE DESCRIPTION:
 GATCAAACAG TTTCTGGAGT GTGCCAGAA CCAGGGTGAC ATCAAGCTCT GTGAGGGTTT 60
 CAATGAGGTG CTGCANAGT GCCGACTTGC AACCGATTG GCCTAATGAA GAAGTTCAAC 120
 50 CTGGAGAGAT GGAATATCAG CTCTCATAAC TANGTTAATT TAGTATAAAA NTAGAATTGA 180
 TAGTGAGGGT ATAAAGTGA ACCATCAGTT AACCTCTCC TGTATTCTT GGCTTCCTTG 240

EP 0 679 716 A1

CTTCAGANTT GAAATGGAAG TGGGGGTGTC CCTACTCTGT AGAATCTGGG NCTGGGCAAA 300
 TGTTTGTGTTG GCCTCCTTAA ACTAGCTGTT ATGTTATGAT TTTTNTTCTT TGTGAGTTAA 360
 TTAGGAATAA AGTCATTTTC TTTCCAAGGG TATGGTTCCA AA 402

SEQ ID NO:510
 SEQUENCE LENGTH:396
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00571

SEQUENCE DESCRIPTION:
 GATCATGAGA AGGAATGGAA ACTAGGCCGG TGCATTTTAC GGTTCCTGA GATTCTGCAA 60
 AAGATTTTAG ATGACTTATT TCTCCACACT CTCTGTGATT ATATATATGA GCTGGCAACT 120
 GCTTTCACAG AGTTCTATGA TAGCTGCTAC TGTGTGGAGA AAGATAGACA GACTGGAAAA 180
 ATATTGAAGG TGAACATGTG GCGTATNCTG CTATGTGAAG NAGTAGCTGC TGTCATGGCC 240
 AAGGGGTTTG ATATCCTGGG AATAAAACCT GTCCAAAGNA TGTAATCCTT CATAGGTTTG 300
 AACTGTGTG TTTTACCCAA GTGGCCATTG GNACTGTTTG CTTTTTTACA ATCATGTGGG 360
 CACAAGCNTA AGAAAGGAAA TTNGCAACCA GGGAAA 396

SEQ ID NO:511
 SEQUENCE LENGTH:384
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00572

SEQUENCE DESCRIPTION:
 GATCCAATCA GATGCAGAGA ATGTGGATAC AGAATAATGT ACAAGAAAAG GACTAAAAGA 60
 TTGGNCGTTT TTNATGCTCG ATGAATGCTG GGAATTCAGA GGAATGTNTT CACTTATACT 120
 TGGATTTGCT CTCTCCCAT TTCTGATGTG NGTATAGCTT TCGATTTTNC TTACAGTAGT 180
 TCCCCCTTAT CTNCGGGAGA TACATTCCAA GGCCCCAGT GAACTCCTGA AACCTCAAAC 240
 AGTACCAAAC CTTTATACAC TGTTTTTCC ATATATATAT ACCTATGATA AAGTATAATG 300
 TATANNTTAA GCATAGCAAG AGATAATAAT AATGTNATAG NCCATTGNTA CNANCTATAN 360
 TAANNNGTTA TGTGANTGTG AAAA 384

SEQ ID NO:512
 SEQUENCE LENGTH:383
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00573

SEQUENCE DESCRIPTION:
 GATCAGAGCA AAACATGCAG AGCCCTTAGC AGAAACCCAC TTAAATGCAT TTTCTTCATA 60
 TCCCTAAAGT TCCTTAAAAA TATGTGACAA TGCATCAGGA AGAGGAGAAC TGAAGAGTAG 120
 AAGTTCCCTT GCAGATTTT TTATCAGTGA CATGTAATGA GCAATTCACA GATGAGCGCA 180
 GGCAGAGCTC TGTGTGCCGT GTACATATGG ACCGTGCTAT GATGTGTCTC ACATTGGATG 240
 ATATTCCACT TTGGGAATTT TAGTATTTGT ATATAGAAAA TGGGTTTAAAT AACTCACCAT 300
 GGTTTTNAAT NGTCTTATAT TCGTTATTTT TAAAACTCT NGTATGTGTT TTTATAATAA 360
 ANAATAAAAG TAAGCCATGG AAA 383

SEQ ID NO:513

SEQUENCE LENGTH:381

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00574

SEQUENCE DESCRIPTION:

GATCCAAAT CATACTGTCA AGACCATCAA ACAAACAAA GAAGCTTAAG TGAAC TAAGC 60
ACAGGGAAAA GTTGT TTTT CACTCGTTCA TTTTGTATC TGCTTCTAGA TGCTGCAATC 120
AAGAAGTAGC AAATGCCCAA GTTGCCATAG TGTTCGAGG AAAAAAGAG AAAAAATAAT 180
AAAAATAAGG AAGGAGCAAT GCCAAAAATT GAAGGAAATA TTATATAATT AANGCAAGAA 240
GNTATCTATC CATTGAGNGA AACAATTTT ATATTATTG CTTTATAGCNG CAAAGCATT 300
GGAATTCTGA GATTGTTATA GCACTAAGAA GGT TTNATT CTGTGTACAC ACTGGAAAAAT 360
TAAATTCTG GGTAAAGGAA A 381

SEQ ID NO:514

SEQUENCE LENGTH:381

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00575

SEQUENCE DESCRIPTION:

GATCCCCCTG GAAGAGGGAC TCCAATGGGC ATGCCCCCTC CGGGAATGCG GCCTCCTCCC 60
CCTGGNATGC NAGGCNTTCT TTNACCCTTG GCCACAGAGT ATGGAAGTAG CTCCGAGAG 120
GCGTGGGCTC GATTCTCTAG GGCCACGTTA CCACAGACCT GTTTGTTTCT NATGCTGTTG 180
TTCGTGGAGT CTCATGGGAT TGTNTGGTTT CCNTTACAGG GCCCNCTCCC CNGGGAATGC 240
GCCACCAAG GCCNTAGACT CATCTGGCC NTCCTCAGCT CCCTGCCTGT TTCCGGTAAG 300
GCTGTACATA GTNCTTTTAT CTNCTGTGG CCTATGAAAC TGGTTTATAA TAACTNTTA 360
AGAGAACATT ATAATTGCAA A 381

SEQ ID NO:515

SEQUENCE LENGTH:377

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00576

SEQUENCE DESCRIPTION:

GATCTGCGTG GGGCTGGTGG TGGTTGGTGT CCTGCTCATC ATCCTGATTG TNCTGCTGGT 60
CGTCTTTCTC CCTCAGAGCA GTGACAGCAG TAGTGCCCA CGGACCCAGG ATGCAGGCAT 120
TGCTCAGGG CCTGGGAAC GACCCAGCTG GTCCTGAAGG AGAAGCCAAA TGGCTGCACT 180
GGCCGATTCT GGTCTCCAGA GGACCTTGGT GTTGCTCTC CCTTGACCA CCCCAGTNAG 240
TGCCAAAGGG CAGCCCCAAC ATGTGCACCC CTGCATTCC TGTATGCCA CAGACTGGCC 300
CTTGAGGGCA GCCTGCTGTA CTGGCCATGC TGGGCCAGCC NCACCTGGAG CTCAGTAAAA 360
ACTGCTGTTT GATTAAA 377

SEQ ID NO:516

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00577

SEQUENCE DESCRIPTION:

GATCACACCA GTTCAGAGAG CTACACTTTA TGGGTAACAG TTTCACCTGT NATACAGTTC 60
 CCTAGAACAT TTTCCCAAAA GTAGTGAAGT GCAAAGTGCT TAGGTTTGAC ATTTATTGTA 120
 GCAGAACAGT AATATCACAG TATGGGACAA AGGTTTACAC TTTGCAGGGT ATTCTTTGGG 180
 GGAATGTTAA ATACTGTAAT AAAACATGT TCAATCATGG TAAATGTTC AACTNGTTAA 240
 ANTTACAAAT GGNCAAAAAA NATTTTTTTC CTNATATATN GCCTAANTAC CAAATGAAGN 300
 GCTTAANCTT AAGNTTCAAT GTGAAANCGA GTAAATNTGT TCCTAAATTT GCAGNAATAA 360
 NAGATANCCN GTANN 375

SEQ ID NO:517

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00578

SEQUENCE DESCRIPTION:

GATCCATGTA CTGTCATGTT TTTTTCAGG AACAAGCACA TCATGATTGA TTTGGGGACT 60
 GGCAACAACA ACAAGATTAA CTGGGCCATG GAGGACAAGC AGGAGATGGT GGACATCATC 120
 GAGACGGTGT ACCGCGGGGC CCGCAAAGGC CGCGGCCTGG TGGTGTCCCC CAAGGACTAC 180
 TCCACCAAGT ACCGCTACTG AGGCGCCTCA GTCTGCGCGG ATAAATGTCG TGGAGCCCTT 240
 TTTGTATGGA AACGTTTTAA GCTATTTAAA GCCTTTGGAA AATACAGGAN GTNCAGGGCT 300
 GGAGCACCTC TGAGATGGAA TTGATAACAT GGTCTTAACT CACCGAAATA AACAAGCACG 360
 TNGTGAGNGG NAAA 374

SEQ ID NO:518

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00579

SEQUENCE DESCRIPTION:

GATCTCACCG TGGGTCCGAT TAGCCTTNC TCTGCCTTGC TTGCTTGAGC TTCAGCGNAA 60
 TTCGAAATGG CTGGCGGTAA GGCTGGAAAG GACTCCGGAA AGGCCAAGAC AAAGGCGGTT 120
 TCCCGCTCGC AGAGAGCCGG CTTGCAGTTC CCAGTGGGCC GTATTCATCG ACACCTAAAA 180
 TCTAGGACGA CCAGTCATGG ACGTGTGGGC GCGACTNCCG CTGTGTACAG CGCANCATCC 240
 TGGAGTACCT NACCGCAGAG GACTTNAAC TNGGCAGGNA AATTGCATCA AAANGACTTA 300
 AAGGTNAAAN GGTTTTACCC CTNNGGTNANT TGCAACTTTG GTTATTTNGN TGGGGGATGA 360
 AGGNTTTGGG TTNN 374

SEQ ID NO:519

SEQUENCE LENGTH:372

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00580

SEQUENCE DESCRIPTION:

5 GATCAGAGAG ATTAGGATTG TATTTTGACA TAGGATTTGG AACCCATCTA AATGTTGAAG 60
 TTCCCTGAGA CAGCTCTCCA GCTGCTNNGC CTGCGCCAGG GGCTANGCAG CCCCTAATGA 120
 GAGGCTCTGC TCCCTTTCCC ACCTCGCCAA TGTGTGTGTT GCTGCCTTTT TGATTTGTAT 180
 CCTCTGTTAT AGACATTTTT NAAAAACGAT TTCCTCTTTC ATTGTGCACA AGTGCTGAGA 240
 GTCTNAGGCC CCATTCTGCG TGTGTATATA TATCCTGACT CGGGGCTTTT ATTCAGCAAA 300
 CTGTTTATTG TTCTGTCAGA CAATGTCATA TTCAACTCTG TTCATATTAA ACCACTTGTN 360
 10 AAGCANTNNA AA 372

SEQ ID NO:520

SEQUENCE LENGTH:371

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS00581

SEQUENCE DESCRIPTION:

20 GATCTGGTCG CTGCCCCAGG GGGACTGATG GGCAGNGTCG CCCCTGTGGC TGGACTGTNA 60
 CCATCCCTGA TGGGGCCTGA CCGCGGGAGC TGAGGAAGCG CCGCTCCACC GTCTGCCCTC 120
 CAAGGACCCG CATGGAGGCA GTGGGCTGGC AGCTTCCTGC TGCTCCGTGT NAGAGTCAAA 180
 GCACAAATCC TCAGGACGGG CTCAAGGGCC AGGGCAGCCG AGGGAAGTNC AGGTGGGGAC 240
 CACGTCTTCC TGAGGTTGGT GCCACTGCTT GGNACCGTTT GCAGTGGGGT GGCCTCCCCT 300
 CTGTTTGCNT GGTGNAGNNA GCGTGGCGTG GGGACGTGAC TGAATAAAGC ACCATGGGTG 360
 25 ATGTGTTGAA A 371

SEQ ID NO:521

SEQUENCE LENGTH:382

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS00582

SEQUENCE DESCRIPTION:

35 GATCTNTGGG ACGTCAGCTG CTGAGAGGAG CAAGCGGTAG TACCACCCCT TAGTTGAGGG 60
 AGTCAGCACA GTCCTTTCTG CAGCTTCTAA CCCAGGACCA TGAATCAGG TGCCTAGAGA 120
 AGCCAGGCAG CNNAAGGACA AGGAATGCTG GGGGCTGTGG GAACAGGAAT GCAGATACCC 180
 TTTGAAGGAG CATTCCTGCT AAAAGAAGCT GAAAATGTAG ACCTATGTGA AGTGCTCTGA 240
 TTTCTAAATA TTGTGAAGGT TAAGAAAAAC ATANATTTN GGGTCTATGG GCTAGGATTN 300
 40 AGNCCCACAG TTGGCCANTT TNTAGNGGT NCCCAAATGG ANTGGTAAA CCNNNGGTTT 360
 NGNTTCCTAG CCTAGGGGTA AA 382

SEQ ID NO:522

SEQUENCE LENGTH:382

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS00583

SEQUENCE DESCRIPTION:

50 GATCAAGAAC AATGCCTCCA CTGACTATNA CCTATCTGAC AAGAGCATCA ACCCTCTGGN 60
 TGGCTTTNTC CACTATGGTG AAGTGACCAA TGACTTTNTC ATGCTGAAAG GCTGTGTGGT 120

55

5 GGAACCAAG AAGCGGGTGC TCACCTCCG CAAGTCCTTG CTGGTGCAGA CGAAGCGGCG 180
 GGCTCTGGAG AAGATTGACC TTAAGTTCAT TGACACCACC TCCAAGTTG GCCATGGCCG 240
 NTTCCAGACC ATGGAGGAGA AGAAAGCATT CATGGGACCA CTGAAGAAAG ACCGAATTGC 300
 ANAGNGAAGA AGGAGCTTAA TGCCAGGNAC AGATTTTGCA GTTGGTGGNN GTCTCAATTA 360
 AGNGTTATTT NNCCACTGGA AA 382

10 SEQ ID NO:523
 SEQUENCE LENGTH:367
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00584
 SEQUENCE DESCRIPTION:
 15 GATCTCCAAG CNAACTCAGC CTCCANCCAA NCTCCCTGTG GGTCTAGCC ACAAGCTCTC 60
 CAACAATTAC TATTGCACTC GCAATGGCCG CCGGGAATCT NTGCCCCCTT CCATCATCAT 120
 CNCGTGCGAG AAGTCGCTGG TGTCAGGCAA GCCAGCAGAG AGCTCTGCTG TAGCTGCCAC 180
 TGAGAAGAAG NCGGTGACTC CAGCTCCTCC CATAAAGAGG TGGGAGCTGT CCTCGGACCA 240
 20 GCCTTACCNG TNACACTGCA CCCTNACGGC ACCNGACTAC TTTGCCTGCT TGGATTTCTT 300
 CCAGGGGAAT GTGACCTAAT TTATGNCAA TACGTAGAGT CAGGTATCAC TTCTAGTTTA 360
 CTNTAAA 367

25 SEQ ID NO:524
 SEQUENCE LENGTH:365
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00585
 SEQUENCE DESCRIPTION:
 30 GATCAAGAGG AAAGAGAACG TAACAACCAG AACCCCTGGA CATTGAGCG AATAGCCACT 60
 GCCAACATGC TGGGCATACG GAAAGTACTG AGCCCATATN ACTTGACCCA CAAGGGGAAA 120
 TACTGGGGCA AGTTCTACAT GCCCAAACGT GTGTAGTGAG TGTAGGAGAT AACTGTATAT 180
 AGGCTACTGA AAGAAGGATT CTGCATTTCT ATTCCCTCA GCCTACCCAC TGAAGTCTTT 240
 35 GGGTAGCTCT TAAGCCATAA CTAAGGAGCA GCATTTGAGT AGATTTCTGA AAAACAATGT 300
 TATTGTGTGA TTTAAAAGA AAAGTGTATT NTTATTAAAT AAAATTAAA CATCACTTCA 360
 GGAAG 365

40 SEQ ID NO:525
 SEQUENCE LENGTH:396
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00586
 SEQUENCE DESCRIPTION:
 45 GATCTATGGG TTGACTAATT AAACAATAAT TCAAGTAGAG TGTCCAGAA AAAAACCCT 60
 TGGGCTCCCT GTTTGGAGTC TGGCTGGCTC TGAGCATTGC CAATGGCCCC TACTCACCTG 120
 ACTTTGTATC CTCTCCTTTT AGAGGCTTTG CATTCTGCAC CCAGCTTCAC TAACAGTGGG 180
 50 CTGAAAACAT CCTTGGGTTG AGTGTTCAT TTGGGAGTTA TTTGGCCAGG GCCTTTTGAA 240
 CAGTAGTGTC CCCATGAAGT GCTAGATAAT ATATGTGTAA GAGTCAGCTT TTTTTTTTTT 300

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TAAACTNTAA CACCNTTNAG AANTTTCTAA CTACTTNGNA ACTGNATGGT TTANCCCGGN 360
GNTAAAAGCN GTTTTAAAA GTNTANGTTT TCCAAA 396

5

SEQ ID NO:526
SEQUENCE LENGTH:360
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

10

CLONE:HUMGS00589

SEQUENCE DESCRIPTION:

15

GATCCGCGGG CTTCCACTNC ACCATCGGAT GTTTGCCACT CAGACTGAGG GGGAGCTCAG 60
AGTGACCCAA ATTCTCAAAG AAAAGTTTCC ACGAGCTACA GCTATAAAG TCACTGACAT 120
TTCAGGCACT AAAAGAAGAA ATCAAAGAGA TGCATGGATT GCGGATATT ACCTCTGTCC 180
CCAAACGCTG ACCACGGCCT GGCTGCATAG ATGCTGCTGC TTAAGACCTT GGATGAACTT 240
CACTGACATC ATTCTTCCT AAGCAGTCAC CAAAAAATT ATATATNTNG CTCATATACA 300
NTNCCATATN ATANTTATAG AAGATGTATA ATCTATTTA GATGTNANTN AAAGGGTAAA 360

20

SEQ ID NO:527
SEQUENCE LENGTH:267
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

25

CLONE:HUMGS00590

SEQUENCE DESCRIPTION:

30

GATCGGGTTT GGCCCCCAGC CCCGCTCAGC CCAGTCCCTC TTCCTCTGCC GGGAGGGTGT 60
TTTCAACTCC AAACCCAGA GAGGGGTGT AGATTGGGTC CAGCTTTGCT TCAGTGTGTG 120
GAAATNTCTC GTGGGGTGGC ATCGGGGCTG CGGGGTGGGG ACCCCAAGGC TTTCTGGGGC 180
AGACCTTGT CCTCTGGGAT GATGGGCACT GCTATCCACA GTCTCTGCCA GTTGGTTTTA 240
TTTNGAGGTT TNTGGGCTTT TTTAAA 267

35

SEQ ID NO:528
SEQUENCE LENGTH:352
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

CLONE:HUMGS00591

SEQUENCE DESCRIPTION:

40

GATCAATCAC CTTCTGCTGC TTGGATGGGT GGATTTGGTG CTCAGCCTCC CCAAGGACAA 60
GCTCCTCCCC CTGTAATACC TCCTCCTAAC CAAGCCGGAT ATGGTATGGC AAGTTACCAA 120
ACACAGTGAG CCGGGACTCT AAAAAAAT TGTAATTCAT GATAGGCTTC GATTTCCTGT 180
GACACTCTGA AGACATGAAA GTAGACATCG GAAATGNAA ATATTTATTT TAAAAATTGA 240
AATGTTTGA ACCTTTAGCA CAGATTGCT TTGGTGAAGG ACACGTGTCT TCTAGTTCTG 300
CCTTTTAAA GTTTNTTGT CATGNTGGAT NTTGAACATN GNTTTTNTT TN 352

45

SEQ ID NO:529
SEQUENCE LENGTH:351
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

50

55

CLONE:HUMGS00592

SEQUENCE DESCRIPTION:

5 GATCAAGCCT TTCTTTCATT CCCTCTCTGA AAAGTATTCC AACGTGATAT TCCTTGAAGT 60
 AGATGTGGAT GACTGTCAGG ATGTTGCTTC AGAGTGTGAA GTCAAATGCA TGCCAAACATT 120
 CCAGTTTTTT AAGAAGGGAC AAAAGGTGGG TGAATTTTCT GGAGCCAATA AGGAAAAGCT 180
 TGAAGCCACC ATTAATGAAT TAGTCTAATC ATGTTTCTG AAAACATAAC CAGCCATTGG 240
 10 CTATTTAAAA CTTGTAATTT TTTTAATTTA CAAAAATATA AAATATGAAG NCATAAACCC 300
 AGTTGCCATC TGC GTGACCA ATAAACATT AATGCTAACC ACTTTTTTAA A 351

SEQ ID NO:530

SEQUENCE LENGTH:348

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00593

SEQUENCE DESCRIPTION:

20 GATCCAGAAT ACCCTGACCT CGCCCCAGTT CCAGCAGGCC CTGGGCATGT NCAGCGCAGC 60
 TTTGGCCTCG GGGCAGCTGG GCCCCTCAT GTGCCAGTNC GGTCTGCCTG CAGAGGCTGT 120
 GGAGGCCGCC AACANGGCG ATGTGGAAGC GTTTGCCAAA GCCATGCAGA ACAACGCCAA 180
 GCCCCAGCAG AAAGAGGCG ACACGAAGGA CAAGAAGGAC GAAGAGGAGG ACATGAGCCT 240
 GGA CTGAGCC ACGCGCCGTC CTCCGAGGAA CTGGGCGNTT GCAGTGC GTT GCACACCTTN 300
 25 ACCTTCNACN TACTGATTAT TAATAAAGTT TTTCTTTTA CCTGCAA 348

SEQ ID NO:531

SEQUENCE LENGTH:347

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00594

SEQUENCE DESCRIPTION:

35 GATCCTGAAG AGATTGAAAA AGAAGAGCAG GCTGCTGCTG AGAAGGCAGT GACCAAGGAG 60
 GAATTTTCAGG GTGAATGGAC TGCTCCCGCT CCTGAGTTCA CTGCTACTCA GCCTGAGGTT 120
 GCAGACTGGT CTGAAGGTGT ACAGGTGCCC TCTGTGCCTA TTCAGCAATT CCCTACTGAA 180
 GACTGGAGCG CTCAGCCTGC CACGGAAGAC TGGTCTGCAG CTCCCACTNG CTCAGGCCAC 240
 TGAATGGGTA GGAGCAACCA CTGACTGGTC TTAAGCTGTT CTTGCATAGG CTCTTAAGCA 300
 40 GCATGGAAAA ATGGTTGATG GAAAATAAAC ATCAGTTTCT ATTTAAA 347

SEQ ID NO:532

SEQUENCE LENGTH:346

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00595

SEQUENCE DESCRIPTION:

50 GATCCGGTNT TGGTGCCAAT GTCTCCAAC TCACTTTTGC TCCTAGCACG ATTATATTTT 60
 ACCTGGGACA TGCTGCTATG CTGGGACTCA TGTATGTCTA CTGGACTCAG CTCAACATGT 120
 TCCAGACCTT GAAGTACCTG GCCATCTTGG GCAGTGTGAC GTTCTGGCT GGCAATCGGA 180
 TGCTGGCCCA GCAGGCAGTC AAGAGAACAG CACATTAGTT CCAGAAGAAA GATGGAAATT 240

55

CTGAAAACTG AATGTCAAGA AAAGGAGTCA AGAACAATTC ACAGTATGAG AAGAAAAATG 300
 GAAAAAATA CCTTTATTTA AAAANGAAAA AAGTCCAGNT TGTAAA 346

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SEQ ID NO:533
 SEQUENCE LENGTH:346
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00596

10

SEQUENCE DESCRIPTION:
 GATCTGTAG CCTAGATAGG ATAGTNTGAC CTTCTAGCAT AGTCTTTTGG GCAAATNATT 60
 TGTGTTTTCA GTGTGTGGGG AAGCTGTCCT GGGGGCTGGG GCGACAGATA GCACATAGGC 120
 TGTCTCTGGG GCTGCAGGGG CTTCCNTGAG CTGGATGTTG TGGGTNTTGC CGTGCTTCAG 180
 GAAGTNTGGC GACCAGAAAG CGTAGACCCG GGGCCAGGG TCTGCCCGCC CCTGCAGCNT 240
 GGCCTCCCCG CACAGGCTGT GGCTTGCACT CCAGCCGNTC TAGTNTCTNA GGAATTTNCT 300
 TGTNACTTGT ACTGTGTAAA TAAAGCTTCC TGGTTCAATA CCNAAA 346

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SEQ ID NO:534
 SEQUENCE LENGTH:345
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00597

25

SEQUENCE DESCRIPTION:
 GATCCTATGG CCATGACCCA GAAGTATGAG GNGCATGTNC GGGAGAGCAG GCTCAAGTAG 60
 AGAAGGAGGA CTTCAGTGAC ATGGTGGCTG AGCACGCTGC CAAACAGAAG CAAAAAATAC 120
 GGAAGCTCA GCCCCAGGAC AGCCGTGGGG GCAGCAAGAA ATATAAGGNG TTCAAGTTTT 180
 AGGTCCCCCT AACTAGCCCC TTTTCTTGGC CCTACGTCTG GATGCCTGGG CTTACACAAA 240
 GAACCACTC TCCGCGAGTT CCAAGGNTC TGTCATTTC TGTCTTATT TTAGACCTGT 300
 TTTGTAAATA AAGCTGTTTC CCAAGGAAAG AGATGAATAT TTAAA 345

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35

SEQ ID NO:535
 SEQUENCE LENGTH:354
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00598

40

SEQUENCE DESCRIPTION:
 GATCGTGTTT ATGGTGAATC CAAGTTGGGA GGAAATGAAA TAGTATCTTT NTTGAAAGGA 60
 ATATTGACTC TTTTGTCTAC TACATAAAG AAAGATACTC ATTTATAGTT ACGTTCATTT 120
 CAGGTTAAAC ATGAAAGAAG CTGGTTACT GATTGTATA AAATGTACTC TTAAAGTATA 180
 AAATATAAGG TAAGGTAAAT TTCATGCATC TTTTATGAA GACCACCTAT TTTATATTC 240
 AAATTAATA ATTTAAAGT TGCTGGCCTA ATGAGCAATG TTCTCAATTT TCGTTTTCAT 300
 TTTGCTGTAT TGAGACCTAT AAATAAATGT ATATTNTTTT TTGCATAAAG TAAA 354

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SEQ ID NO:536
 SEQUENCE LENGTH:343
 SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS00599

SEQUENCE DESCRIPTION:

5 GATCCGTGAC AAGCGCACAG GCAAGACCAA GGGCTACGGC TTCGTGAGCT TCAAGGACCC 60
 CAGCGACTAC GTGCGCGCCA TGCCTGAGAT GAATGGGAAG TATGTGGGCT CGCNCCCCAT 120
 CAAGCTTCGC AAGANCATGT GGAAGGACCG GAATCTGGAC GTGGTCCGCA AGAAGCAGAA 180
 10 GGAAAAGAAG AAGCTGGGCC TGAGATAGGG TCTGTGGCCA GGCACCCGCT CCCACCTGGC 240
 CGGGCGCTGG CTCCTCCCTC AGTTCTCTTT GGGAAAACCC CCAGCTNGTC CACCCATCCN 300
 NTGCCCCAAA ACCAGTTTCA GTAAATTAC GTTCATTTC AAA 343

SEQ ID NO:537

SEQUENCE LENGTH:341

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00600

SEQUENCE DESCRIPTION:

20 GATCGAACGG ACTGTGAAAT CCGCTCTTTG TCGGAAGCTG AGCAAGCTGT GGCTTTTTTC 60
 CAACTCCGTG TGACGTTTCT AAGTGTAGTG TGGTAGGACC CCGGCGGGTG TGGCAGCAAC 120
 TGCCCTGGAG CCCAGCCCC TGCNTCCATC TGTGCTGTGC GCCCCACAGT AGACGTGCAG 180
 ACGTCCCTGA NAGGTTCTTG AAGATGTTA TTTATATTGT CCTTTTTTAC TGGAAGACGT 240
 25 ACGCATACTC CATCGATGTT GTATTGTCAG TGGCTGAGGA ATTCTTGAC GCAGTTTTCT 300
 TTGGCTTTAC GAAGCCGATT AAAAGACCGT GTGAAATGAA A 341

SEQ ID NO:538

SEQUENCE LENGTH:339

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00601

SEQUENCE DESCRIPTION:

35 GATCCTCGGG TGTCTTCCC ATCAGATAAA ATAGTTCACT ACAGACAGAT GTTTTTATCT 60
 ACTGAACTAC AAAGAGTAGA AGAGCTTTAT GATTCATTAT TACAAGCTGT TGCCTTCTAT 120
 GANTTAGCAG TGTTGACTC TCAGCCTTAG AATTCTGAGG TTAACGTGCT AAAGTATAAT 180
 TNTTAGCTCT AACGTAACAC CAACTGTTGT GAACATCCAT GTTATTGGAA AAGAACACAT 240
 TTTCACTGTA TTTTAGATGT TTAANTTCTG ACTTTTGGCT ATTAAATGGT TTACACAATA 300
 40 AGCCAAGACC AAATCAATAA ACATTTTNTG AGAACGAAA 339

SEQ ID NO:539

SEQUENCE LENGTH:339

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00602

SEQUENCE DESCRIPTION:

50 GATCATCATC CGAGTGCAGA CCACGCCGGA CTACAGCCCC CAGGAAGCCT TTACCAACGC 60
 CATCACCAGC CTCATCAGTG AGCTGTCCCT GCTGGAGGAG CGCTTTCGGG TGGCCATAAA 120
 AGACAAGCAG GAAGGAATTG AGTAGGGGCC AGAGGGGGCT CTGCTCGGCC TGTGAGCCCC 180

55

EP 0 679 716 A1

5 GTTCCTACCT GTGCCTGACC CTCCGCTCCA GGTACCACAC CGAGGAGAGC GGCCGGTCCC 240
AGCCATGGCC CGCNTTGTGG CCACCNTCA CCCTGACACC GACGTGTCCT GTACATAGAT 300
TAGGTTTTAT ATTCCTAATA AAGTATAGCG GAAGAGAAA 339

10 SEQ ID NO:540
SEQUENCE LENGTH:339
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00603
SEQUENCE DESCRIPTION:
15 GATCGTTATG AATATCAAAT GTCCATTCT ATNGTAATGA ATTCAGTGA ACCATCACAC 60
AAAAGCACAC AAAGACCTCC TCTCCACAG GGGAGACAGA GGTGGGGAGG CTCTCTTGGC 120
TCACATAATC GTGTCTGTGT CACAAATAAT CATTAAATTA GCTATTTTCA GCTAACACAT 180
TTGTNGTTGC ACTTGAAAAA GAGTTAGTGA GCCTGTCTTG GAGTTTAAGT AGTTTCAAAT 240
AAAAAAAGGC TACAGTGCCT CACAAAGGAT GTTCCCAGCA AGTNGTTTAA ATTCCCAGCA 300
20 AGTTGTAAAA GTGTAAATAN AANTATATGA ANTTGTAAA 339

25 SEQ ID NO:541
SEQUENCE LENGTH:355
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00604
SEQUENCE DESCRIPTION:
30 GATCCTGAAA TCTACTAGAG ACACCCCTAA GCCATGAATG AACTACATCC AAATACCTGA 60
NTTTTGGAA TCTGTTTCAT GGATTTTNCA TCTTCTACCG TATGTNAAAT TGCAAGTNTT 120
TGAAGATTTA TAAGTACAAA TTTGGGAACA TACAAATCTT TTAGGTAGTA GAGTTTAAAG 180
TGTATAAGCT AAAAGTGAAG GTAAGTGAAG GTTCTCTTGT TTCTTTGCAT TAATGTAACT 240
GTGTGGTTTG CCTTTGTCCC CCTGGATAGA ACGTGCATTT AAAGAATATA TTGTACTTAC 300
TGTGACAGCA GATAATAAAC CAGTCTCTTG GAGGGCACAA CCCTTATTG ACAA 355

35 SEQ ID NO:542
SEQUENCE LENGTH:331
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
40 CLONE:HUMGS00606
SEQUENCE DESCRIPTION:
45 GATCTTTTT ANATAAANNT TATGTATTGT GGCATAATCC TTTTTTGAG CTCTACAGAG 60
AACAGTCTTT TGGTAATAGT GGCAGGTATT TATCCTTCT GAATATATAC CCCATTATAG 120
GAATAACTGT TACTTATTTA GGATTCCATC ATTGAAAATT TTNACCCAAG GCACAGCAGT 180
GAANTTTATA GTNCTCANTT TAGTTGNCAT TATTGACAGG CATTGGNATT ATTAGTCATT 240
GCTAAGCAAC TAAAACTTCA TCAGTTCAAN TAAGTTTIAN TTGTCANATG GCNGTATAAN 300
CACATGANCT TTCTAGGAAA TATTCCTCN N 331

50 SEQ ID NO:543
SEQUENCE LENGTH:330

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00607

SEQUENCE DESCRIPTION:

GATCGGTGTG CCCCGCTGCG AGGGGCCCC CATGGGGCTG NTGGCCNTC CGCAGTCAGG 60
 ACATCCCAAC CCCTGGNTGG GACTGAACCA CCCAGAGCGG AGGGCNTCCC TTTNAGCCT 120
 TGTNAGTCAC CTGGCAGGCC CCAGCTGGGC TGCTGTCCG TGTCCCTCAG CCTGGNTGGT 180
 GATTCCTTGC AGGCCAGAAA TNAAGAGTCC CTGTAGGTTT TGGTTTGTG TGTATTATT 240
 TGTTCTTTCA CCTTTTTTCC TCATTAAAA AAAANGNCC CTGNGGAGTG TACTNATTNA 300
 TTTTTGATN AAAGGGANGT AAAATGNAAA 330

SEQ ID NO:544

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00608

SEQUENCE DESCRIPTION:

GATCCAGACT GTAAGATGTT GTTTtagggg CTAAAGGGGA GAAACTGAAA GTNTTTTACT 60
 CTTTTCTAA AGTGTGGTC TTTCTAATGT AGCTATTTN NTTGTTCAT CTTTCTACT 120
 TCAGTACACT TGGTGTACTG GGTAAATGGC TAGTACTGTA TTGNCNCTGT GAAAACATAT 180
 TTNTGAAAAG AGTATGTAGT GGCTTCTTTT GAACTGTTAG ATGCTGAATA TCTGTCCACT 240
 TTTCAATCCC AATTCTGTCC CAATCTTACC AGATGCTACT GGACTTGAAT GGTTAATAAA 300
 ACTGCACAGT GCTGTTGGTG GCAGTNAAA 329

SEQ ID NO:545

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00609

SEQUENCE DESCRIPTION:

GATCACTAGA TTTATGGAGG AATTNGTCAC AAATNACTTN TAGAAAAATG CTGTCATATA 60
 GTTCATTCA TCATTTCTG TTGCAGGAAG CCACTCCACC ACAGAATGCT AATATGCCAG 120
 TGGTACCCAG TACCTCTGT ATATAGGTTA TTGCAAATAT TGTNCTGAAA TGCTTAACCT 180
 CAGAATTACA TTTTAAAG TAAATAATTG TTTAAATCT ATTTGTAAA GNTATAAAGT 240
 ACAATAGAAT TTCTGGAGTA CAGATTAAAC TATTGCACT AACACACGTG CCGTGCATGA 300
 TTTAATAAAA TANTNNACT CTCNTAAA 329

SEQ ID NO:546

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00610

SEQUENCE DESCRIPTION:

GATACCGTG TGCTCAGGCC AGGTGTGAAT CCTGAGGTCC ATGGAGGTGC AGAGATGAGA 60
 TTACTCCTAT TCACGTTGAA GTGATTGCT TTGTTACAA AAAATTGCAG CTATTGTCTA 120

EP 0 679 716 A1

5 GCTTTCATTT TTTTACTGAG AACTTTAAAT TAGTCCCCTA TTAGAATAGG GTTGCTACTC 180
 ANCTNTTTTN AAAAACCGAA TTTCATCATT TATCTAAAGA GNAATATGC AGANTAAGTG 240
 GTCTTGTTAA GAGTGCAATA TTATATNNNN ANGTAAGT AAAANTNAAT TTGGGGGGAT 300
 TATTATNCA GCATGANACC TANTNTGN 328

10 SEQ ID NO:547
 SEQUENCE LENGTH:328
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00611
 SEQUENCE DESCRIPTION:
 15 GATCCCNNGG ACGTGAGACT TANNCTTCCA GCCAGTGTGA ATCATTGTAT TTTGTCTCAT 60
 AATCACAGCA CNCCTGCATG ACACAACAAC GTGCAGCATT TTTTACATAA AAATATGGTA 120
 GANTTAATTT ATGACATGGA AATGCCCTTAC GTGGTATCAC ACTTAGTCTT GAAAAAACA 180
 CCNAGGTGAC GTTTAAATTT TTTAGTACAT ATCCTCAAAT TGGAGCTAAG TTATACTTCT 240
 TTTATAACCT TTTGGGCATC TGGTCGAGAG AAGACAAGAT TTTNTCTATT TACAGTGATG 300
 CAATAAATAT GTTGGCCACC TTTGGAAA 328

20 SEQ ID NO:548
 SEQUENCE LENGTH:322
 SEQUENCE TYPE:nucleic acid
 25 TOPOLOGY:linear
 CLONE:HUMGS00612
 SEQUENCE DESCRIPTION:
 30 GATCTTGAAG AGACCGCTGG CAGCACCAGT ATTCCAAGA GGAAGAAGTC TACACCCAAG 60
 GAGGAAACAG TTAATNACCC TNAGGAGGCA GCCACAGAAG TGGCTCCAAG AAAAAAGGA 120
 ATTNTCCAAA GAGGAGCCGG TCAGCAGTGG NCCTGAAAGA GCGGGCTGGC AAGANCAGCT 180
 CCAAGAAGAA GAAATGTTC CATAAAGCAT CCCAGGANGA TTAGAATCAA ATGGACANTC 240
 TCTNGGAGGT GGGNATACCA TAGNCCAAGG TNCATTTCCT ACCNTGTGCC GTGTTCCCAA 300
 TAAANACAAA TTCACAAGGA AA 322

35 SEQ ID NO:549
 SEQUENCE LENGTH:318
 SEQUENCE TYPE:nucleic acid
 40 TOPOLOGY:linear
 CLONE:HUMGS00614
 SEQUENCE DESCRIPTION:
 45 GATCCACCTA GCCTCAGCCT CCCAAAGTGC CGCCGGGATT ACAGGCGTNA ACACCATGAC 60
 TGGCCTTCAT TATCTCTNTT TTAATAATGA AAAAGTTTAT AATTACATT CAGTAAATC 120
 ACCCTTTTAA GTGTCTAGTC TGTGAATTTT GACAAATGCA TGGTTTTGTA ACCAATCGAT 180
 AGGNACAGTT TGCCACCCAG GACATTCCCN TCTGTTCTC TGTCTCTC TTCTCTGCC 240
 CCCTAGCAAC CACTGGTGTT TTCTGTCCNT CTGTTTCATT TGACATTAT TTTAAATAA 300
 AATATTTTAA AATCTAAA 318

50 SEQ ID NO:550

55

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00615

SEQUENCE DESCRIPTION:

GATCCTCACC GTGGAGGACC ATNATAATNA AGGTGGCATT GGTGAGGCTG TGTCCAGTGC 60
AGTAGTGGGC GAGCCTGGCA TCACTGTCAC CCACCTGGCA GTTAANCGGG TACCAAGAAG 120
TGGGAAGCCG GCTGAGCTGC TGAAGATGTT TGGTATCGAC AGGGATGCCA TTGCACAAGC 180
TGTGAGGGGC CTCATNACCA AGGCCTAGGG CGGGTATGAA GTGTGGGGCG GGGGTCTATA 240
CATTCTGAG NTTCTGGGAA AGGTGCTCAA AGATGTACTG AGAGGAGGGG TAAATATATG 300
TTTTGNGNAN AATGCAAA 318

SEQ ID NO:551

SEQUENCE LENGTH:314

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00616

SEQUENCE DESCRIPTION:

GATCCCTCT CTGAAGAGAA AGGAGGAAAG AAAAGAAAA AACAGAAACA GAAGCTCCTG 60
TTCAGCACCT CAGTCGTCCA CACCAAGTGA CACTACTGGN CCAGGCTACC TTCTCCATCT 120
GGTTTTNTT TTTTNTTTT TTTCCCCAT GCTTTTGTTT GGNTGCTGTA ATTTTAAAGT 180
ATTTGAGTTT GANCAGATTA GCTCTGGGGG GAGGGGGTTT CCACAATGTG AGGGGGAACC 240
AAGAAAAATT TAAATACAGT GTATTTTCCA GCTTCCTGTC TTTACACCAA AATAAAGTAT 300
TGACACAAGA GAAA 314

SEQ ID NO:552

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00617

SEQUENCE DESCRIPTION:

GATCCCTACT TGGNAGTTAA CCCTAACTAC TTGCTCGAAG ATTGAGATAG TGAAAGTAAC 60
TGACCAGAGC TGAGGAACTG TGGCAGAGCA CCTCGTGGCC TGGAGCCNGG CTGGAGCTCT 120
GCTAGGGACA GAAGTNTTNC TGGAAGNAT NCTTCCAGGA TTTNTTTTTC AGAAACAAGA 180
ATTGAGTTGA TGGTCCTATG TNCACATTC ATCACAGGTT TCATACCAAC ACAGGCTTCA 240
GCACTTCCTT NGGTGTGTTT CTNTCCAGT GAAGNTGGAA CCAAATAATG TGTAAGTCTCT 300
ATANCCANTA CCN 313

SEQ ID NO:553

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00618

SEQUENCE DESCRIPTION:

GATCTTAGCT AGTTCATCAC TTCCTCAGGG AAACATTCCC TAATTTCTGT CACAGAGTAA 60

EP 0 679 716 A1

5 GACCCGTTGT TATACGTCTC ACCTGACCAT GTACCTCTAC TTAGCATTTA ACACGTGTAA 120
 TTTTGTATGT ATTGGTTTGA TTAATGTCAG ANCCACTAGA TTGTAACTC CATGAGGACC 180
 GGAATTNGT TTCTGTCATT GTCATTGTTT AACTTTGTAT TTTTATGCC TCATACAGTG 240
 CCTGGCACAT AGTAGGTGCT CAATTAACCT NATTGAAAG AATAAATGA ATGGATGAGG 300
 TATCAAGAAA 310

10 SEQ ID NO:554
 SEQUENCE LENGTH:310
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00619
 SEQUENCE DESCRIPTION:
 15 GATCTGGGGG CCACCACCCT GTGCCGGTGG CCTCTGGGCT GCCTCCCGTG GTGTNAGGGC 60
 GGGGCTGGTG CTCATGGCAC TTCCTCCTTG CTCCCACCCC TGGCAGCAGG GAAGGGCTTT 120
 GCCTGACAAC ACCCAGCTTT ATGTAAATAT TCTGCAGTTG TNACTTAGGA AGCCTGGGGA 180
 GGGCAGGGGT GCCCATGGC TCCCAGACTC TNTCTGTGCC GAGTGTATTA TAAATCGTG 240
 20 GGGNAGATGC CCGGCCTGGN ATGCTGTTTG GAGACGGAAT AAATGNTTTC TCATTCAGTC 300
 TNCAGTCAAA 310

25 SEQ ID NO:555
 SEQUENCE LENGTH:308
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00620
 SEQUENCE DESCRIPTION:
 30 GATCCNGTGC TGAAAGAGAA ACCAAGAAAA AAGATGACAT TCCAGAAGAA GACAAAGGAA 60
 ATGTAAACA ATGTGAAATC AATTATGTAA AGAAATTCA GAGCTTCAA GACCACAAAC 120
 TAAAATAAG TAAAGANGAC AGTAAATTN TAAAAAGGC TCGGAAAGAT GGATTTTTC 180
 ATGAGACGCT TCTGGACAGG NGAGCCAAAT TGAAAGCCGA CAGATACTGC AAGTNACTGG 240
 GATTTTNTT TCTGCCTTAT CTTNCTGTNG TTTTCTGA NTAAATATT CAGAGGAATG 300
 35 CTTTAAA 308

40 SEQ ID NO:556
 SEQUENCE LENGTH:300
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00621
 SEQUENCE DESCRIPTION:
 45 GATCTTCCTG AAGTNTCTCC CCGTTTNGTG CAGCTGGCCA TACCCAGGT GGACATNATG 60
 AGTCAGGCTG ACTTAATTNC TCATGAGCAG ACCATCCCAG TGAATGCAA GGCATGGGC 120
 TCCACAGCCT GGACCCTGGC ATGGAGTCCA GCNNCTGCT CACCGGCCAG GAGGCCTGGG 180
 GCGGGGTCAC TTACCCTTNT NAGCCTCANT TTCTNTTCT GGAAGCGGAG ATGGTAATAG 240
 CTTTACATT NGAGGTGAAT GTNAGAATTA AACTTGGGCA CATGGAGGAA TACACCTAAA 300

50 SEQ ID NO:557

55

SEQUENCE LENGTH:299

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00622

SEQUENCE DESCRIPTION:

GATCACTTGT CCTATTACCC TATACCTAGC ACTTGTGACA CCACCCCTAA ATCACTTTGA 60
 GCCTGGGAAA TAAGCCCCT CAACTACCAT TCCTTCTTTA AACACTCTTC AGAGAAATCT 120
 NCATTCTATT TCTNATGTAT AAAACTAGGA ATCCTCCAAC CAGGCTCCTG TGATAGAGTT 180
 CTTTAAAGCC CAAGATTTT TATTTGAGGG TTTTGTGTT TTTAAAAAA AATTGAACAA 240
 AGACTACTAA TGACTTTGTT TGAATTATCC ACATGAAAT AAAGAGCCAT AGTTTCAA 299

SEQ ID NO:558

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00623

SEQUENCE DESCRIPTION:

GATCTGCTTC TCCAGTTTT GAGGAGCCAG CCAGGGGTCC AGCACAGCCC TACCCCGCCC 60
 CAGTATCATG CGATGGTCCC CCACACCGGT TCCCTGAACC CCTCTTGGAT TAAGGAAGAC 120
 TGAAGACTAG CCCCTTTTC TGGGAATAA CTTCTCCTC CCCTGTGTTA ACTGGGGCTG 180
 TTGGGGACAG TGCCTGATTT CTCAGTGATT TCCTACAGTG TTGTCCCTC CCTNAAGGCT 240
 GGGAGGGTGN TAAACACCAA CCCAGGANTT CTCAATAANT TTTNATTAC TAAACCTGAA 300
 A 301

SEQ ID NO:559

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00624

SEQUENCE DESCRIPTION:

GATCAGATTT TGCTAAATGG AAATAATATA ACAATGCTGG TTCCTGGAGG AGAAGGACCT 60
 GAAGTGTGAA TGAGTTTCCT TGACTTACAC TAGATTTTGT TTTGGCTTAT AATGACAAGA 120
 AAATGGAATT TTTTTTCCC ACTTTCTAAT GTTAAATCC CATAAAGCTA AGTTTCCCGT 180
 TAAAGGGAAG TGCTTTGAAG ATGTGTACCC ATTTTGTAA GTTAATCATG ATTATCCTGG 240
 AAAAGAAGA AAAGAGCTTC TTCTTTCAG ATGAAAAATA AGGTGTTTTT GGTTAA 297

SEQ ID NO:560

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00625

SEQUENCE DESCRIPTION:

GATCTATTTG TAGATTAGGA TTAATGGA TTTAATCCAT TTTAAGGCT GTGTGAATTT 60
 TTCTAAACAA GAACCATTTG CAATATGGAT TTCTTAGAGA TTAACCAAT TATACTTAT 120
 TAGCAGTCGC GAGCACATGT TCATATAGTC AATGTAAAA TACACTAATG AGTATTTGGT 180

AAATCCCAGT AGGCTTTTAC CATTAGCATA ATTTTGTGTT GTACAATTAA GTTACAATTA 240
CATCTCTAAT TTTGGATAAT ATTCAATTGGT TAACANTANA GTGACAAAAG CTCATGCCTT 300
CAAA 304

SEQ ID NO:561

SEQUENCE LENGTH:301

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00626

SEQUENCE DESCRIPTION:

GATCTGGAAC TTTGCACATG TCACTACTGG GGAGGTGTT CTGCTCTAGC TTCCACGATG 60
AGGCGCCCTC TTTACCTATC CTCTCAATCA CTA CTCTTCT TGAAGCACTA TTATTTATTC 120
TTCCGCTGTC TGCCTGCAGC AGTACTACTG TCAACATAGT GTAAATGGTT CTCAAAAGCT 180
TACCAGTGTG GACTTGGTGT TAGCCACGCT GTTACTCAT ACAGTACGTG TCCTGTTTTT 240
AAAATATACA ATTATCTTA AAAATAAATT AAAATCTGTA TACTTACATT TCAAAAAGAA 300
A 301

SEQ ID NO:562

SEQUENCE LENGTH:294

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00627

SEQUENCE DESCRIPTION:

GATCTNAGGA GCTTTAGGGA GAAGACTTGG TGGGGCTGGA GCACACCTTG GGNCTCANTG 60
GTTTCTGTGT CCCNGTGGTG CCANTCCTTC TGGGCAGTGC AGGCGGCTGC CAGGCCCAGC 120
CCTGACTTCC ACTCTGGCTC AGCAACCTGG TTATTTATGT GGGGCCGTGC AGGCATGGGC 180
CCACTGCCTG TCCATCCTGT TTCTNTTATA AATTGAACT CACCATTGCC CTATCCTTGT 240
GTCTCCACCC GCTTCCATGT GTTGAATAAT AAAAGGTGGG AAAGTGCTGT CAAA 294

SEQ ID NO:563

SEQUENCE LENGTH:296

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00628

SEQUENCE DESCRIPTION:

GATCTGCCAT AAGAAAATCT AGTTCAACTC TAATTTTATG TAGTAAATAA ATTGGCAGGT 60
AATTGTTTTT ACAAAGAATC CACCTGACTT CCCCTAATGC ATTAAAAATA TTTTATTTA 120
AATAACTTTA TTTATAACTT TTAGAAACAT GTAGTATTGT TTAAACATCA TTTGTTCTT 180
AGTATTTTTC ATTTGGAAGT CCAATAGGGC AAATTGAATG AAGTATTATT ATCTGTCTCT 240
TG TAGTACAA TGTATCCAAC AGACACTCAA TAACTTTTT GGTGTGTTAA CTGAAA 296

SEQ ID NO:564

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS00629

SEQUENCE DESCRIPTION:

5 GATCGACTAC AGAGTACTTN TTTCTTATGA TGATTGGTGT AGAAATGTGT GATTGGGGTG 60
GGCTTTTACA TCTTGCCCTAC CATTGCATGA AACATTGGGG TTTCTTCAAA ATGTGTGTGT 120
CATACTTCTT TTGGGAGGGG GGTGTTTTTTC TTCTGTTTAT TTTCTGAGAC TCCTACAGGA 180
GCCAAATTG TAATTAGAG ACACTNAANT TTGTTAATCC TGTCTGGGAC ACTTAAGTAA 240
10 CATCTAAAGC ATTATTGCTT TAGAATNNNC AAATAAAATT TTCCTGACCA AATTGTTTTG 300
TGGGAAA 307

SEQ ID NO:565

SEQUENCE LENGTH:296

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00630

SEQUENCE DESCRIPTION:

20 GATCTTGCTC CTTCAGACTC TGACCTGAGT GGAGACCTTT CCACCAGACA CAGCTCGGGC 60
CTGTGTAATT GTAGGAGAAG ACATCAGCA GTGATTGCCA TGGCACAGAG CCGTGGTCAT 120
TGTTGCTGTT ACAAAGAAGA AAACCATCTG AGTTCTAACT CTTGGTTGC TTAAGTAG 180
TTCCCAAGAG TCTGAGAAGC TATTCTATT TTTAAGAGTC ATTTTGTGA ATNITTGTAA 240
NACAAAAGTA CCAATCTGTT TTGTAAATAA AANTCATCCT AAAATTCGAN GTTAAA 296

25 SEQ ID NO:566

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS00631

SEQUENCE DESCRIPTION:

35 GATCTTTNGC TAGGTGGATG ACTAGTNATA TTCAAAGCCT TTTCTCAAAG CCCTTTCAGT 60
TACAACCACC CCACTATGGA ATCAGTATTT AGTTATACAT TTGTATAAGA NCCTGTATTT 120
TGAAAAACAC ATTCATGTAT ATTTATTCCT GGAATTATTT GCCTGTTAAA CAGTGTCTTT 180
CATGTTCTCT CCCAGATTG TAAACTCTGT AAGAAGCTGC TNGTATCTGT ATCCCTTGTT 240
GAAACTCTGA AAACACTGAA TAACTAAANT CTTCTTCTCA TCCNTAAA 288

40 SEQ ID NO:567

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00632

SEQUENCE DESCRIPTION:

45 GATCTTGATA TTCTGTACAA GTTGATGTAA TACCCTGATG CGTTTTAGAG GACTTGGCAT 60
AAAATNAAAG NTTGGCAAAG GCCCTTGAGG GGCTTGGGGA TGAGAGTATG GAACTGTCTG 120
CATTGGACCC TAAACTGGAC TAGANGAGGC ATCTTCAAGG TTCATACGTT GTCCAGCTGT 180
AAGTTCATTT GAGTAGCAGA GCTAACAAAT ATTTGAGGTC AAAACCCCTAC CATGTAAAA 240
50 CAAACAAAAA CTTATCATGT TAATAAAAGT ATTCATTGTC TTGANANANA AA 292

55

SEQ ID NO:568
 SEQUENCE LENGTH:291
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00633
 SEQUENCE DESCRIPTION:
 GATCCTGACA AGAAGAAAAT NAAGCTCAAA GTCAAAAAAT CTCGTGAAAA ACGGAGTTTG 60
 GCCTCTCATC TCAGTGGATA TATCCCTNCC AAAAGGAAAC AAGGGCAAGG CTTATCTTTG 120
 TGTCAAAACG GAGAGTCACC CAACTGTGTG GAAGACAAGA TGCTCTCGAC AGTTGCAGTA 180
 CTTACCCTTG GCTAAGAACT GCACTGCTTT GTTTAAAGGN CTGCAGACCA AGGAGCGAGC 240
 TTTCTCTCAG AGCATGCTTT TCTTTATTAA AATTACTGAT GCAGANAAAA A 291

SEQ ID NO:569
 SEQUENCE LENGTH:285
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00634
 SEQUENCE DESCRIPTION:
 GATCANGCTG GCTGCAAAGA AGGGACTGGA CCCATACAAT GTACTGGCCC CAAAGGGAGC 60
 TTCAGGCACC AGGGAAGACC CTAATTTAGT CCCCTCCATC TCCAACAAGA GAATAGTAGG 120
 CTGCATCTNT NAAGAGGACA ATACCAGCGT CGTCTGGTTT TGGCTGCACA AAGGCGANGC 180
 CCAGC NNTGC CCCCGCTNGT GGAGCCCATT ACAAGCTNGT NCCCCAGCAN CCTGGCACAN 240
 TGAGGNACCT GCACTAAATT ACTNAAAAAT TGCTGTAAAG NTTTN 285

SEQ ID NO:570
 SEQUENCE LENGTH:285
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00635
 SEQUENCE DESCRIPTION:
 GATCACCCCTT GTAATGTGTT ACGGGTCCAT TTTTCCTGGA ATCGTTTAAT CTAAAGCAGT 60
 TTCCCTGTGTT TTGGAGATTT TNTAGTAAAT TTTAATTTG GCTATTGTTT GGAAAAGATG 120
 AGCTGTCTGT GTAGATATGA AGTATAGTTT TTNCCATAAA ACAGATGTTT ATTTGTATT 180
 AAAAAATACC ACTGTACTTG TTTTACACCA TTTGTATACA TGTGGTGATA TTAATGCTAA 240
 ACTGTAAAT TCAGGAATTA AAATGTGACC CTGTAATTC ATAAA 285

SEQ ID NO:571
 SEQUENCE LENGTH:287
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00636
 SEQUENCE DESCRIPTION:
 GATCTAACCA TTTTCATACT CTAACTGAT TGAAACAGAT TCAAAGAAGT ATCGAGTGCT 60
 ATGCATTGAA ACTTGTTTTT AAATGTTAGA TGGCACTATG TATATTAATG TAAANCAATG 120
 TTAATTTACT CAAGTTTCA GTTTGTACCG CCTGGTATGT CTGTGTAAGA NGCCAATTTT 180

NGTGTATTGT NACAGTTTCA GGTNATTNAT ATTCGATGTT TTGTAAANCT CAAATANCGA 240
CTATACTNAT GGGNCCAAAT AAATGGGCAT CTGCATTCTN GGTAAA 287

5

SEQ ID NO:572
SEQUENCE LENGTH:282
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

10

CLONE:HUMGS00637

SEQUENCE DESCRIPTION:

15

GATCTNTGGT GGCAATGNCT GACCAGTAGA CTGGTGGCTC ACTTCTNCCC ACCTGCCGGC 60
AACACCAGTG CCAGGAAAAG GCCAAAAGAA TGTNTGTTTC TAACAAATCC ACAAATAGCC 120
CCGAGATTCA CCGTCCTAGA GCTTAGGNCT GTTTCCACC CCTCCTGACC CGTATAGTGT 180
GCCACAGGAC CTGGGTCGGT CTAGAACTCT CTCAGGATGC CTTTCTACC CNATCCCTCA 240
CAGCCTCTTN CTGCTAAAAT AGATGTTTCA TTTTNTGGA AA 282

20

SEQ ID NO:573
SEQUENCE LENGTH:279
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

CLONE:HUMGS00638

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SEQUENCE DESCRIPTION:

30

GATCTACTGG CGAGCGATGA AAATGTTGCA GGGAGAGTCA GCAGAGGCAT TTGTAGCTAA 60
ACATGCTATG CATCAGACTG GCCATTATG AAGATGAAGA ATACAGTCAG CTTGTGAAA 120
TAGTATTGCA AGCAAGCCCC GTGGGCAAAAT TTGTATTGAG TCCATCTGTA ATTTGCTCAG 180
TGATGGCAGA CAAGATGGCT GTCTGGTTTT GAGACACACT TTAATTTTAT GTTAACTTGT 240
TAAATCTTTT TAAAAATTAA AAAATTTTTA TGATTGAAA 279

35

SEQ ID NO:574
SEQUENCE LENGTH:279
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

CLONE:HUMGS00639

SEQUENCE DESCRIPTION:

40

GATCATTGCA TTTTCCTGTA TTTTCTAAAA TGGCTCCAAT TTTGTNTTTT AAGCTTCAGC 60
TTAAGAGGAA GTTTATGTTT TAATTCCTGA CTGAGAATAC AGTATTGAGA TTCTNTGTTT 120
TACAGATAAC AACTGGTTTT TATTACTCAT TAAGTTCATT TGCATCCCGT AGCCCTCTGT 180
AAATGTTTCC CCTAGTTGTA TGTACGTAAA TGCACGCTTA TCCAGTNTAT ATTAGACATT 240
TTTGTGCTAA AATATATTAA GTGGGATTTT TGTAGCAA 279

45

SEQ ID NO:575
SEQUENCE LENGTH:280
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

50

CLONE:HUMGS00640

SEQUENCE DESCRIPTION:

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GATCTTTGCA AGGGCAAAAC TACAAGTAAC GAGTTTATA TAATTAATTT AAATTTNTNA 60
 CAGGTTTTCA TGTTCAGGAT AAACCATACT TCCACCTTGG GTGAGAACAC TTGCAACAGT 120
 TTATTAATGA GGTGACTTTC ACCTTAGGAC AACTGTTGCA TGCCAAGTTT TTTGTGTGTG 180
 TGAAACACTN TCAAACTGA TTAAAAAGAT GTAAATTTAA AATTGGTTGT ATCTAATATG 240
 CCCCAGGTTC GGTAAATAAA CAATTCCTTT TAAAAACAAA 280

SEQ ID NO:576
 SEQUENCE LENGTH:300
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00641

SEQUENCE DESCRIPTION:
 GATCTGCCTG TCCCTTTTTC CCCTGGGGTT TGACACACAG GCTCCTCTCA GCATGAGGTG 60
 GAGCAGTGAC CAGGTGGAGC AGTGACCAGG ACGCCTCTGG CCCAGTGCTG CCCAGCCTCC 120
 CCGNCCGCTC CCAGGCGCCC CATGTCCTCA CAGGCCAGGA CGCCATGNCA GGATGGAGAG 180
 GACTTGTGTG ATTTTGTGTT CTTCCTGAC CTCAGTTTCA TGAAAGAAAG TGGAAGCTAC 240
 AGAATTATTT TCTAAATAAA AGGCTGAATT GTCTGAAAAA TAAATATAT TGTATTAAA 300

SEQ ID NO:577
 SEQUENCE LENGTH:278
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00642

SEQUENCE DESCRIPTION:
 GATCTGGGAC GTGGTTCGGC GGANAGTCCC CAGCCCGGCC CCCTGCCTGG GACCACCAGG 60
 CCCCCAGGAG AAGCCGCTG AGCCACAACC TTGCGGCATG CAAATNAGAT GGCCGCTCCA 120
 GGCTTGAAT GTTCCGTGGC TGGGCCCCAC GGAAGCCTG ATGTTCAGGG TTGGGGTGGG 180
 ACGGGCAGCG GTGGGGCACA CCCATTCCAC ATGCAAAGGG CAGAAGCAA CCCAGTAAA 240
 TGTAACTGA CTTCCAGCCT CACCCGTGGG CGGTCAAA 278

SEQ ID NO:578
 SEQUENCE LENGTH:277
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00643

SEQUENCE DESCRIPTION:
 GATCAGGGCC CACTGATGAT GGTGAAGAAG AGATGGAAGA AGACACAGTC ACAAACGGGT 60
 CCTGAGCAGT GAGGCAGATG TATAATAATA GGCCCTCTTG GAACAAGTNT TGCTTTTNGA 120
 ACATGGTATA ATAGCCTTGT TTGTNTTAGC AAAGTGAAT CTATCAGCAT TGTGAAATG 180
 CTTAAGGCTG CTGCTGATAA TTTNNTAATA TAAGTTTGA AATCNAAATG TCAATTTNCT 240
 ACAAATNATA AAAATAAACT CCACTCACNA TGCTAAA 277

SEQ ID NO:579
 SEQUENCE LENGTH:277
 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00644

SEQUENCE DESCRIPTION:

GATCCGAGTC GTCCGGAAAT CCATTGCCC GTNTTCTCAC AGTTATTAAC CAGACTCAGA 60
AAGAAAACCT CAGGAAATTC TACAAGGGCA AGAAGTACAA GCCCCTGGAC CTGCGGCCTA 120
AGAAGACACG TGCCATGCGC CGCCGGCTCA ACAAGCACGA GGAGAACCTG AAGACCAAGA 180
AGCAGCAGCG GAAGGAGCGG CTGTACCCGC TCGGGAAGTA CGCGGTCAAG GCCTGAGGGG 240
CGCATTGTCA ATAAAGCACA GCTGGCTGAG ACTGAAA 277

SEQ ID NO:580

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00645

SEQUENCE DESCRIPTION:

GATCAGGACC CACCTNCACT NCTTCTGAAA GTGTGACAGT GTCCAGCCGG TTCTGCAGCA 60
CTAGGGGAGG GGCAGATGG TGGTTGCATG GGCTTCCTGG GTCTCCACTC TCCGTCTGGC 120
CTAAAGGTGA TGTATTTGGT GTTTGGCCCT GCAGTCCCCA CTCTTGAGGC TTAAGGCGCA 180
TGTGGCAGAN CACTNCTTCC AGCAGTAGTC GCTTTACTGT TACCNGTTTA GGCCTAGAAG 240
TTTTCCNNCA TCTGTAATG TGATTTAAAA TNTAAA 276

SEQ ID NO:581

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00646

SEQUENCE DESCRIPTION:

GATCTACTTA CTCAAGTCTN ATGAATNCTG NGCCTTTCAT CACATTCCTA GCCCACTCTC 60
ATCATTACTG CAGAAGGGTG TTGTGATGAC CAGTNTTATA CTGTGTTTG ATATGTCTAG 120
CAATAACTTA AAGAAAAAA AACCTGGGAA ATCTTCAACA TGNNTNGGA ACATATATGT 180
ATGTATTAAT GNATATACAT GGCTTAACTT ATACGGTTAT GGCAGCNCCT GTATACAGTT 240
TGAACATCATG NACCTGAAAA ANAATTCTTA ANTTN 275

SEQ ID NO:582

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00647

SEQUENCE DESCRIPTION:

GATCGCCATC ATGAACGACA CCGTAACTAT CCGCACTAGA AAGTTCATGA CCAACCGACT 60
ACTTCAGAGG AAACAAATGG TCATTGATGT CCTTCACCCC GGGAAGGCGA CAGTGCCTAA 120
GACAGAAATT CGGGAAAAAC TAGCCAAAAT GTACAAGACC ACACCGGATG TCATCTTTGT 180
ATTTGGNTTC AGAACTCATT TTGGTGGTGG CAAGACAACT GGCTTTGGCA TGATTTATGA 240
TTCCTGGNT TATGCAAAGA AAANTGGAAC CCNAACATAG NCTTGCAAGT CATGGCCTGT 300
ATGNNGN 307

SEQ ID NO:583

SEQUENCE LENGTH:272

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00648

SEQUENCE DESCRIPTION:

GATCTGAATT TTTTCCTCCT TTTGGTTTTA TTTTGTGGT TTATTTTGTG TTTTCTTTTC 60
 TCCTTTTGG GGGGTATTCA GAGTGGGCTG GGGCCCTGGG CGAGACACAG CTACCTCTGT 120
 TGGCATCTTT TTAATACCAG GAACCCAGCG GCTCTAGCCA CTGAGCGGCT AAATGAAATA 180
 AAGTGGAAAA AAAAAAANGG GAAAAACCCA AAGGNTTAAA AACCCACNGG AATTTNTTG 240
 TNGAAANTNG AAAATAAAGG TTTCCNNGTA AA 272

SEQ ID NO:584

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00649

SEQUENCE DESCRIPTION:

GATCTATACC AATTAAACAT TTTCATAGTT CTGCCTATTG TCCTTCCCTG AGGCTCCATT 60
 GCTGCTTGGT GGCCATTCTC TGCCTTTTTA CAGTCACCTG AACAATGACC CATCATCTCT 120
 TGCTTGCTTG AAATCTTGCT GAAATGTTCT CATTTCCTGT TTGCTGTATG GGCTCGGGTG 180
 GGATGTTTGT TGGCTCTGTT GTGTTTATTC ACCAATTGT ACATTATTG TTGTCCTTTA 240
 CTACTGTAAA CAGTAAATAT AGTTTGGTAT TCTGTCAA 279

SEQ ID NO:585

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00650

SEQUENCE DESCRIPTION:

GATCCAGAC TGGTTCTTGA ACAGACAGAA GGATGTAAAG NATGGAAAAT ACAGCCAGGT 60
 CCTAGCCAAT GGTCTGGACA ACAAGCTCCG TGAAGACCTG GAGCGACTGA AGAAGATTCG 120
 GGCCCATAGA GGGCTGCGTC ACTTCTGGGG CCTTCGTGTC CGAGGCCAGC ACACCAAGAC 180
 CACTGGCCGC CGTGGCCGNA CCGTGGGTGT GTCCAGNAAG AAATAAGTCT GTAGGCCTTT 240
 GTCTGTTAAT AAATAGTTT ATATACCTNN AAA 273

SEQ ID NO:586

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00651

SEQUENCE DESCRIPTION:

GATCTNCCAC GTCTCCATCT CAGTACACAA TCATTTAATA TTNCCCTGTC TTACCCCTAT 60
 TCAAGCAACT AGAGGCCAGA AAATGGGCAA ATTATCACTA ACAGGTCTTT GACTCAGGTT 120

CCAGTAGTTC ATTCTAATGC CTAGATTCTT TTGTGGTTGT NGCTGGCCCA ATGAGTCCCT 180
AGTCACATCC CCTGCCAGAG GGAGTTCTTC TTTTGTGAGA GACACTGTAA ACGACACANG 240
AGAACAAGNN TAAACAATA ACTGTGTGTG TTAATA 275

SEQ ID NO:587

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00652

SEQUENCE DESCRIPTION:

GATCTTATGG ATAAACTCA GAAAGTGAAG GTGAAGAAAG AAACGGTGAA CTCGCCAGCT 60
ATTATAAAT TTCAGAGTCG TCGAAAACGT TGACGTGTTA TAGATAAGCC TTGTCATTNT 120
GTATCAAAAA TCTGTTGTG TTTTCTAGTA ACTTCAAATT CCATTACTCC AAATGGCATG 180
GTTTCCGGT TTGTAACCAT AACTAAATG TCAGTCTGAC ATTTAATGTC TTTCTATGGA 240
CAACATTAATA TCNCCCTCCC TTCTGTAAA 269

SEQ ID NO:588

SEQUENCE LENGTH:272

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00653

SEQUENCE DESCRIPTION:

GATCAAGTGG CTTTCCCTGG GACCTGCCCA GCTTTGAGAA TCTCTNCTCA TCCACCCTCT 60
GGCACCAGC CTCTNAGGGA AGGAGGGATG GGCATAGTG GGAGACCAG CCAAGAGCTG 120
AGGGTAAGGG CAGGTAGGCG TGAGGCTGTG GACATTTTCG GAATGTTTG GTTTTNTTTT 180
TTTAAACCG GGCAATATTG TGTCAGTTC AAGCTGTGAA GNAAAATATA TATCANTGTT 240
NNCCAATANA ATACAGTGAC TANCTGAACA AA 272

SEQ ID NO:589

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00654

SEQUENCE DESCRIPTION:

GATCGTCAAA TCTTTNCAA ATTTAATNTA TATGTGTATA TAAGGNAGTA TTCAGTGAAT 60
ACTTGAGANA TGTACAAATC CTTATCCAT ACCTGTGCAT GAGCTGTATT CTTACAGCA 120
ACAGAGCTCA GTTAAATGCA ACTGCAAGTA GGTTACTGTA AGATGTTTAA GATAAAAGTT 180
CTTCCAGTCA GTTTTCTCT TAAGTGCTG TTTGAGTTTA CTGAAACAGT TTACTTTTGT 240
NCAATAAAGT TTGTATGTTG CATTTAAA 268

SEQ ID NO:590

SEQUENCE LENGTH:267

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00656

SEQUENCE DESCRIPTION:

GATCAAAAAT AAAATGTTAT TTTTAAAGTT TCTNTTGGAG ATTTTNCCTA AGTTTTGGTA 60
 GATATTCTTA AGTTTTAGTG ACCTCAGTTT GGAATTAAG TAAGCTAAAC ATTGTGTCCT 120
 TATTATNAGT TATATAAAAC TATGCTTTAG ACTTTGTNAG AAATTCTGC CCCACCTGA 180
 CTGACTGCTT TNCCATTTNT GGTGTACAA AATGAATTCA CACTTTAATG CTATGGCCAC 240
 CTTTAAATAA AGTACAGCGT GACTAAA 267

SEQ ID NO:591

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00657

SEQUENCE DESCRIPTION:

GATCTAGATT CTACATGTTA CCATTGGTTT ATTCTGTGC TTTCTGTATT TAAACTTTG 60
 GCTGTACTAA GCAAATGCAA GGTATAATT TAGCTAATAG TAGTTTACAG ACAATTCTGA 120
 TGATTATGAT TTCATTTGGT TTAACAAAGC TGTACTAGTT CATTTTATAA GGAAATGATA 180
 CTGTAGACAA ATGTAAATAA AGCCTGTGAG TCAAGCATCA AGTGGTGGT GTTAGAAATA 240
 ANCTAGAGAT TTTTAACTC TGAAA 265

SEQ ID NO:592

SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00658

SEQUENCE DESCRIPTION:

GATCTGGGGC CAGCTCACCG CTCACGTCCC CGTCATCGAC AACTCCACCC TNTACATCAG 60
 TAGAGCATGC ACCATTTTGA ACGTGACATT TNCGGTAAAG TAACTATGC TGATTTCTCA 120
 GACTTTAAAG ATGCTCTNNT TCTGTGTGN AAATAGGACC CAAAGTGTCT CGATTGCTGA 180
 AGTGATGAAC AAGTGGGAAA GCAGATTTGA GACTATTTCC TTATCTGAAT ATTTAAATGA 240
 AATACAGCAT CTTTAAAANG CAAA 264

SEQ ID NO:593

SEQUENCE LENGTH:262

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00659

SEQUENCE DESCRIPTION:

GATCTTTTAA AAAGATGATG CAGTTCTGTA TTTATTGTGC TGTGTCTGGT CCTAAGTGGA 60
 GCCAATTAAN CAGGTTTCAT ATGTATTTN CCAGTGTGTA ATCTCACACA CTGTACTTTG 120
 AAAATTTCTT TCCATCTGA ATAACGAATA GAAGAGGCCA TATATATTGC CTCCTTATCC 180
 TTGAGATTTC ACTACCTTTA TGTTAAAAGT TGTGTATAAT TGTTAAAATC TGTGAAAGAA 240
 TAAAAAGTGG ATTTAAATTA AA 262

SEQ ID NO:594

SEQUENCE LENGTH:260

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00661

SEQUENCE DESCRIPTION:

GATCCATCCA AAAACAAGGA CTGCAGCCTA AATTCCAAAT ACCAGAGACT GAAATTTTCA 60
GCCTTGCTAA GGGAACATCT CGATGTTTGA ACCTTTGTTG TGTTTGTAC AGGGCATTCT 120
CTGTACTAGT TTGTCGTGGT TATAAAACAA TTAGCAGAAT AGCCTACATT TGTATTTATT 180
TTCTATTCCA TACTTCTGCC CACGTTGTTT TCTCTCAAAA TCCATTCCCTT TAAAAAATAA 240
ATCTGATGCA GATGTGTA 260

SEQ ID NO:595

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00662

SEQUENCE DESCRIPTION:

GATCCCTTTA TGAAACCTTG TGAATAGATG AATGTNTGGA GATGGCGACT AGTGGACAAC 60
AGAACAATAT TGGAATGGTG GTAATACGAG GAAATAGTAT CATCATGTTA GAAGCCTTGG 120
AACGAGTATA AATAATGGCT GTTCAGCAGA GAAACCCATG TCCTCTCTCC ATAGGGCCTG 180
NTTTACTATG ATGTAAAAAT TAGGTCATGT ACATTTTCAT ATTAGANTTT TTGTAAATA 240
NNCTTTTGTA ATAGTCAAA 259

SEQ ID NO:596

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00663

SEQUENCE DESCRIPTION:

GATCNGGCT AAGCCAGCCA GCCCNCCCGC GCCAGGNAAA ACAGGGCTGC AGGTGTCCTG 60
TCTCCAGCC TCATCTGGCC GGCCTCCCA AACATTTGCC TGTCCATCAG CTCTTCCTCC 120
TTTCGAGTCA TGTGAAAGG GACAGGNCCA AGTGGCCTTG GTGTTTAAAT CTTGCCCTAA 180
ATTGTAATC ACATGATTAT TTAAAGTCAC TAGANATAAG TAAGCACAGC AATAAAGNTT 240
TAATGGAATA AAAGAAA 257

SEQ ID NO:597

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00664

SEQUENCE DESCRIPTION:

GATCCCAGAA TTCAACCTGT ATTTATAAAT GTATAATGTA TTTAGCTACT TTTTGGTTTA 60
AATGAACTTG TTGGGTTAGC TTGGTAAATG TTATAATTTT NACTATTTTC TACAAAGAAA 120
ATATTTTCTA ATTAAAGTTG GAGCTATCTG TGCAGCAGTT TCTCTACAGT TGTGCATAAA 180
TGTTTTNCT ATAAAATGAG CTAATGTATA ANATACTGCT GTATACCATA ATAANGATAG 240
TAATACTTGA AA 252

SEQ ID NO:598

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00665

SEQUENCE DESCRIPTION:

GATCATTAGT TGAATCGGTA TCATCTTCAC CAAATAAAGA AAGTAATGAA GAAGAGCAAG 60
 TGTGGCACTT CCTTGGCAAG TGATTGAAAC ATCTGAAATT CTGCTGTCAA GATTCCCATC 120
 TCTAAGGACT CCAAGTGCTA GAGACAAGGG GGTCTATGAG CATTTACTGA CTCCTGTTA 180
 AAACCTTCATT TTTTCAAAC TTTTGAGCTA TGCAATATAT AANTAAACAG TAAGAATTTT 240
 AAATTACAAA 250

SEQ ID NO:599

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00666

SEQUENCE DESCRIPTION:

GATCCTTCTT CCTTCACTG GTCGTGCCTC CCANNAGGTG CAGAGATTCT TAGAAGAGGA 60
 GGTGTATCCC CTGTTAAAAC CATATGAAAG CGTGATGAAG GTGAAAGCAG AATTATGTCT 120
 GTAGAGTTGG AAGAGAATTA AACGAAAATC ATTGTTAATT GCTGAGGCAT GAAAATTGTG 180
 TTACTATAAT GCCTTATTTT ACCTCGAGAA TTGTTACCTT AAATTAGTAC AGCACTTTCT 240
 TCTTCCCAA 250

SEQ ID NO:600

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00667

SEQUENCE DESCRIPTION:

GATCCTTCAG TTACATACAA TTTGTTTAAAT GAAATGTCAT GGCTCTGTTC ATATTTTNTT 60
 NTTGTNCTTC CAATTGGTAT ATACAACTTT CAGAGCCTCT TGTATTTGGA AGGCTGGAAG 120
 GGCCCAGACT TTGGAATAGT GTCTTGTTTT CACTGTTTTN GTTTTGATTT TTTTTTTGTT 180
 TNGATTTTTT TAAAACTAAA GCTATATAAA GCTTGNGGAT TAANCAGANT AAATTCCTAA 240
 ATTTAAA 247

SEQ ID NO:601

SEQUENCE LENGTH:246

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00668

SEQUENCE DESCRIPTION:

GATCCAGGGT GTGTGTGAGT TGAGGGTGGG TGGAGGGGTT TGCAGTGTGG GAATGTGGCC 60
 CTGCAGTTGA CCTGAGCTGC TTCACATGGT TGTCCATTCT GGGGCTTAAA GAACTGGGAC 120

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CAGACCAAGT AGAGGCCTTG GTGCTGNTTG GGGTGGGGCC TGCAGANTCT TAGTTACTGA 180
TTTCATTTC AATAAATGTA GGTTTGTAC ATGAGTTTCC CAATTAAAAA AAAAATGACT 240
TCTAAA 246

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SEQ ID NO:602
SEQUENCE LENGTH:284
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

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CLONE:HUMGS00669

SEQUENCE DESCRIPTION:

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GATCAGAATT TCACCAGGGA GTAAAATTAC CTGAAAACGT AAGANGTTTT AAACAGCTTT 60
TCACACAAAT TAGATGCAAC TGTTCCTCATG TCTGAGTACT TATTTAAAAG AAAGGTAAAG 120
ATTGGCCTGT TAGAAAAAGC ATAATGTGAG CTTTGGATTA CTGGATTTTT TTTTTTTTNA 180
AACACACCTG GNGNGGNCAT TTGAAAACAC TTTTCTTACC CTCGANCCCT GATGTGGTNC 240
CATTATGTAA ATATTTCAA TTTAAAAAT GTATATATTT GAAA 284

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SEQ ID NO:603
SEQUENCE LENGTH:249
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

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CLONE:HUMGS00670

SEQUENCE DESCRIPTION:

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GATCGAGGTG GAGAAGCCCT TTGCCATCGC CAAGNAGTAG GGCACAGGGA CATCTTTCTT 60
TNAGTGACCG TCTGTGCAGG CCCTGTAGTC CGCCACAGGG CTCTGAGCTG CACTNGCCCC 120
GGTGCTGGCA TCTGGTGGAG CGGACCCACT CCCCTCACAT TCCACAGGCC CATGGACTCA 180
CTTTTGTAA AACTCTTAC CAACACTGAC CAATAAAAAA AAATGTGGGT TTTTTTTTTT 240
TTAAATAAA 249

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SEQ ID NO:604
SEQUENCE LENGTH:244
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

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CLONE:HUMGS00671

SEQUENCE DESCRIPTION:

GATCGGAATG GTGGAGAACT TCAACCAGGC ACTCAAGGAA ATTGGGGATG TGGAGAACTG 60
GGCTCGGAGC ATCGAGCTGG ACATGCGCAC CATTGCCACT GCACTGGAAT ATGTCTACAA 120
AGGGCAGCTG CAGTCTGCCC CTTCTAGCC CTTGTTCCT CCCCCAACC TATCCCTCCT 180
ACCTCACCCG CAGGGGAAAG GAGGNAGGCT GACAAGCTTG AATAAAACAC AAGCCTCCGT 240
TAAA 244

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SEQ ID NO:605
SEQUENCE LENGTH:244
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

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CLONE:HUMGS00672

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SEQUENCE DESCRIPTION:

5 GATCCCTTT CCGTAAAAGC GTGTAACAAG GGTGTAAATA TTTATAATTT TTAATACCTG 60
 TTGTGAGACC CGAGGGGCGG CGGCGCGGTT TTTNATGGTG ACACAAATGT ATATTTTNC 120
 AACAGCAATT CCAGGCTCAG TATTGTGACC GCGGANCACA GGGGACCCA CGCACATTCC 180
 GTTGCCCTTAC CCGATGGCTT GTGACGCGGA GAGAACCGAT TAAAACCGTT TGAGAAGCTC 240
 CAAA 244

SEQ ID NO:606

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SEQUENCE LENGTH:242

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00673

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SEQUENCE DESCRIPTION:

GATCTTTCCC ATNTCTACCT AAGTCAGCTT TCATCTTTGT GGATGGTGTC TCCTTTACTA 60
 AATAAGAAAA TAACAAAGCC CTTATTCTCT TTTTNTTGT TCCTCATTCT TGCCTTGAGT 120
 TCCAGTTCCT CTTTGGTGTA CAGACTTCTT GGTACCCAGT CACCTCTGTN TTCAGCACCC 180
 TCATAAGTCG TCACTAATAC ACAGTTTGT ACATGTAACA TTAAGGCAT AAATGACTCA 240
 AA 242

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SEQ ID NO:607

SEQUENCE LENGTH:245

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00674

SEQUENCE DESCRIPTION:

30 GATCCGGGTG GATGCACAGC CCGTCAAGGT CTATGCTGAC GNCTCCCTGG TCTTCCCCCT 60
 GCTTGTGGCT GAAACCTTTG CCCAGAAGAT GGATGCCTTC ATGCATGAGA AGAACGAGGA 120
 CTGAGCGGCT GCGGTCCCAG GAAGGTCTTA CCCCTCTNC TATTATNAA TTTGCAGACC 180
 CAGCCNTCC CCTACTTTTT GGTGAGCTAC GNCTCTAGAA TAACNCCCGG TATCTGAAGT 240
 CCAAA 245

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SEQ ID NO:608

SEQUENCE LENGTH:245

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS00675

SEQUENCE DESCRIPTION:

45 GATCTCTACC ATTTAATTAA GAAAGCAGTT GCTGTTGAA AGCATCTTGA GAGGAACAGA 60
 AAGGATAAGG ATGCTAAATT CCGTCTGATT CTAATAGAGA GCCGATTCA CCGTTTGCT 120
 CGATATTATA AGACCAAGCG AGTCCTCCCT CCCAATTGGA AATATGAATC ATCTACAGCC 180
 TCTGCCCTGG TCGCATAAAT TTGTCTGTGT ACTCAAGCAA TAAATGATT GTTTAACTAA 240
 ACAA 245

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SEQ ID NO:609

SEQUENCE LENGTH:241

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00676

SEQUENCE DESCRIPTION:

GATCTAAAAT GTCACATTCA GATTTTNAGG AAGAAAATCT TCATTACAGT GGAGCACAAA 60
 TTTTCCATAC AAGACATCAT TGAGGNAGCA TGCTGTCCCC TTCTAACCTG AAACACATTG 120
 TTTCCCATCC NGGTTGGGCT TCTNTACCNC CTTATTAATT TATGAACCNG AAGTTGCTTG 180
 AAGTGTTTTG GGCTTAATAA ATGGGGTGAA AGTATAGGTA GCAGTAACAC CTACATGNAA 240
 A 241

SEQ ID NO:610

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00677

SEQUENCE DESCRIPTION:

GATCTTCTGA GGTCAGGAGT TTGAGACCAG CCTGACCAAC ATGGAGAAAC CCAGTCTCTA 60
 CTGAAAATAC AAAATTAGCC GGGCATGGTG GTGCACGCNT GTAGTCCCAG CTAATTGGGA 120
 GGCTGAGGCA GGAGAATCGC TTGAACCCAG GAGGCGGAGG TTGCGGTGAC CCTCCAGCTT 180
 GGGCAACATG TTATGANTGA AACTCCATCT CAAAAAATAA AAAAAAAAAA GGGNNGCAAA 240

SEQ ID NO:611

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00678

SEQUENCE DESCRIPTION:

GATCTGTGAA GGCTTCCCTG ACCNNTGCCC AGGAAGAGTT CACTGGTCGC TCTGTTGTGC 60
 CCCACAGCAC TTTGTTATAC CTCTGCCACA CACTTCACGC AGCGCGTTGT AACTCATGTG 120
 TTTACATGTC TGTCNCCCA GACTGTNAGC TCCTTGAGGG CAGGGACTGT ACATTCTCCA 180
 GCTCTGTGTC CCCAGGGCCT GGCACATTGT AGACGCTTAA TAAATTTCTG TTAAATGAAA 240

SEQ ID NO:612

SEQUENCE LENGTH:242

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00679

SEQUENCE DESCRIPTION:

GATCAGCTCC TTGACCTCTG AGGGGCAGGN GTGCTTCCTG GTGTGTGTAT TAGAATCCCT 60
 TCCTGCCTTG TTTCATGGCA GTGAAATGCC TCTTGGTCCT GTCCAAGTGT ATCTTTCCT 120
 GATTTCTGNA TCATGNTCTA GTTGCTTGAC CCTGCCANAT GGGTCCAGTG TTCATCTGAG 180
 CATAACTGTA CTAAATCCTT TTTCCATATC AGTATAATAA AGGAGTGATG TGCAATAGCA 240
 AA 242

SEQ ID NO:613

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SEQUENCE LENGTH:239
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00680
 SEQUENCE DESCRIPTION:
 GATCGCAACA ATNAGCCATC CACATNCGTT TTTCAGGGTC ACACCCAAGT AATTGAAAAG 60
 AACTCCTCC ACTTATCCCC TCCNTAATAT GGCTCTNCGC ATGCTGAGTA CTGGACCTCG 120
 GACCAGAGCC ATGTAAGAAA AGGCCTGTCN CCTGGAAGCC AAAGGACTCT GCATTGAGGG 180
 TGGGGGTAAT TTTTCTTGG NGGGCCAGT TAGTGGGCTT NCGNANTGTN TGTATGNGN 239

SEQ ID NO:614
 SEQUENCE LENGTH:238
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00681
 SEQUENCE DESCRIPTION:
 GATCCAAATA AACAGACCCC GTCTGGCAAG AAATGCATTG CAGCCAAAAA AATTAAACAG 60
 TCGGTGGGAA AAAAAAGCAT GTCCTTTCCA ACTGGAAAGT CAGACAGAGG CTTCAGGTAC 120
 AACTGGCCAC AGAGATAGTC CTGGAAGACA CGTGGCGCCT GTGGACCGGA AGCACCAAAT 180
 GCTGGTGCTG CTTTGTACA TACATATTTT TAAACCATTA AAATTCTTCC TGAAGAAA 238

SEQ ID NO:615
 SEQUENCE LENGTH:254
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00682
 SEQUENCE DESCRIPTION:
 GATCCATAGT CAGAAAAGTT ACTGCAGCTT AAACAGGAAA CCCTTCTTGT TCAGGACTGT 60
 CATAGCCACA GTTTGCAAAA AGTGCAGCTA TTGATTAATG CAATGTAGTG TCAATTAGAT 120
 GTACATTCCT GAGGTCTTTT ATCTGTTGTA GCTTTGTCTT TTTCTTTTTC TTTTCATTAC 180
 ATCAGGTATA TTGCCCTGTA AATTGTGGTA GTGGTACCAG GAATAAAAAA TTAAGGAATT 240
 TTAACTTTT CAAA 254

SEQ ID NO:616
 SEQUENCE LENGTH:247
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00683
 SEQUENCE DESCRIPTION:
 GATCAAAGAA AGAAGGCATA CGCNGATTTT TACAGAACT ATGATGTCAT GAAAGATTTT 60
 NAGGAGATGA GGAAGGCTGG TATCTTTCAG AGTGTAAGT AATCTTGGA TATAAAGAAT 120
 TNCTTCAGGT TGAATTACCT AGAAGTTTGT CACTGACTTG TGTTCTGAA CTATGACACA 180
 TGAATATGTG GGCTAAGAAN TAGTTCTCTT TGATAAATAA CCANTTAACA AATNCTTNG 240
 ACAGAAA 247

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SEQ ID NO:617
 SEQUENCE LENGTH:235
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00684
 SEQUENCE DESCRIPTION:
 GATCTGCACC TGAGCCAAAG AAACCTGAGG AAAATCCAGC TTCTAAGTTC AGTTCTGCAA 60
 GCAAGTATGC TGCTCTCTCT GTTGATGGTG AAGATGAAAA TGAGGGAGAA GATTATGCCG 120
 AATAGACCTC TACATCCTGT GCTTTTNTCC TAGTTTCTCT CCACCCTGGA ACATTGAGA 180
 GCAAATCAAA ACCTCTATCC AGACAAGACA AAATAAACT CAACATCTCC TGAAG 235

SEQ ID NO:618
 SEQUENCE LENGTH:238
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00685
 SEQUENCE DESCRIPTION:
 GATCTGTTCC TTGGCAGTGG ACTCAGAAAG CCAACATGTG GCTCCTCCCA GCCCATAACC 60
 AGTATTTTTC CTGCTTCTAA ATACAAATNG GTTGGTTTAA ACTTCANATT GANCTTACTG 120
 TAGCCTCAAA TGATTCCCC CCTCCGCCTC CAGGAAGAAA GAATGTNACT GCCTTAATAA 180
 AAAATGAAAA GAGAATGATG CTCAAAATCT TTCCAAATAA AATGTTCCCT ATATTAAA 238

SEQ ID NO:619
 SEQUENCE LENGTH:234
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00686
 SEQUENCE DESCRIPTION:
 GATCCGCCCT CGAATGGACA CATTACCAGT GAAGGGGCAT TTNTNGTCAA TGTAGGTGCC 60
 CTCAATAGCC TCCTTGGGTG TTTGGAAGCC CAGACCGATG TTCTGTAGT ACCGCGGGAG 120
 CTTCTCCTTG CCAGTTTCTC CCAGCAGGAC CCTCTTCTNG TTTTGAAAGA TGGTCGGCTG 180
 CTTTTGGTAG GCACGCTCAG TCTGAATGTC CGCCATCTTC CCGGCCGGCT GAAA 234

SEQ ID NO:620
 SEQUENCE LENGTH:251
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00687
 SEQUENCE DESCRIPTION:
 GATCCCCAAG CCTGGCAAGG GAATTTNTTC AACTCCCTGC CCCCCAGCCC TCCTTATCAA 60
 AGGACACCAT TTTGGCAAGC TCTATCACC AAGAGCCAAA CATCCTACAA GACACAGTGA 120
 CCATACTAAT TATACCCCTT GCAAAGCCCA GCTTGAAACC TTCCTTAGG AACGTAATCG 180
 TGTCCCTAT CCTACTTCCC CTTCTAATT CCACAGCTGC TCAATAAAGT ACAAGAGCTT 240
 AACAGTNAA A 251

SEQ ID NO:621

SEQUENCE LENGTH:241

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00689

SEQUENCE DESCRIPTION:

GATCCATCAT CCGNCAATGT TAAAAGGCCCG CGTGCGCGAG GCGGACGTGC TCACCCCTTTT 60
 GGAGTCAGAG CGAGAAGCCC GGAGGTTGCG CTGAGCTTGG CTGCTCGCTG GGTCTTGGAT 120
 GTCGGGTTTCG ACCACTTGGC CGAGGGGAAT GGTCTGTAC AGTCTGCTCC TTTTTTTGT 180
 CCGCCACACG TAACTGAGAT GCTCCTTTAA ATAAAGCGTT TGTGTTTCAA GTTAACTCAA 240
 A 241

SEQ ID NO:622

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00690

SEQUENCE DESCRIPTION:

GATCCTCCTG CCTNGGCCTC CAAAAGTGCT GGGATTACAT GCATACCTGA NCTACTGAGC 60
 ACTTTNATCT TGAATGAGTG TTGGATTTTG TCAAATGCTT TTCCTGTACC TATTAATACA 120
 ATCATGATTT TNNCTCTTT AGTATGTTGA TATGATGGGT TACATTAATT GATNNTCAAA 180
 TGTGGAATCA GTCCTGCATA CCTGGAATAA ATCCCACTTG GTCATAATAA A 231

SEQ ID NO:623

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00691

SEQUENCE DESCRIPTION:

GATCTATGAA ATCTGTGTAG GTTTTAAATA TTTTAAAAAT TATAATACAA ATCATCAGTG 60
 CTTTATAGTAC TTCAGTGTTT AAAGAAATAC CATGAAATTT ATAGGTAGAT AACCAGNTTG 120
 TCNCTTTTTCG TTTAAACCAA GCAGTTGANA TGGCTATAAA GACTGACTCT AAACCAAGAT 180
 TCTGCAAAATN NTGATTGGNA TTGCACAATA AACATTGCTT GNTGTTTTAA A 231

SEQ ID NO:624

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00692

SEQUENCE DESCRIPTION:

GATCCCATTT AGGAANCGGC ATTCACTTCA GAAGGTACTT TTAACTGCT CAGTTTTTGA 60
 CTATTTTAAA TAGTTTGCTG AAAACTCCTG ATAACACTTG CTACATATCA TGTTTAAATT 120
 GCTTGTACAG TTAACCTTTA ATTTTATTTA GTAAAGTGTA TCAAAGTAGG ACTTTTTTGA 180
 ATTGTAAATA GGTGGTTTAA TTAAATAAAA GTCAATGTAA AAATTGTAA A 231

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SEQ ID NO:625
SEQUENCE LENGTH:230
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00693
SEQUENCE DESCRIPTION:
GATCCGGAGG GAAATGTGTT AGAGGGTCTG GAAAATTCAG TGCTTTTGAG TTAAGTGTGTT 60
TTATTAAAAA TTCTCTACA AAAGAGAGTC CTCAAGTTGT GGCTGTTCTT GGGAAAGGGG 120
TCACCGTGTC TGACAAAGTG TAACCTTAAA AAGCACGTTG ATTTTTCACA AATGTAAGTG 180
TGCTTGGGAA TTCCTTAAAT TTTGTGCAAT AAACATTTT TTGAAGAAA 230

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SEQ ID NO:626
SEQUENCE LENGTH:202
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00694
SEQUENCE DESCRIPTION:
GATCCAATCA TATTNCTGT AGGGTGGAGG AGGTTTCAGA CCATCCCGCT CTGTTATATC 60
GAAGACCACA ATGGAAGACA AAGGCTTCTA AAGTATACCC CACAGCACGT GCATCGCGGA 120
NAGCCTNCTT GGGATAAAAT ATGTTTACAA TAACTTGCCT ATTGCTGAGA TTAAACCTTA 180
CAGGCTGCGT TATTTAGCA AA 202

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SEQ ID NO:627
SEQUENCE LENGTH:226
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00695
SEQUENCE DESCRIPTION:
GATCCATTGT ATCAGTACCT CACAATCAGA GTTGGCAAAT GATGGATGAG TGATTCAAGC 60
AGTGACCCG GTGGAAGCTG AAATCCATCT GTGAATGGAA CTGAAGTGAA CGTGAATATG 120
CTGACTATAT CCTGGAAGCA TTTTATACC ATCTTGAAT TTCAACANAC TGGCTTTTGC 180
CAGTTAATCC AGCTGTCTTT CAAGAATAAA AGTTGGGGTT TTCAA 226

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SEQ ID NO:628
SEQUENCE LENGTH:226
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00696
SEQUENCE DESCRIPTION:
GATCACCTGA GGTCAAGAGT TCGANACCAG CCTGGCCAAC AGGGTGAACC CCGTCTCTAC 60
TAAAAGTACA AAAATTAGCT GGGCGTGGTG GCGGACGCTG TAATCTCAGC TACTTGGNAG 120
GCTGAAGCAG GAGAGGTGCT GGAACCTGGN AGGCGGAGGT TGAAGTNAGC CGAGATTGCC 180
CTATTGCACT CCAGCTCGGG CGNCAACTGC AAGACTCCAT CTCAAA 226

SEQ ID NO:629

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00697

SEQUENCE DESCRIPTION:

GATCTGTAA TTTCTATCT AATAAATGCC TTNAATTGTN CTCATAATNA AGAATAAGTA 60
GGTATCCCTC CATGCCCTTC TGTAAATAAT ATCTGGAAAA AACATTAAAC AATAGGCANA 120
TATATGTNAT GTGCATTCT AGAAATACAT AACACATATA TATGTCTGTA TCTTATATTC 180
AATTGCAAGT ATATAATAA TAAACCTGCT TCCAAACAAC AATAAA 226

SEQ ID NO:630

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00698

SEQUENCE DESCRIPTION:

GATCAGAGTA ATTCTTTTGT ACATTGAAAT NAGGGGCTTG GTTTAAAAA AGACCTTTCC 60
CTCTCCCTGC CCCTAGAACA ACCAGTATTA GAAGGTGCCA CCATTGGTGC TGCCTTCTNT 120
TCCCACAGCC TGTAAGTCAG TGTTTTGTAC TTCACTGAAT TGTGATGGNT AGAAACTTCG 180
TGGGTAGNNN NTGGGAATCA TCCNGTTAAA CAANACGGGN TTAAAA 226

SEQ ID NO:631

SEQUENCE LENGTH:222

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00699

SEQUENCE DESCRIPTION:

GATCCTTGGT GACTGAGCA GTTCTTTTGG GGCTTTTTCT TTCTGGGAAG CGGGAGGGAA 60
AGGAGCAAGG TGTCATCCTG CTCTTCATT GTATTTTGGT CCCAAAATGT AAATACAATT 120
TNTATGTGA CTTTTTTGTG GTAAGTACCG AGATGAATAT TTAAATTAGA TAAGTTATAT 180
GAAAAGGAAA ATTCCATGTC TAAATAAAAA ACAAACTCCA AA 222

SEQ ID NO:632

SEQUENCE LENGTH:222

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00700

SEQUENCE DESCRIPTION:

GATCTTCTGG ACAAACTTCT GCGATACGAC CATCAACAGA GACTGACTGC CAAANAGGCC 60
ATGGAGCACC CATACTTCTA CCCTGTGGTG AAGGAGCAGT CCCAGCCTTG TGCAGACAAT 120
GCTGTGCTTT CCAGTGGTCT CACGGCAGCA CGATGAAGAC TGAAAGCGA CGGGTAATGC 180
GGCATTGATG CTTNCCAATA AAACCAACCA ACCAAACACA AA 222

SEQ ID NO:633

SEQUENCE LENGTH:221

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00701

SEQUENCE DESCRIPTION:

GATCCACCCA GTTCTTTAGG CAACCACTGA TAGCATTTTC TTAAGTATTC TTCCAGATAT 60
CGTCTATGCA TATGTAAAAG TATCTGNCTT TCTCCNTTTA AAAACACAAT TGGNAATATA 120
TCATACTNGC TGGTTTGAC CTNGCTTTT TTGCTTAATA TATCTAGTTT ATAATGNCCN 180
AATGNGCAAA TTTTNGCATC NGCCCTAAAT ATCTACTGGN N 221

SEQ ID NO:634

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00702

SEQUENCE DESCRIPTION:

GATCACTCGT TTAAGTCCTT AGTTGTATGT NATCTCTTCT CTAGCAGGAA TTGGCAAAC 60
TTTTTGTAAG GGGGTAGAAA GTGAAGATTT TAAGGCTTTG CAGGCCATAT ATCCTCTNCT 120
GCAAAATNCTC AGCCCTGCTG TTGTAATGTA AAANCTNCCA CAGACACTAC ATGAACACGA 180
ATGAGTGTGG CTGGTGTTC AATAAACTT TATTACAAA 220

SEQ ID NO:635

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00703

SEQUENCE DESCRIPTION:

GATCATCAAA CCAGTCCACA AGCACAGGGA GATGCGTGGG CTGACATCTG CAGGCCGAAA 60
GAGCCGTGGC CTTGGAAAGG GCCACAAGTT CCACCACACT ATTGGTGGCT CTCGCCGGGC 120
AGCTTGGAGA AGCGCAATA CTCTCCAGCT CCACCGTTAC CGCTAATATA NGTAAAGTTT 180
NGTAAATTC ATACTTAATA AACAATTTAG GACAGTCAAA 220

SEQ ID NO:636

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00704

SEQUENCE DESCRIPTION:

GATCCACATC TCAAAGAAGT GGGGCTTCAC CAAGTTCAAT GCTGATGAAT TTGAAGACAT 60
GGTGGCTGAA AAGCGGCTCA TCCAGATGG CTGTGGGGTC AAGTACATCC CCAGTCGTGG 120
CCCTCTGGAC AAGTGGCGGG CCCTGCACTC ATGAGGGCTT CCAATGTGCT GCCCCCTCT 180
TAATACTCAC CAATAAATTC TACTTCTGT CCACCTAAA 219

SEQ ID NO:637

SEQUENCE LENGTH:215

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00705

SEQUENCE DESCRIPTION:

5 GATCCTCTCT CGACTNGCCA TACATTTCTT TCACAGCATT TACATAGTCC ATGATAGTTT 60
 ACTTGTGGGA TTATTTGGTT AATCTTTGCC TTAAACACCA GGGTTCCTTG GGTGAAGGAG 120
 CTTCTTTATC TNGGTAACAG CATTATTTCA AGCATAACTN GTAATATAGT NATATTACAT 180
 ATATANCATA TATATATATN NCANANCANA TATAN 215

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SEQ ID NO:638

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS00706

SEQUENCE DESCRIPTION:

20 GATCTGGTTT CTTAGCAAAT TTCCCAGTAG GATGTCATGT AAGTNCCTTC CCCCTCTTAG 60
 AGATTGAAGG CTGTAAGAGT CCAGATGGTG GAGCCAGGCT GTCTGGGTTC AAATGCCATC 120
 TTTGACACTT GCAAGCTAAA TNACATTACT CAAATTAATC GTTCTGCACT TCAGCTTCCTN 180
 TGTCTATCAA ATAAAAAGAA TAGTACCNGC CAAA 214

SEQ ID NO:639

SEQUENCE LENGTH:215

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00707

SEQUENCE DESCRIPTION:

30 GATCATTGTA GATGANCTGA AGCAAGANGT TATCAGTACC AGCAGCAAGG CAGAACCACC 60
 CCAAGTCACC TCCTTGGCCT GGNCTGCTGA TGGCCAGACT CTGTTTGCTG GCTACACGGA 120
 CAACCTGGTG CGAGTGTGGC AGGTGACCAT TGGCACACGC TAGACGTTTA TGGCAGNGCT 180
 TTACATGTGG GGAATAACN TGGCTTTTCT GTAAA 215

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SEQ ID NO:640

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS00708

SEQUENCE DESCRIPTION:

45 GATCAAACCA AGGCCCAGGC TGCAGCCCA GCTTCAGTTC CAGCTCAGGC TCCCAAACGT 60
 ACCCAGGCCC CTACAAAGGC TTCAGAGTAG ATATCTCTGC CAACATGAGG ACAGAAGGAC 120
 TGGTGCGACC CCCCACCCCC GCCCCTGGGC TACCATCTGC ATGGGGCTGG GGTCTCCTG 180
 TGCTATTGTG ACAAATAAAC CTGAGGCAGG ATTTGTAAA 220

SEQ ID NO:641

SEQUENCE LENGTH:210

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS00710

SEQUENCE DESCRIPTION:

5 GATCGAGAAC CACATCCTCA AGCTCTTCGA GAGCAACCTG GTGCCCCTA AACCTGAGT 60
 GAAGGCCGCC TGCCGGGGAC TCAGACACTC AGGGAACAAA ATGGTCAGCC AGAGCTGGGG 120
 AAACCCAGAA CTGACTTCAA AGGCAGCTTC TGGACAGGTG GTGGGAGGGG ACCCTTCCCA 180
 AGAGGAACCA ATAAACCTTC TGTGCAGAAA 210

10 SEQ ID NO:642

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00711

15 SEQUENCE DESCRIPTION:

20 GATCTGGTTT TATTCTGTA ATTCAGCCAC CTGATTTTGT GAGGGGGGGG AATAATATGT 60
 GGTTTTGTG CAAACATGTT TCTCAGTGTG TTGTNATTTT GGAAAAATG AGGGGAGGGA 120
 GTTTGGCAAG AATGGAGAAA ATGAATGAAG AAGGCCTAAT CTCTCTCTTT TTCAGTNAAT 180
 AAATGGAACA CCATTCTGG ATTCTAAA 208

SEQ ID NO:643

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS00712

SEQUENCE DESCRIPTION:

30 GATCTGTACA TTGTAAAACA CCATTCAAGT GTCAGAATCA TTATTTTCCA CCACTTATCA 60
 TGGTGCTTGA CAAGTCTTCC CAATAAATAC TGAATGAACA AATGAATGGC AGAAACATTA 120
 AAATGAACAC TATGGGGAAA GGGGAAGAGA GGCAGAATCA GAAATTATCC NGAATAAATA 180
 TTTATNCCAT TTGTCATCCN NCNAAA 206

35 SEQ ID NO:644

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00713

40 SEQUENCE DESCRIPTION:

45 GATCTATGTG GTGAAAATGC ACAGGAGCTT GTAGACTGC GGGGGAAAGA GAGAGCTCCT 60
 TTCGCCATGT TTTACCAGTN TGCTGTTATA ACCTCTTAGG TTGTATCCTT TAATTTCCAG 120
 CCTTTTAGGT TAGTTTCTGT AACAGAACAA GTGAGTCTGG GATGAAGTCC TCAAAGTACT 180
 TCAAAATGGTA ATTTTTTGT TTTTGTAAATA GCTNAACAAA TAAACCNAGG GTTCTATAT 240
 TAAA 244

SEQ ID NO:645

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

50 TOPOLOGY:linear

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CLONE:HUMGS00714

SEQUENCE DESCRIPTION:

5 GATCTATGAA TGANAGGAGG GCAGACCACA TTGCTTTTNA CATCCATTTC CCCTCCTTCC 60
 CATGGGCAGA GGACCAGGCT GTAGGAAATC TAGTTATTTA CAGGAACTTC ATCATAATTT 120
 GGAGGGAAGC TCTTGGAGCT GTGAGTTCTC CCTGTACAGT GTTACCATCC CCGACCATCT 180
 GATTAAATG CTTCTCCCA GCATAGGATT CATTGAGTTG GTTACTTCAA A 231

SEQ ID NO:646

10 SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00715

15 SEQUENCE DESCRIPTION:

GATCTACATC TTTTCTAAA GAAAAGTGGG GCTTGCCTCC AGTTCAATTC ACAAGAGCAT 60
 TTTCCCTCCC ATGCCACCT TTTCTGTGG CTGTCGCTAG GAAGGATGCA GAGGCTGTGT 120
 GGTITACCAA ATGCTTAAC TTAGCAGTGA ATGACAACTG TCAAACACAT GTTGAGGGGA 180
 AATTTTACT GATTCACAAA 200

SEQ ID NO:647

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

25 TOPOLOGY:linear

CLONE:HUMGS00716

SEQUENCE DESCRIPTION:

30 GATCTGCCGC AAGTGCTATG CTCGCCTTCA CCCTCGTGCT GTCAACTGCC GCAAGAAGNA 60
 GTTGGGTAC ACCAACAACC TGCCTCCCA GAAGNNGGTC AAATAAGGTT GTTCTTTCCT 120
 TGAAGGGCAG CCTCTGCCC AGGCCCCGTG GCCCTGGAGC NTCAATAAAG TGTCCCTTTN 180
 ATTGACTGGG GNNGNANAAA 200

SEQ ID NO:648

35 SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00717

SEQUENCE DESCRIPTION:

40 GATCCAGAAG GGGTTTGGTC TGGGACTTCC TTGCTCTCCC TCTTCTCAAG TGCCTTAATA 60
 GTAGGGTAAG TTGTTAAGAG TGGGAGAGAG CAGGCTGGCA GCTCTCCAGT CAGGAGGCAT 120
 AGTTTTTACT GAACAATCAA AGCACTTGA CTCTTGCTCT TTCTACTCTG AACTAATAAA 180
 TCTGTTGCCA AGCTGGAAA 199

45 SEQ ID NO:649

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

50 CLONE:HUMGS00718

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SEQUENCE DESCRIPTION:

GATCTTTTGT CCTCACTGCT TTCTAATGGG GAGGGCTGAG GGTTCCTGT CCCACAGCA 60
GGTATGTTGG GNTCTGCCCC AGCCCCACAC TTGCTCTGAA AACCAAGTGN NAGAGCCCCT 120
TCCCCTTGTT TTTATTTTAC TGTTATAATA ATTATTAAC TCCCTGTAAT AGAAATAAAG 180
TTTGTACTTG GAGTTCAGCT CAGAAA 206

SEQ ID NO:650

SEQUENCE LENGTH:201

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00719

SEQUENCE DESCRIPTION:

GATCCTCGTT TTCTNGGTTT TGGTGATGTT GGAGGAGTAC CCCCCAGCCC ACCGCCCCGA 60
TTCCTTTTGG CTTCTGGTTT GGAGCTCCGG ACCAGGACCT TCGTCCTGTT CAGTTTTTAA 120
ATAATNATTT AGCAGTGTA CTTTTAAACC TGCCTGACAT CTACANNNG CCCAATAAAG 180
AAAGAGGAAG CCACGGTCAA A 201

SEQ ID NO:651

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00720

SEQUENCE DESCRIPTION:

GATCTGTTAT CTAGCTGAGT TCATTTTCATC TCTCCCTTTT TTATATCAAG TTTGAATTG 60
GGATAATTTT NCTATATTAG GTACAATTTA TCTAACTGA ATTGAGAAAA AATTACAGTA 120
TTATTCTCA AAATAACATC AATCTATTTT NGTAAACCTG TTCATACTAT TAAATTTTGC 180
CCTAAAAGAC CTCTTAA 198

SEQ ID NO:652

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00721

SEQUENCE DESCRIPTION:

GATCTTAAAC ATCGGTCAGA TGAGTCATAC ATTGGGTTAT TTTTATATA CATGTATACA 60
CAAAATATTT CAAATTGAAA GCAACATCTT AATGGATTCA AAATATTAC AAGCTGTTGT 120
CTAAACAGG TGAGAAAAA ATTTATAACT GTAAANCAA ATGCACATAT TGATATTTAA 180
AATGCGTAAT TAAGAAA 197

SEQ ID NO:653

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00722

SEQUENCE DESCRIPTION:

5 GATCTGGACT GTCCTGGCAT CGAACTCTCC CTCTGTGTGT AATTGGAGGA GACCACAAGC 60
 TGTGTTTTG GGTGACTGAA GTATAAAGTG TTNCTGTAC CTTAGATTCA CAAACTTTGT 120
 ATTTNAGTA CATATTTNNA AGAATTTCTA TAGTACATAT NTNNAAGAAT TTNATATCA 180
 AATATACCGT ATACTNN 197

10 SEQ ID NO:654
 SEQUENCE LENGTH:201
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00723
 SEQUENCE DESCRIPTION:
 15 GATCACC GCCAGTAAAA AAGGCTCCAG CCCAGAAGGT TCCTGCCCAG AAAGCCACAG 60
 GCCAGAAAGC AGCGCCTGCT CCAAAAGCTC AGAAGGGTCA AAAAGCTCCA GCCCAGGNNN 120
 GCACCTGCTC CAAAGGCATC TGGCAAGAAA GCATAAGTGG CAATCATAAA AAGTAATAAA 180
 GGTTCCTTTT GACCTGTAA A 201

20 SEQ ID NO:655
 SEQUENCE LENGTH:199
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00725
 25 SEQUENCE DESCRIPTION:
 GATCTGCAGT TTAAGTTGCC ATGCTGCTAG GAAATTGTCC TTTNCTTTC TAGCTGTAA 60
 CCTACTTCTT GAAAAAAGTA GTAGCTCTCT GTAGCATTAT GGAGTTTCAG TGGAACCAAA 120
 TTTTGGCCAT TAAAAACTGG CATTATACTG AACTATACAT TGAGAAATCA ATCAAAATAA 180
 30 AATTTTNNAC TTTCACAAA 199

35 SEQ ID NO:656
 SEQUENCE LENGTH:196
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00726
 SEQUENCE DESCRIPTION:
 40 GATCTGGTTT CTAGCAAATT CCCAGTAGGA TGTCATGTAA GTCCTTCCCC CTCTTAGAGA 60
 TTGAAGNTGT AAGAGCCAGA TGGTGGAGCA GGCTGTCTGG GTTCAAATGC ATCTTTGCAC 120
 TTNAAGCTAA ATGACATACT CAAATTAATC GTCTGACTCA GTTCCTTGCT ATCAAAATAA 180
 AAGATAGACC TGCAAA 196

45 SEQ ID NO:657
 SEQUENCE LENGTH:201
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00727
 50 SEQUENCE DESCRIPTION:
 GATCTGCCTG CCTCAGCCTC TCAAAGTGTT GAGATTACAG GCGTGAGCAN CCGCTCCCTG 60

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CCCAACACAT ATACCATCTG AAAATGTTAG AATTCTGAGT TGTGATTTTA TTGACTTGTT 120
 GCTTGCTTTT CCTNAGGCTT TGTAACCTGT AATATGTAA AGTGACTAT CTAATAAAC 180
 TGAATACTTT GGTATCTTAA A 201

SEQ ID NO:658

SEQUENCE LENGTH:197

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00728

SEQUENCE DESCRIPTION:

GATCCTCCAT TGGAGTGGCC CAAATCTTTC CATCTAGGGC AAGTCCTGAA AGGCCCAAGG 60
 CCCCTCCCC AGTCTGGCCT TGGCCNCCAG CCTGGAGAAG GGCTAACATC AGCTCATTGT 120
 CAAGGCCACC CCCACCCAG AACAGAACCG TGTCTCTGAT AAAGGCTNTT GAAGTGAATA 180
 AAGTTTAAA ANCTAAA 197

SEQ ID NO:659

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00729

SEQUENCE DESCRIPTION:

GATCGTNTT GTTTGTTTT TAAAGAAAGG TGAGATTGGC TTGGTTCTTC ATGAGCACAT 60
 TTNATATAGC TCTTTCCTG TTTTNCCTG CTCATTTCTG TTTGGGGAAG AAATCTGTAC 120
 TGTATTGGGA TTGTAAAGAA CATCTCTGCA CTCAGACAGT TTACAGAAAT AAATGTTTTT 180
 TTTGTTTNC AGAAA 195

SEQ ID NO:660

SEQUENCE LENGTH:196

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00730

SEQUENCE DESCRIPTION:

GATCTCAAAC TCCAGGCTCA GAACTGTGAA GACTGTTTCC AGCCTGGCTG TGAGCCAAGA 60
 CCTGGTTCCT GGTGGACCCT GAGGACAAAG TGTGATAAAA CCTCTGGCTC AGACTTGCTC 120
 TACTGAAGGC TTCTTGGTTA TAAGATGCAT AAAGTCACTG GGGCTAGCTA AACAATAAAG 180
 AGTTTATTGT GAGAAA 196

SEQ ID NO:661

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00731

SEQUENCE DESCRIPTION:

GATCTAATGT ACTGTAACTT TATCAGTGAA AGGTAAATC TCAAATAACA AGTACAAACA 60
 TTGAACAATT ACCTATAAAG ATTTNTAAAA GTAAAAATTT TCCAATAGAT TTCATTCTTG 120

TCATTTTGTA AGACGACCCT GCAGTCCACC NGTTTGTAAC TTTTSTAATA AAATAGACAT 180
CTGTATTACT GAAA 194

5 SEQ ID NO:662
SEQUENCE LENGTH:246
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
10 CLONE:HUMGS00732
SEQUENCE DESCRIPTION:
GATCAAGAAA ATAAGGACAA CGTGAAGTTT AAAGTTCGAT GCAGCAGATA CCTTTACACC 60
CTGGTCATCA CTGACAAAGA GAAGGCAGAG AAAGTGAAGC AGTCCCTGCC CCCCAGTTTG 120
GCAGTGAAGG AACTNAATAA ACCAGACACA CACAGAACAG GCGATTATTT ATTTGTTTTT 180
15 AATTATTTT GTCATATTTT TGTAACCGG CAGAAATGCA ATAAACCTA TATTCAACA 240
GTGAAA 246

20 SEQ ID NO:663
SEQUENCE LENGTH:192
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00733
SEQUENCE DESCRIPTION:
25 GATCATATTT TATACATGTG TAATAGATAA AAATAAACCA GATTGCAAAT CCTTTTTTAA 60
AATCCTAAAC CATGTACCAA GTTTTGGTC CAAATTATGT AGGATAAGTT AAACCTAAAT 120
TGCATTCTAT TAACCAATAT GAGTGTATTT CTGTAAGCAT AGTTATGTG AAATAAAGTT 180
TTAAAAACCA AA 192

30 SEQ ID NO:664
SEQUENCE LENGTH:191
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
35 CLONE:HUMGS00734
SEQUENCE DESCRIPTION:
GATCTTCACA CTAATGATGA GTGTGTGGCT ACATACAAAG GAGTTCCTTT TGAGGTGAAA 60
GGGAAGGGAG TATGTAAGGG CTCAAACCAT GAGCAACAAG TGGAATCAAA TAAATGCTT 120
40 CCACNACCAA AAGACATTAG AGAAAACCTT AAAAGTAATA AAGNGAAATA TATTNTCAC 180
TTATACCTAA A 191

45 SEQ ID NO:665
SEQUENCE LENGTH:188
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00735
SEQUENCE DESCRIPTION:
50 GATCTGAATC TNCCGGGGCC CCAGCCCACT CCACCCTGCC AGCAGCTTCC AGCCAGTCCC 60
CACAGCCTCA TCAGCTCTCT TCACCGTTTT TTGATACTAT CTTCCCCCAC CCCCAGCTAC 120

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CCATAGGGGC TGCAGAGTTA TAAGCCCCAA ACAGGTCATG CTCCAATAAA AATGATTCTA 180
CCTACAAA 188

5 SEQ ID NO:666
SEQUENCE LENGTH:186
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
10 CLONE:HUMGS00736
SEQUENCE DESCRIPTION:
GATCTNAAAC CCAAGGGTCT GAGGCCAGGG CCGACTGCCG TAAGATGGGT GCTGAGAAGT 60
GAGTCAGGGC AGGGCAGCTG GTATCGAGGT GCCCATGGN AGTAAGGGGA CGNCTTCCGG 120
GCGGATGCAG GGCTGGGGTC ATCTGTATCT AAAGCCCCTC GGAATAAAGC GCGTTGACCG 180
15 NCGAAA 186

SEQ ID NO:667
SEQUENCE LENGTH:184
20 SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00737
SEQUENCE DESCRIPTION:
GATCTGTAAA TAATCATTGC CAGTNTGACT TTTGTTCAAC AAAAGGATTG TACTGTATTA 60
25 AGAACCAGATG AAAAAAATTN TCCTGTAACA TTTTTTAAAG AAAACTTTGT TTGTTTAAAG 120
AAAAAGTATT GTATAANTNA TAATTTTAAT TTAAATAAAC CTAAATGCT TTGTGCTAAG 180
GAAA 184

30 SEQ ID NO:668
SEQUENCE LENGTH:180
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00738
35 SEQUENCE DESCRIPTION:
GATCCCAGAA AAGTTCTAAT TTTCAATTAGC AATTAATAAA GCTATACATG CAGAAATGAA 60
TACAACAGAA CACTGCTCTT TTTGATTTA TTTGTACTTT TTGGCCTGGG ATATGGGTTT 120
TAAATGGACA TTGTCTGTAC CAGCTTCATT AAAATAAACA ATATTTGTAA AAATCATAAA 180

40 SEQ ID NO:669
SEQUENCE LENGTH:179
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
45 CLONE:HUMGS00739
SEQUENCE DESCRIPTION:
GATCTATCCA AGGTTTTGAC ATGTATCGAG AGTTTATTCC TTTTATTGTC TGAATAGTAT 60
TAATATTCTA TAGTATGGAT GTAACATAGT GTGTTTAAAC ATTGCCTGT TGAAGGACAC 120
50 TTGGGTTGTT TCCAGTTTCA GGTTCTTACA AATAAAGCTA CTCTGTGTGT TCATGTAAA 179

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10
SEQ ID NO:670
SEQUENCE LENGTH:179
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00740
SEQUENCE DESCRIPTION:
GATCAAATGC CAGTGTCAAT TTGTACTTAA GTTCCAAAGT AGGAACATTN TATACTTTTT 60
NCTGTATTGT AATAGGTAGT TTTGTATGAA ATCTTTTCTC CTCTCCCGTT GTACCGCATT 120
CTTTCAGCA TTGTGCTTTT TCCCTGGNCT TATTTGAAAA TTTTACTGTT TTATACAAA 179

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20
SEQ ID NO:671
SEQUENCE LENGTH:177
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00741
SEQUENCE DESCRIPTION:
GATCCAAGAA ACCAGGGCCA TGACCAGGTC CACTGTGGAG CAGCCATCTA TCTACCTGAC 60
TCCTGAGCCA GGCTGCCGTG GTGTCAATTC TGTCATCCGT GCTCTGTTTC CTATTGGAGT 120
TTCTTCTCCA CATTATNTTT GTTCCTGGGG AATAAAACT ACCATTGGAC CTAGAAA 177

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30
SEQ ID NO:672
SEQUENCE LENGTH:175
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00742
SEQUENCE DESCRIPTION:
GATCTGCAAG TCCCGGAGAG CAACAGCACA GCTCTGCCTG ACGCTCTCAT TAAATCTAT 60
GCAGCCAAGC TCGGCACTTT GTAGCAGCCG GCCTTGCGAA GCCTCCTCAG CTCGGGGGGC 120
CGGGGACCCA GTGAGCCGAG AGCCCTCTGG NCTCCACTTA TGCATATGCA CCAAA 175

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45
SEQ ID NO:673
SEQUENCE LENGTH:180
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00743
SEQUENCE DESCRIPTION:
GATCCGGAGA ATAGGGCANN AATATGTGCC GCCAGTGTTT CCGTCAGTAC GCGAAGGATA 60
TCGGTTTCAT TAAGTTGGAC TAAATGCTCT TCCTTCAGAG GATTATCCGG GGCATCTACT 120
CAATGAAAAA CCATGATAAT TCTTTGTATA TAAATAAAC ATTTGAAAAA ACCCTTCAAA 180

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SEQ ID NO:674
SEQUENCE LENGTH:176
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00745

SEQUENCE DESCRIPTION:

GATCTATTCA GATGGTTCTG ATGAAGTGAA ACGNGCCATG AACAAATCCT TTATC>NNGT 60
 CCGGTGGTAC AGTTTTGAGT ACCAACTGGT CTGATGTAGG TAAAAGGAAA GTTGAAATCA 120
 ATCCTCCTGA TGATATGGNN NGGAAAAAGT ACTAAATAAA TTAATTGCT CTCAAA 176

SEQ ID NO:675

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00746

SEQUENCE DESCRIPTION:

GATCAAAACC AGTTTGATT GGAATCTTC CCCTTTCCAA ATGAAATAGA GATGCAGTAC 60
 TTAACTTTCC TTGGTGTG TAGATATTGC CTTGTGTATT CCACTTAAAA CCGTAATCTA 120
 GTTGTAATAA GAGATGGTGA CGCATGTAAA TAAAGCATCA GTGACACTCT AAA 173

SEQ ID NO:676

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00747

SEQUENCE DESCRIPTION:

GATCCTAGCA TCCCTTTTCA CATGGTTTCT CCATGTATAT AACAGAATCA AGAAACAAAT 60
 TTNAATTAAA CAATCTGTAA CAGAATCAAG AAACAAATAC ATTTTAATTA AACAATCTAT 120
 ATGGAACAAA CATTCCCAA TNCTAAGAAT AANTNTTCNT NTAAGTTTTC AAA 173

SEQ ID NO:677

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00748

SEQUENCE DESCRIPTION:

GATCCAAATA ATTTATTAAA TGACTGGTCT CAGAACTGA ACTCATTAAT GTCTCTGGTT 60
 AACAAACTA CGCATCTCAT AGCCAAAGAG GAGATGATAC ATAATCTACA ATAAGGGTCT 120
 TAGTGCTTTA GAAAAAAGTT AAAATTGGAA GTCATTAAAA AAAGACTGTT ATAATGGTGA 180
 AA 182

SEQ ID NO:678

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00749

SEQUENCE DESCRIPTION:

GATCTTATGA GAAGAGGAAG GAGAGANGTC TCTNCCTATG CTCACACACA AAGGAAAGTC 60
 CACATGAGGA CACAAGGAGA AGCCAAGAGN GCCCTTACCA GGANTTAAAC CTGCTAATCC 120
 CTATTTTAAT TAGAACAGTG AGAAANTAAA TATCTGTATT TAAGCCTCAC AAA 173

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SEQ ID NO:679
 SEQUENCE LENGTH:173
 SEQUENCE TYPE:nucleic acid
 5 TOPOLOGY:linear
 CLONE:HUMGS00750
 SEQUENCE DESCRIPTION:
 GATCCAGAGA AAGCCAAAGC TCTTAGTAAA CACTTGCCAT CGTCAGTNTN ATGTCTCTAA 60
 10 AAGTAGATGT TGAGGCTCTT NAAAATNCTC CTGGTGCTAC ATACATTCGG AAGAAGGGTG 120
 GAAAAGTTAC TGGAGATAGT CAACCAAAGG AACAAGGACA GGNAGATTG AAA 173

SEQ ID NO:680
 SEQUENCE LENGTH:172
 15 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00751
 SEQUENCE DESCRIPTION:
 GATCCAATCC ATTCAGCAGT CCATTGAAAG GCTCTTAGTC TAAACCTGTG GCCTCTGCCA 60
 20 CGTNCTCTCC TGCCAGCTTC CCCCTGAGG TTGTGTATCA TATTATCTGT GTTAGCATGT 120
 AGTATTTTCA GCTACTCTCT ATTGTTATAA AATGTAGTAC TAAATCTGGA AA 172

SEQ ID NO:681
 25 SEQUENCE LENGTH:170
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00752
 SEQUENCE DESCRIPTION:
 30 GATCAAATTT AAACCTCATT TTGGGGGGTA TTTTGGTACT GTAATGGGGT CATCAAATNA 60
 TTAATCTGAA AANAGCAACC CAGAATGTAA AAAAGAAAAA ATTGGGGGGA AAAAGACCAG 120
 GTCTACAGTG ATAGAGCAAA GCATCAAAGA ATCTTTAAGG GAGGTTTAAA 170

35 SEQ ID NO:682
 SEQUENCE LENGTH:239
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 40 CLONE:HUMGS00753
 SEQUENCE DESCRIPTION:
 GATCGGAACA GTCCTTACT CTGAGGAAGT TGATTCTTAT TTGATGGTGG TATTGTGACC 60
 ACTGAATTCA CTCCAGTCAA CAGATTCAGA ATGAGAATGG ACGTTTGGTT TTTTTTGGT 120
 TTTGTTTTTG TTTTTCCTT TATAAGGTTG TCTGTTTTTT TTTTNAAAA AATNGCANCA 180
 45 GTNCATGGCC CCCATCATT ANANGNGAGG ANTNCANCAG AAAATAAAAT ATNCACTCN 239

SEQ ID NO:683
 SEQUENCE LENGTH:170
 50 SEQUENCE TYPE:nucleic acid

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EP 0 679 716 A1

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 TOPOLOGY:linear
 CLONE:HUMGS00754
 SEQUENCE DESCRIPTION:
 GATCCAGACA GCCATCAGGG AAAGCTTGTN TTTAACCGAA CTGTCACACT GAAGGAAGAC 60
 CCAGGAAAGG TGTGAGCTGG AAGCACTGAA CCTACCTCAT CCTCCTGGAG GGTGTGGCTA 120
 CCCTCGCCAC CCCAAATTCC ATGTCAATAA AGAACAGCTA AATTCTCAA 170

10
 SEQ ID NO:684
 SEQUENCE LENGTH:168
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00755

15
 SEQUENCE DESCRIPTION:
 GATCTTTCCA TTGGAATATA CTGGAAGTGA AGAGGTTTTG TTGCTTGATC AGTGTCAGAT 60
 GAGGAACACC ACTATCTTAA TTTTGTGATA CACTGCATTT GCTGGTGCTA TTTTNATACA 120
 GTGAAGCAAC AGCTTTGCAG CAAAATAATA AAATACTTCT ANGTAAA 168

20
 SEQ ID NO:685
 SEQUENCE LENGTH:169
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

25
 CLONE:HUMGS00757
 SEQUENCE DESCRIPTION:
 GATCCATCGT NATGTCTTAT TTAAGGGGAA CGTGTGGNCT ATTTAGGCTT TATGGCCCTG 60
 AAGTAGGAAC CAGATGTCCG ATACAGTTCA CTTTAGCTAC CCCCAGTNT TATGGGCCCG 120
 30 GAGCGAGGAG AGTAGCACTT TTGTNCGGGA TATTGATTTC ACGGAGAAA 169

35
 SEQ ID NO:686
 SEQUENCE LENGTH:171
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00758

40
 SEQUENCE DESCRIPTION:
 GATCTGCTAC TAAACAGAGT TCAAAAACCT TCCAGAGTAA TTAATATGTA AAGCCANGTA 60
 ACTAACAAAN GATTGCTTT AGAGATAATT ATTTGGAATT TTTATAGCTN ACTTCACAAT 120
 GTGCCCAGGT CAGCTGTATA AAATAAATAC TGCATTNTNG TTTCTTTCAA A 171

45
 SEQ ID NO:687
 SEQUENCE LENGTH:167
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00759

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 SEQUENCE DESCRIPTION:
 GATCCTGACA CTAAGGAAAT GCTGAAGCTT TTGGACTTCG GCAGTCTGTC CAACCTTCAG 60
 GTCACCTAGC CTACAGTTGG GATGAATTTT AAAACGCCTC GGGGACCTGT TTGAATTTT 120

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NCTGTAGTGC TGTATTATTT TCAATAAATC TGGGACAACA GCAGAAA 167

5 SEQ ID NO:688
SEQUENCE LENGTH:166
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00760
10 SEQUENCE DESCRIPTION:
GATCAGCGAT GAAGAGGAAG AAGATGATGA TTGAAGTATG AAATATGAAA ACATTTTATA 60
TATTNATTG TACAGTTATA AATATGTAAA CATGAGTTAT TTTGATTGAA ATGAATCGAT 120
TTGCTTTTGT GTAATTTTAA TTGTAATAAA ACANTTTAAA AGCAAAA 166

15 SEQ ID NO:689
SEQUENCE LENGTH:175
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
20 CLONE:HUMGS00761
SEQUENCE DESCRIPTION:
GATCTATTG GTCTTTCTCA TGTCCTGTAC CCCAGGGAGC GGGTGCTTGT 60
ACTGTGTGAA TCCAGTGTTT ACATTACAC TTAATGACTT CCTTGGCACC AATCATGTAT 120
25 TTCACCGTTT GCACTTNTTG TATTTCAATA AAAATGTTGA TGCAAAACTG CTAAA 175

SEQ ID NO:690
SEQUENCE LENGTH:165
SEQUENCE TYPE:nucleic acid
30 TOPOLOGY:linear
CLONE:HUMGS00762
SEQUENCE DESCRIPTION:
GATCGACTCT ATCATCCAAC GCTCCGAGGA CAGCCCATGT CCCCACCCCN GNGACCCGGA 60
35 CCCGGCCAGC AGGACCCACT GAGANGGGCT GCCCGGGNCT NCTCAGCTGC CCACCCCAC 120
ACTGTCCAGC ATCTGGCACA ATAAACATNC TCTGTTTTGT AGAAA 165

SEQ ID NO:691
SEQUENCE LENGTH:164
40 SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00763
SEQUENCE DESCRIPTION:
GATCAAGAAA TAAACATAAA CATCTCAGAA TGCTCCTTCA TTACCAGAGT CACTACCTGA 60
45 TTATGTCTTA ATGGGTTACA TAATGACAGA GGGTATCTCA TATATGTNCT TTTCCAAACA 120
TAAAATAACT TTTGTTTTG TTTGATTGAA AAAAAATTTA GAAA 164

50 SEQ ID NO:692
SEQUENCE LENGTH:171
SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS00764

SEQUENCE DESCRIPTION:

5 GATCCAGATT CTCACCTAAT GGGGTTTATA TGGACTTTCT TCTCATAAAT GGCCTGCCGT 60
CTCCCTTCCT TTGAAGAGGA TATGGGGATT CTGCTCTCTT TTCTTATTTA CATGTAAATA 120
ATACATTGTT CTAAGTCTTT TNCATTAATA ATTTAAACT TTTCCCATAA A 171

SEQ ID NO:693

10 SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00765

15 SEQUENCE DESCRIPTION:

GATCGACTCT ATCATCCAAC GCTCCGAGGA CAACCCNTGT CCCCACCCCC GGGACCCGGA 60
CCCGGCCAGC AGGACCCACT GAGAAGGGCT GCCCGGNTCA CCTCAGGGGG NCACANTTTA 120
CACTCTCCAG CATCTGGCAC AATAACATN CTCTGTTTTG TAAA 164

20 SEQ ID NO:694

SEQUENCE LENGTH:168

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25 CLONE:HUMGS00766

SEQUENCE DESCRIPTION:

30 GATCTAATGG TCTAAAACT GGAGTTTCCG GACACAAGCT CTCCTTTNC CTGCAACCAT 60
CCATGCAAGA TGTNACTTGC TCCTCTNTGC TTTCTGCCAT GATTGTAAGG CCTCCCCAGC 120
TACATGGAAC TNTAACTCCA TTAAACCTCT TTNTTTTGTA AATTGAAA 168

SEQ ID NO:695

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS00768

SEQUENCE DESCRIPTION:

40 GATCCGCCCA CCTCAGCCTC CTAAGTGCT GGGATTACAG CTGTGAGCCA CCCTGCCCGG 60
CCACTTTTGT ATGATTCTTA ATGTATTTGT AATTACCTA ACAAAATTGCC TAATCTGCTA 120
TGTTAATGTA TTTATGAATT AAAATAAATA CGACTGCAAA 160

SEQ ID NO:696

SEQUENCE LENGTH:161

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00769

SEQUENCE DESCRIPTION:

50 GATCCGTAGC GGCATGTTCT GGCTGCGCTT CTAGGCGGGA AGCCTATGTA AGCAAGAGGG 60
CAGGGCCCGG GTTTGTGGTC CCCCCCCAC CACAAACACA GCACTTCGGC TCCTCTAACC 120

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TGTGCCACAG GTGACCACCA ATAAATCCT CTGCTGAGAA A 161

5 SEQ ID NO:697
 SEQUENCE LENGTH:159
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00770
 10 SEQUENCE DESCRIPTION:
 GATCTCCCTG CCCCCACCCC AGTTCCCCAA CCCACTCCCT TCCAACAACA ACCAGCTCCA 60
 ACTGACTCTG GTCTTGGGAG GTGAGGCTTC CCAACCACGG AAGACTACTT TAAATGAAAA 120
 AANGAAATTG AATAATAAAA TCAGGAGTCA AAATTCAAA 159

15 SEQ ID NO:698
 SEQUENCE LENGTH:159
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 20 CLONE:HUMGS00771
 SEQUENCE DESCRIPTION:
 GATCTTTTNN TTTTTTTTAA GTCTCACAAG ACATGGGGCA TCTCCACAAA TTAAAGTTCC 60
 TGTCCATTG GAAATTTGTT TCTATGTGTA CAGTTTGTC GAGAAAAACA AAGTTTTTGT 120
 25 ATGANTACAG AATGTGATTT ACGCAAGATT TGACAGAAA 159

SEQ ID NO:699
 SEQUENCE LENGTH:161
 SEQUENCE TYPE:nucleic acid
 30 TOPOLOGY:linear
 CLONE:HUMGS00772
 SEQUENCE DESCRIPTION:
 GATCTACCTA TCTCAGGAT GGAACCTGG GGAAAAATAA AATTGAGGGG AAGTAAAAAG 60
 35 TATGTAACAC TTCCAGTTGT GAGCCAAGAT TGTAACCAGA GAGCAGCCAG GAGCTTCCTG 120
 TCAGTAACCA TTTTTTCAAT AAATACTCTT TCATGTACAA A 161

SEQ ID NO:700
 SEQUENCE LENGTH:157
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00773
 SEQUENCE DESCRIPTION:
 45 GATCCTCTCA CCTCAGATTT CCAAAGTGTT GGATTATAGG TGTAAGCCAC TGAGCCCAGT 60
 TTGAATGCTT TTTTATATAT TTTTGGCCA TTTGTATGTC ATCTTTGGAG AAATGTCTAT 120
 NCAAAATCCNT TGCTCATTAA AATNATTTNC TGATAAA 157

50 SEQ ID NO:701
 SEQUENCE LENGTH:160
 SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS00774

SEQUENCE DESCRIPTION:

GATCTGGCCG TNAGCCGCGA NCCGCTGNGA ACTCCACTCG GGGAACTCCT TTCCAAGCTG 60
ACCTCAGTTT TCTACAAGA ACCCAGTTAG CTGATGTTTT ATTGTAATTG TCTTAATTG 120
CTAAGAACAA GTAATAAGTA AATTTTAA AAGCCTTAAA 160

SEQ ID NO:702

SEQUENCE LENGTH:161

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00775

SEQUENCE DESCRIPTION:

GATCAAAATTG TGCAGTACTT TGTGCATTCT GGATTTTAAA AGTTTTTNAT TATGCATTAT 60
ATCAAATCTA CCACTGTATG AGTGGAAT AAGACTTTAT GTAGTTTNA TATGTTGTAA 120
TATTNCTCCA AATAANTCTC TCCTATAANC CACCAGGAA A 161

SEQ ID NO:703

SEQUENCE LENGTH:154

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00777

SEQUENCE DESCRIPTION:

GATCAGAGCT TATACTTAAT TAAGGTTTTA TACACACCAG TTCCCCAGTA AATNCAAATT 60
TAACAAGAAA ATCAGACATG TCATATGTNC AAAATGCTCA TGGCAAACAA TCATTTTGCA 120
TTCCTGCAAA TAAAATTGTT TTATACTGTA GAAA 154

SEQ ID NO:704

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00778

SEQUENCE DESCRIPTION:

GATCTGTTTG TTCCCTGAGC TTTTAAATA CCCTGTGAAA ATTTTNTTC CTCCCTTGGT 60
CATCATGCAT CTAATTGTGG GGAATGTTT GTCAAACCA CCTGCAAAGC AGCATGGTGT 120
AGTTGAGAAG AATAACAGA GAAGACTGGG AAA 153

SEQ ID NO:705

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00779

SEQUENCE DESCRIPTION:

GATCTTTGGA CAGAAGCAGC TCTTTCCGA ACATTGTGG CGTCTGGNAC GGCCCCACCC 60
NTCCCCCAC ACTCCCTCCC ACGGGGCTCC GGGAGACAGG CCGGCCCTGC ACCTNACCCC 120

ACCGTGACCT CAATAAACGT TGAAACTNCA AA

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SEQ ID NO:706

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00780

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SEQUENCE DESCRIPTION:

GATCTATCCT TTA CTGAAA GCTTTTGAAA AGTGGAAAGG TCATTTTGTT GCATTTCCCC 60

ATTTCTTGTT TTTAAAAGAC CAACAAATCT CAAGCCCTAT AAATGGCTTG TATTGAACTT 120

TTACATTGA ATTAAGATG TTAACATGA AA 152

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SEQ ID NO:707

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS00781

SEQUENCE DESCRIPTION:

GATCTAGTAT GCTCCTGCTC TAATGCATTT ACATTGTTTA GGTAAGTGGT TCCTAATAAA 60

AAGAATTATA AAATACCCTC AAATTAACAA TTCAATNGCA TATAATAGCC TAACTCAGTA 120

AGANTATTAA AACTTACTAT TATNCTTCAA A 151

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SEQ ID NO:708

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS00782

SEQUENCE DESCRIPTION:

GATCTANTCT GTGCTACCTG ATTAACCTAC AGCAGGCTTA CTGANTGGCT TCATTTGAGA 60

TTTAGTTGAT TTCTCCACCA AATNCATGTC ATGTATTCTC AATAGGCTGT ATTCCCAGCA 120

GNCAATAAAT GGAACACCCG TANAANCNA AA 152

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SEQ ID NO:709

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00783

SEQUENCE DESCRIPTION:

GATCCCAGG GTTCTTTGT CTTATTTATG GAGAAAAACC GGTCACCTTG TCCAGCGCAC 60

TGTGAGGCCC CCACTCAGGC CAGCCCTGGC CCCCCTTGG TACTTGGAAC CGAAGTTACA 120

GATTATATTA AAATAATAAT GTACAAA 147

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SEQ ID NO:710

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

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 TOPOLOGY:linear
 CLONE:HUMGS00784
 SEQUENCE DESCRIPTION:
 GATCTTATAA AAGGAAATTC TAGCAGTTTT AGAAATAGGT GGGAAAAACT CAAATATTCC 60
 TCCTATCTGC ACCAAAAAGT TTATTTGTGG TATATAAAAT GAATATTGTT TTATAATAAC 120
 TTGTTAATAA AGTACTTTCT AATAAA 146

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 SEQ ID NO:711
 SEQUENCE LENGTH:145
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00785
 15 SEQUENCE DESCRIPTION:
 GATCAATGAA GTGAGAAATT GTTGAGAAGG ATACAGTTTG TTTTATAGATG TCCTTTGTCC 60
 AATGTGAACA TTTATTCATA TTGTTTGTAT TACCCTCGTG TTAATAACAAG ATGGCAATAA 120
 ATACTATGGG ATTGTTTGTG TTAATAA 145

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 SEQ ID NO:712
 SEQUENCE LENGTH:145
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 25 CLONE:HUMGS00786
 SEQUENCE DESCRIPTION:
 GATCTCCCTT CAGCAACTTA TTTTGCTTTA ATTGCTTTAA ATCTTAAGCA ATATTTTAA 60
 TTCAGTAAAC AAATCTTTT ACAAGGTACA AAATCTTGCA TAAGCTGAAC TAAAATAAAA 120
 NTGAAAAGGA GAGATTAANG GTAAA 145

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 SEQ ID NO:713
 SEQUENCE LENGTH:145
 SEQUENCE TYPE:nucleic acid
 35 TOPOLOGY:linear
 CLONE:HUMGS00787
 SEQUENCE DESCRIPTION:
 GATCTAGAAG CAGAGGAATC CCAGCGCCTT TAAAAGTTG TTATGTGGTT TTCTTTTAAA 60
 AAGCTCCTGT TTTTGAAAAG TAGAATTTAT GGGTACAACG TATGTTCAAT ATTTGTACAT 120
 AAAATAAAAC CATTTAATAA GTAAA 145

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 SEQ ID NO:714
 SEQUENCE LENGTH:154
 45 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00788
 SEQUENCE DESCRIPTION:
 GATCTATGCC TAACAGAGCC CCAGTACAAC TATTTTNCAG AATGGCTGTT ACCCTAGAAT 60
 50 TACTATAGCA CATATTGAGA TATAGTTGTA CTCCCTAGTA GATAGGAACT GACCCCAACA 120

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ATAAACTTTG ATAATAAAGA AAAAAAANCG NAAA

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SEQ ID NO:715

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00789

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SEQUENCE DESCRIPTION:

GATCAACCTT AAAGGAACT GCTATCCGAA CTTGGCTATC TCACAGCAGA GCCAGTTTGA 60

CGAATGGGTA AACCTAAGG ACATGCTGGG TCCAAAGTGA TTTACATAAA TNTATAATGA 120

AAATAAACAT GTATAANATT TAAA 144

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SEQ ID NO:716

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS00790

SEQUENCE DESCRIPTION:

GATCCGTGAT GCCACTTACC TGTGTGTTTG GTAACAACAA ACCAACATCA TGGAGGTCCC 60

TGGATTGAAA AAGGAGCCTC TCCCACTCCT CCTACCACCA AAGTGGTTAG GACNCTATAT 120

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AANTAAAAAC AAGGCTTTTG GAAAAATAAA 149

SEQ ID NO:717

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS00791

SEQUENCE DESCRIPTION:

GATCTGGCTG AACCACTTCC ACAAGGTTAC TGTATACATA GCCTGAGTTT AAAAGGCTGT 60

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GCCCACTTCA AGAATGTCAT TGTTAGACTT TGAAATTCT AACTGCCTAC CTGCATAAAG 120

AAAATAAAAT CGTTTTAAAT CAAGAAA 147

SEQ ID NO:718

SEQUENCE LENGTH:115

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00792

SEQUENCE DESCRIPTION:

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GATCTGGGGC AGCCACCTTG CTACCATGAA GGAAAGGCCA AGACAATCAT CCACAGCTAT 60

TCCCTCCAGC ATCTGGTTCT GTACAAAAAT TAAATGCTTA TTTNTTTAAG TCAAA 115

SEQ ID NO:719

SEQUENCE LENGTH:142

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SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS00793

SEQUENCE DESCRIPTION:

5 GATCGCCACT GTAAAGGTCC TAGAGTTGCC TGTGTGCTC TGGAGATGGA ATTAAACCAA 60
 ATAAAGAGCT TCCACTGGAG GCTTGTATTG ACCTTGTAAC TATATGTAA TCTCNTGTTA 120
 AAATAAAATA TAGCTTGTGA AA 142

SEQ ID NO:720

10 SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00794

SEQUENCE DESCRIPTION:

15 GATCTGTGCC TACNTTTTAC CACCCCTCTG ATTGGAGCTT TTGTNATGCA GCTACCATNN 60
 TTCAAAAAA TTAATAAATA AAAAAAAAAA ATCTGCCACT TATCCAAGTC CACTAGAGGC 120
 CACTGTCTTC AAAGNTTNTN TN 142

20 SEQ ID NO:721

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00795

25 SEQUENCE DESCRIPTION:

GATCCAGGTG ACTCTGAACA TCATTAGAAG CATGCCAGAA CAGACTGGTG AAAAGTAAAC 60
 CTTTTCACCT AAAAAATTC ACCTGCAAAAC CTAAACCTG CAAAATTTTC CTTTAATAAA 120
 ATTTGCTTGT TTTAANAACA NNNGAAA 147

30 SEQ ID NO:722

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS00796

SEQUENCE DESCRIPTION:

40 GATCCAGAGC CTCCTGGGCC TTCTCCGGTG TCCTGTACCA ACTCTTCTAT TTAAGAGAAC 60
 CTCAGATGAT GTACCTGAGC CTCAGGGTTT TGTTTCAGAG GGATATAAAT NATTTAAAAA 120
 TTAAATGAAA ACGTTGCAAA 140

45 SEQ ID NO:723

SEQUENCE LENGTH:150

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00797

SEQUENCE DESCRIPTION:

50 GATCGGCCAC TACCTGGGCG AGTTCTCCAT CACCTACAAG CCCGTAAAGC ATGGCCGGCC 60
 CGGCATCGGG GCCACCCACT CCTCCCGCTT CATCCCTCTC AAGTAATGGC TCAGCTAATA 120
 AAGGCGCACA TGACTCCAAA AAAAAATAAA 150

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SEQ ID NO:724
 SEQUENCE LENGTH:140
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00798
 SEQUENCE DESCRIPTION:
 GATCAGGGTA AGGCAGTCAG GCGGGTGTTC ACCACTGCCT TTCCTTCCTC TGAGCGTGAG 60
 AACACTGAAC CCAGCCACTG CCCCTGGGTC CCTGTCTGG AAATNGTCTA ATAAATCCTT 120
 TNCCCTTCTT GAGCTACAAA 140

SEQ ID NO:725
 SEQUENCE LENGTH:141
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00799
 SEQUENCE DESCRIPTION:
 GATCCGAATC GAGGCCAACG AGGCCCGGGA TGAAGGCCCN GGAGTAGGCG AGCCAGACGA 60
 CAAGGTTGAC CTCAGCTTCG GAGCCACCTC TGGATGAACT GCCCCAGCC CACGNCCNAT 120
 TAAAGACCCG GAAGCCTGAA A 141

SEQ ID NO:726
 SEQUENCE LENGTH:136
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00800
 SEQUENCE DESCRIPTION:
 GATCAGCTTT ACCTATGGTG CTTTGCCTTT AACTAGAGTG TGTGATGGTA GATTATTTCA 60
 NATATGTATG TAAAACTNTT TCCTGAACAA TAAGATGTAT GACCCGGAGC AGAAATAAAT 120
 NCTTTTCCTA ATTAAA 136

SEQ ID NO:727
 SEQUENCE LENGTH:135
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00801
 SEQUENCE DESCRIPTION:
 GATCATGTCA TTCAATTCCA GTCACCTCTT CTGCAATCAT GACCTCTTGA TGTCTCCATG 60
 GTGACCTCCT TGGGGGTCAC TGACCCTGCT TGGTGGGGTC CCCCTTGTA CAATAAAATC 120
 TATTTAAACT TTAAA 135

SEQ ID NO:728
 SEQUENCE LENGTH:135
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

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CLONE:HUMGS00802
SEQUENCE DESCRIPTION:
5 GATCTTAAAC ATTGTTTTGT AGTGTATATT ACTTGTCAT TCCTTTAAGG GGAGCAGCCT 60
GCACTCTTTT GTAGATTACT TTGGGGGAT ATATTNNAG AATNATGAAA CGGAATAAAA 120
TTGTAAAAAA CTAAG 135

SEQ ID NO:729
10 SEQUENCE LENGTH:134
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00803
15 SEQUENCE DESCRIPTION:
GATCATGTTA CCATATCAAG CTGAAAATGT CACCACTATC TGGAGATTTC GACGTGTTTT 60
CCTCTCTGAA TCTGTTATGA ACACGTTGGT TGGCTGGNTT CAGTAGGGGG NTATTNNAGG 120
CCTTTCTTTT TAAA 134

SEQ ID NO:730
20 SEQUENCE LENGTH:134
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
25 CLONE:HUMGS00804
SEQUENCE DESCRIPTION:
GATCTANGTT GCCTACCTTG AATTTTTTTT TAAATATATT TGATGACATA ATTTTGTGT 60
AGTTTATTTA TCTTGATCAT ATGTATTTTG AAATCTTTTA AACCTGAAAA ATAAATAGTC 120
ATTTAATGTT GAAA 134

SEQ ID NO:731
30 SEQUENCE LENGTH:134
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
35 CLONE:HUMGS00805
SEQUENCE DESCRIPTION:
GATCTCACTA AAGGATTCTT ATTTGCTGTC AGTTAAAAAT AAAGCCCTAA ATACATTTTT 60
ATTCTTTCTA CTGAGGGCAT TGTCTGTTTT CTTTGTAAT GCCGTACAAT AAACAAATTA 120
TTTAATAACC TAAA 134

SEQ ID NO:732
45 SEQUENCE LENGTH:137
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00806
SEQUENCE DESCRIPTION:
50 GATCTTGCA CTCTCCATGT TCTCTACAAG AAGCTGTGGT GATTGGCCCT GTGGTCTATC 60
AGGCGAAAAC CACAGATTCT CCTTCTAGTT AGTATAGCGG ACTTAATAAA AGAGGAAAAA 120
ACTCTTGCTT CAGTAAA 137

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SEQ ID NO:733
SEQUENCE LENGTH:134
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00807
SEQUENCE DESCRIPTION:
GATCCTCGAA CGGAAAGCCA AATCTCGCCA AGTAAGGAAA GGAAAAGGGC AAATACAAGG 60
AAGAAACCAT TGAGAAGATG CAGGAATAAA GTAATCTTAT ATACAAGCTT TGATTAAAAC 120
TTGAAACAAA GAAA 134

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SEQ ID NO:734
SEQUENCE LENGTH:132
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00808
SEQUENCE DESCRIPTION:
GATCAGTGGC TTTGAATGAA ATACAGATGC ATTATCCAGA ACTGAAGTTG CCCTACTTTT 60
AACTTTGAAC TTGGCTAGTT CAAAGATAGA CTCTTCTTTT GTAAAGTAAA TAAATTCTTC 120
AAAATGCTTA AA 132

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SEQ ID NO:735
SEQUENCE LENGTH:132
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00809
SEQUENCE DESCRIPTION:
GATCNAACC TTTTCAATAA AAGGCAAAAC AAACCAATNT CCNAACATAG CATTACAGCC 60
TTTAAACCA TTCACTNCTC ATAGTGATTC ACAGAGGACA AGAGATTAAA GTGCTGGATT 120
TTAAATGTCA AA 132

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SEQ ID NO:736
SEQUENCE LENGTH:131
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00810
SEQUENCE DESCRIPTION:
GATCANATGC AACNCACAA CCTCGGCTGA GTCTTGAGAC TGAAAGATTA AGCCATAATG 60
TAAACTGCCT CAAATTGGAC TTTGGGCATA AAAGAACTTT TTTATGCTTA CCATCTNTTT 120
TTTTTCTTAA N 131

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SEQ ID NO:737
SEQUENCE LENGTH:383
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

CLONE:HUMGS00811

SEQUENCE DESCRIPTION:

5 GATCATACAC CTGCTCACAG GCGAGAACCC TCTGCAGGTC CTGGTGAACG CCATCATCAA 60
 CAGTGGTCCC CGGGAGGACT CCACACGCAT TGGGCGCGCC GGGACTGTGA GACGACAGGC 120
 TGTGGATGTG TCCCCCTGC GCCGTGTGAA CCAGGNCANN TGGCTGCTGT GCACAGGCGC 180
 TCGTNAGGCT GCCTTCCGGA ACATTAAGAC CATTGCTGAG TGCCTGGCAG ATGAGCTCAT 240
 CAATGCTGCC AAGGGCTCCT CGAACTCCTA TGCCATTAAG AAGAAGGACG AGCTGGAGCG 300
 10 TGTGGCCAAG TCCAACCGCT GATTTTCCCA GCTGNTGCC AATAAACCTN GTCTGCCCT 360
 TTTGGGGGAA GCCCGAAGC AAA 383

SEQ ID NO:738

SEQUENCE LENGTH:128

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00813

SEQUENCE DESCRIPTION:

20 GATCCAGCTG CCAGAGGATG AGTGACCAGT TGCTAAGTGG GGCTCAAGAA GCACCGCCTT 60
 CCCCACCCC TGCTGCCAT TCTAACCTCT TCTCAGAGCA CCTAATTAAG GGGGCTGAAA 120
 GTCTGAAA 128

SEQ ID NO:739

SEQUENCE LENGTH:128

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00814

SEQUENCE DESCRIPTION:

30 GATCTGGATT ACNATGTAAA TTCACAGCAG TAAGATAATA TAAATTTTGT TGAATGTATT 60
 AACATCATAT GGTCTGAAAA TGTGGGTTT NATTTGGCAC ATTAAATAA AATGTTTCTA 120
 ACTAGAAA 128

SEQ ID NO:740

SEQUENCE LENGTH:128

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00815

SEQUENCE DESCRIPTION:

40 GATCAAGAAT GAAAAAGACA TCATATGAAN NGGGAGAAAC TATTTGCACA CCATCTATCT 60
 CATGGTTTGG TTAATATTCA AACTATATNA GCAGAATGTG TAAGGATATC CTACAACTCA 120
 ATAGCAAA 128

SEQ ID NO:741

SEQUENCE LENGTH:138

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00816

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SEQUENCE DESCRIPTION:

5 GATCCAAGGG GAAACTGCAG GTCAAGGGCT GATAACGGCC ATGCAGGATG CTTGATGCTG 60
 CGTCCCCCGC TGCTTGCCGC CCCCCACCCC GCCATTTTGT ATAATAAAGC TCCCTGTGTA 120
 TTCTCAAAAA AAANCAAA 138

SEQ ID NO:742

SEQUENCE LENGTH:127

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00817

SEQUENCE DESCRIPTION:

15 GATCCCTGAG ACTGAGGGGT TTACGGGCTG TGAATGGACC TTCAGCCCTN CCCACCCCTC 60
 CTCCCCACTG CTGCTGAGTC TGTCTGATGT TTTGTTGTG TGAATAAATA TAATCCCCT 120
 CTGGAAA 127

SEQ ID NO:743

20 SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00818

SEQUENCE DESCRIPTION:

25 GATCGGGTAG CTCAAAAGAA GGCAAGCTTC CTCAGAGCTC AGGAGCGGGC TGCTGAGAGC 60
 TAAACCCAGC AATTTTCTAT GATTTTTTCA GATATAGATA ATAAACTTAT GAACAGCAAC 120
 TAAA 124

SEQ ID NO:744

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00819

SEQUENCE DESCRIPTION:

35 GATCAGAAAT TCTCTTGCTT GAGAGATTTT TTTTGTCTT CTGTTGACTA CATAGTTTCA 60
 AATCTCTCTN TATTTTCATGA TGATATATAA ATNGCTTTTA ATTATATNAA ATNTTAATTN 120
 NCCN 124

SEQ ID NO:745

SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00820

SEQUENCE DESCRIPTION:

45 GATCTCATT A CCTGTTTCC GAATTCTGCC GTGTGTATCC CCAACCCCTG ACCCAATGAC 60
 ACCAAACACA GTGTTTTTNA GCTCGGTATT ATATATNTTT TTCTCATTAA AGGTTTAAAA 120
 CCAAA 125

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5 SEQ ID NO:746
 SEQUENCE LENGTH:123
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00821
 SEQUENCE DESCRIPTION:
 GATCCGTGGC TTAAGACAGG AGATTATCTC TNTACTCCAG TGGCATCTCC TTAGCCAAGA 60
 10 TGTGAAATTA AAATCATAGT TCGCCTCATT TAAAAATNCT AATAAAGCAC TCAAACCTTG 120
 AAA 123

15 SEQ ID NO:747
 SEQUENCE LENGTH:122
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00822
 SEQUENCE DESCRIPTION:
 20 GATCCAAATC TGGTTCAAAC ATTCAAAAC TCAAAGATAA TTCATCTTTC AGCTAATGCT 60
 TGTGGTCTCTG TTGTTCCCTT GAAAAAAAT AAAACAGTT GCCTTCNGGG AAAANTTNNA 120
 AA 122

25 SEQ ID NO:748
 SEQUENCE LENGTH:122
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00823
 SEQUENCE DESCRIPTION:
 30 GATCTTGTGT TTAGGNTGG GCATTTTCAC TCTTCTGCCT TAAATCCCTA ACCCCATGGA 60
 GCTGACATTC TAGTGCGGCT GAGGGGAGGG GAAACATTGT AAAATAAATC ATAAAAATTA 120
 AA 122

35 SEQ ID NO:749
 SEQUENCE LENGTH:122
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00824
 40 SEQUENCE DESCRIPTION:
 GATCTCTGGG CTGGGGACTG AATTCCTGAT GTCTGAGTCC TCAAGGTGAC TGGGGACTTG 60
 GAACCCCTAG GACCTGAACA ANCAAGACTT TAAATAAATT TAAAAATGCA AAAACTCGGA 120
 AA 122

45 SEQ ID NO:750
 SEQUENCE LENGTH:122
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 50 CLONE:HUMGS00825

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SEQUENCE DESCRIPTION:

GATCNTAGAA GGGCTTCCCA ACCNNATTTG CAACATCCAA ATTGTCTTCA ATTNAAGGAA 60
GGCCTTATCA GTTCATAGAT GANCTTCATT GTAAAAATAA ATGTACTTTG CACCACTTCA 120
AA 122

SEQ ID NO:751

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00826

SEQUENCE DESCRIPTION:

GATCCACTTC TGTNATTANG TAAATGGATG TNCGTGATG CGTCTACAGT TATTTATTGT 60
TACATCCTTT TCCAGACACT GTAGATGCTA TAATAAAAAT AGCTGTTTGG TAACCATAGT 120
TTCACCTGTN CAAAGCTGTG TAATCGTGGG GGTACTATCT CAACTGCTTT CGTATTCATT 180
GTATTAAGAAG AATCTGTTTA AACAACTTTT ATCTTCTCTN CGGGTTTAAG AAACGTTTAT 240
TGTAACAGTA ATTAAATGCT GCCTTAATTG AAA 273

SEQ ID NO:752

SEQUENCE LENGTH:144

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00827

SEQUENCE DESCRIPTION:

GATCAAAAAG AAACCTTGTGTT TTTCCGCAAT TGAAGGTTGT ATGTAAATCT GCTTTGTGGT 60
GACCTGATGT AAACAGTGTC TTCTTAAAT CAAATGTAAA TCAATTACAG ATTAAAAAAA 120
AAAGCCTGTA TTAAAGAAC GAAA 144

SEQ ID NO:753

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00828

SEQUENCE DESCRIPTION:

GATCAGAGGA AAAATCCAGT GTGACAGAGT GCAAGTNAGA AGACCTGGCT TTTNATCCCA 60
GCTTTGAAAC TTGGAACCTT TTGATTGACA AATTAATAAA CCTCTCTATG CCTCAGGCTC 120
CTCATCTGTA AA 132

SEQ ID NO:754

SEQUENCE LENGTH:117

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00829

SEQUENCE DESCRIPTION:

GATCTAGGCT TGAGCTTGGT TGGGATTGCT NTTTTCTTCT TCTTCTTAT AAACGATTCT 60
NTGTAACTNT TTGTATTGAC AGTTTCAAAC TTACAGTAAA ATTGCAACAC GAGTAAA 117

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SEQ ID NO:755
SEQUENCE LENGTH:117
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00830
SEQUENCE DESCRIPTION:
GATCAGTACA TAGCATTTGG CTCNTGAACN NAATTNTAAA CTTTCAGGTA TTTTGTACA 60
AATAAGGGAC TGATGTTCTG TTTCTTGTA TTAGAAATAA ACATTAATAC AGTGAAA 117

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SEQ ID NO:756
SEQUENCE LENGTH:119
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00831
SEQUENCE DESCRIPTION:
GATCTATCAT TACTGCAAAA ACCTGCTCTG TTGTGCTGGC TGGNAGGCCC TGTGGCTGCT 60
GGCTGAGGGT TCTGCTGTCC TGTGGCACCC CATTAAAGTG CAGTCCCTC CGGGCCAAA 119

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SEQ ID NO:757
SEQUENCE LENGTH:167
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00832
SEQUENCE DESCRIPTION:
GATCTGAAAT TAAATACTCA ACAGACTCCT CCTTTTTTAG CTGTATTTT CAGGTACTGT 60
GTGGTGACCG CCCCACTGGT GTCTATTACA GGCCACTTTG GTAGTTGTGT ATCTGNTCAT 120
GTATGTGATT TGACAAACCA GTTTTTTAAA ATAAATGGCT TTTTAAA 167

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SEQ ID NO:758
SEQUENCE LENGTH:379
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00833
SEQUENCE DESCRIPTION:
GATCCAATA GAAATGAATG GAAGATGATG GGAAATATGA CTTACCAAG GAGCAATGCT 60
GGGATTGCAA CTGTAGGGAA CACCATTTAT GCAGTGGGAG GATTGGATGG CAATGAATTT 120
CTGAATACGG TGGAACTCTA TAACCTTGAG TCAAATGAAT GGAGCCCCTA TACAAAGATT 180
TTCCAGTTTT ANCAAATTTA AGACCCTCTC AACTANCAG GCTTAGTGAT GTAATTATGG 240
TTAGCAGAGG TACACTTGTG AATAAAGNGG GTGGGTGGGT ATAGATGTTG CTANCAGCAC 300
CACAANGCTT TTCCATATTN GCNTCCTNTT AACCATGCNT GTCCATAAAC CCNGGGANGN 360
NNANTTGNGG GGTNAANN 379

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SEQ ID NO:759
SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00834

SEQUENCE DESCRIPTION:

GATCTACTAC TNGGCCTTCA GTGCGAAGAG CCACATCCAG GCCTGAGGGC GGCACCCCAG 60
CCCTGCCCTT GCTTCCTTCA ATAAACATCA CAGGACCTGG GACTGCACAG GNCCTGGGAA 120
A 121

SEQ ID NO:760

SEQUENCE LENGTH:303

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00835

SEQUENCE DESCRIPTION:

GATCGAAGCA ATTGANGTAT CATGGATTGG ATTGTTACTG ATTCAGTAA AGTATGTTTT 60
GCCAATTAGA TACATATATA CAAGATAAAG GAATAGGATG GTAATATATT TGTNTGAAAT 120
TAAATTACTG TTTTNATTAA AAAATACTGC TTCATTGGGC TGATTTTGTAA AAATGTAATG 180
AGTAAAATGA ATTACTGTAT TTNCCCTTTT ATGTCCACAG AATGAGAGTC ATATGTNGTN 240
ATATNCTAAA TNTNCATTAA ATATTCATGT CACCTTGAGT TGTCATGATA AGTATGTTTT 300
AAA 303

SEQ ID NO:761

SEQUENCE LENGTH:373

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00836

SEQUENCE DESCRIPTION:

GATCTACTAT GTNATGTCAG GGCCTGCGTG GCAACTCATG CAGCAATTCC AGAACCCCTGA 60
CTTCCCACNC GAAGTAGAGG AACAGGATGC CAGCACCTG CCTGTGTCTT GTGCCTGGAA 120
GAGTGGGATG AAACGCCACA GAGCAGCCTG TGCTTCGGCT AGTATTAATG TGTAGATAGC 180
ACTCTGGTAG CTGTAACTG CAAGTTTAGC TTGAATTAAG GGATTTGGGG GGACCATGTA 240
ACTTAATTAC TGCTAGNNNN GGAATGTCTT TGTAAGAGTA GGGTCGCCAT GATGCAGCCA 300
TATGGAAGNC TAGGGTATGG GTCACACTTT ATCTGTGTTT CTATGGAAAC TNATTTNGNA 360
TATTTNGNTT TGN 373

SEQ ID NO:762

SEQUENCE LENGTH:406

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00837

SEQUENCE DESCRIPTION:

GATCTAGGGA GATGTGGAAG AAAGTGTGAC TACTATAGAA ATTGATGAAG AAACATATGA 60
AGAGATATAT AAATCAACGN AACGGAATAT TCCAATGCTC TTTGTCCGGG GAGATGGCGT 120
TGTCCTGGTT GCCCCTCCAC TGAGAGTTGG CTGAAACAAA GAATTTGTCC TGTATGAAAA 180
NCGNNNNNNN GGTGTACAGT GGCCTCTCTA AAAGTACAAA ACATTCATAA GAGAAACCCG 240

CATACATTTT GATATTAAGA AATAATTCGG GGGATTCTTC CACTCCTGAA ATGAGTTGAT 300
 TTGCAGATAA CTCACAACCT CTTAAGCTAA ATGGTATTTT CATTTTCTC AAGCTCTCCN 360
 ATAANTATGG CCACCNNGG NNANNGNGTG GGGAAAAAA NAATTN 406

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SEQ ID NO:763
 SEQUENCE LENGTH:120
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

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CLONE:HUMGS00839
 SEQUENCE DESCRIPTION:
 GATCCCCACG CCACAGCCCT TTTGTCTCTG CAACTGCCT TCTTCGGAAA GAAGAAGGTG 60
 GGAGGNTGTN AATTGTTAGT TTCTGAGTTT TACCAAATAA AGTAGAATAT AAGACGNAAA 120

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SEQ ID NO:764
 SEQUENCE LENGTH:115
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

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CLONE:HUMGS00840
 SEQUENCE DESCRIPTION:
 GATCTTGATG GTGTTTCTTT CCCCCAAAAT TGACTTAGAT ATTAATAATT GGTGCTTATA 60
 AGAGAGAGTT AAAAAAAAT AGGATTGCTT CAATTAAAT TACAAAAGAG NCAAA 115

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SEQ ID NO:765
 SEQUENCE LENGTH:113
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

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CLONE:HUMGS00841
 SEQUENCE DESCRIPTION:
 GATCCAGTGA CAGCAGGTGT CATGGGTCAA GCATAAATCA TATATAGCAT TTTCAGGCAT 60
 GTTCCTGGTA GTTCTTTTGA GTCTGACATT CTAATAAAAT AATTGTAGG AAA 113

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SEQ ID NO:766
 SEQUENCE LENGTH:112
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

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CLONE:HUMGS00842
 SEQUENCE DESCRIPTION:
 GATCTTTGTG AGGATTAGGA ATTAGGTAA AAGAAATTAA GAACCATCTT CAAGCAAAAN 60
 TTAAACTTTA TTTCTNCTTA ANCAATAAAT ACACCTGANT TAGTTTTCCA AA 112

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SEQ ID NO:767
 SEQUENCE LENGTH:112
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

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CLONE:HUMGS00843

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SEQUENCE DESCRIPTION:

GATCAAAGAC CCAAAGGAAT GCAACANTTT ATCTNTTATC TACCTATNAC CTGCGAGCTG 60
 CCCACCACCC CCANGTTGTN GCGCCTTTCC AGACAGAACC AGTGATACATC TN 112

SEQ ID NO:768

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00844

SEQUENCE DESCRIPTION:

GATCCAAAAC TTAAATACAT CTATGAATTT CCTGGGGCTA TTGTGAGTAC TGTGTATGTA 60
 TTTAGCAAAT ATTTAAGACC TAGTAAGTGC TCAATAAATT GTAGCTGTTA TTGCTGTTGT 120
 NGTTTGTA 130

SEQ ID NO:769

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00845

SEQUENCE DESCRIPTION:

GATCGTGCCA CTGCTCTCCA GCCTGCATGA CGGGAGTNAG ACACCATCTC AAAAAATACA 60
 TATAATAATA TAAATAAAAA TATCTTTTNN GAAAATAATT TAATATNNCN N 111

SEQ ID NO:770

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00846

SEQUENCE DESCRIPTION:

GATCNAGTAN TGNAGGGGCT GTTAGGAGCT TCCTGCAAAT CCCTGAGAGG GCAGAAGATA 60
 GCTTCTGTTA ATTCATTATT CTTCCAATAA ATGTTGATTG AGTACCTAAA 110

SEQ ID NO:771

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00847

SEQUENCE DESCRIPTION:

GATCACCGNC CAGTAATGGG CTCAGAGCAG GTCTTCATCA TGCCTTGTC TTTTTTAACT 60
 GAGAAAGGAG ATTTTTTGAA AAGAGTACAA TAAAAAGGAC ATTGTCAA 109

SEQ ID NO:772

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS00848

SEQUENCE DESCRIPTION:

5 GATCTTCTTC AATATGTGAA TTTGGGCTCA CAGAATCAAA GCCTATGCTT GGTTTAATGC 60
TTGCAATCTG AGCTCTTGAA CAAATAAAAT TAACTATTGT AGTGTGAAA 109

SEQ ID NO:773

SEQUENCE LENGTH:109

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00849

SEQUENCE DESCRIPTION:

15 GATCAACAAG GTTGGCCACT GCTTGATTA CCAGGGACTG GTTACAACCA TTATTTCTNT 60
TCATTTGCTT GGCTTATCTC ATATTAAAGT GAGTTTGAG TTCTCCAAA 109

SEQ ID NO:774

SEQUENCE LENGTH:110

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00850

SEQUENCE DESCRIPTION:

25 GATCCAGTTC TAAACTTTGG GATATTTTTT TTCAATTTTG AAGAGAAAAT GGTGAAGCCA 60
TANGAAAAGT TACCCGAGGG AAAATAAATA CAGTGATATT CTTACGCAAA 110

SEQ ID NO:775

SEQUENCE LENGTH:108

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00851

SEQUENCE DESCRIPTION:

35 GATCTGTGTG CTCTTATCAC CAATCAGTTC AGACCTGGTT GATTTTGTAC TTTGGAACGT 60
TACCTTGGAT GGTTTGTGTT ATTTAAAGAG AAACCTGAAG TACTCAAA 108

SEQ ID NO:776

SEQUENCE LENGTH:108

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00852

SEQUENCE DESCRIPTION:

45 GATCACCATC TTAAATTTA CTTCAAAATA AAAGCATGTA AGTNACTGTT TTTCAAGAAG 60
AAATGTGTTT CATAAAAGGA TATTTATATC TCTNTNGCTT TGACTNNN 108

SEQ ID NO:777

SEQUENCE LENGTH:106

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS00853

SEQUENCE DESCRIPTION:

5 GATCCCCCTC GGAAGAGGGA CTCCAATGGG CATGTCCCCT CCGGAAATNC GGCCTCCTCC 60
CCCTGGAATG CNAGGNCCCC CTCCCCGGN AATNCGCCA CCAAGN 106

SEQ ID NO:778

SEQUENCE LENGTH:130

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00854

SEQUENCE DESCRIPTION:

15 GATCCCATCA TGAATTCATT GGAATTTGTG TTGCATGTAA GGCAATCTTT TCCNTGTTGT 60
AAATCTTCG TTTTAAATG TACATATATT TTGAAAATA TGAATAAACA TGAATTTTA 120
AAAGCTGAAA 130

SEQ ID NO:779

20 SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00855

SEQUENCE DESCRIPTION:

25 GATCATGGTG GGTGAGCTGT ACTGATTGTN ATCCTGACTT TGGCATTGGC AGCTCTTATA 60
TNCCGACGAA TATATCTGGC AACNNATAC ATATNTAACT TTAN 104

SEQ ID NO:780

30 SEQUENCE LENGTH:107

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00856

SEQUENCE DESCRIPTION:

35 GATCTTTTCA CAGTATCCAT TTATTATGTA ATNCTTNTNA GAAAAGAATC TTATAGTACA 60
TNTTANTATA TGCAACCAAT TAAATGTAT AAATTAGTGT AAGCAAA 107

SEQ ID NO:781

40 SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00857

SEQUENCE DESCRIPTION:

45 GATCAAAATG AAAGAAAATC ACAGAAATTA TCCTATGTGT ACTCCTCATC CCTCCTGCTG 60
TATATNTTCT NATTTTTTGC GTAATAAATN ATGTTAATTA CCAAATAAA 109

SEQ ID NO:782

50 SEQUENCE LENGTH:125

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear
 CLONE:HUMGS00858
 5 SEQUENCE DESCRIPTION:
 GATCTCCAAT GTTTTGGGGA TGCTTTGAGT CTCAAAAAA ATTGATAATC AGAAAAGTAA 60
 TTTTGTGTTG TTTGTTAAT GTATCCCTGT TCTGTTTTTA ATTAACTCC AAGTCTCATT 120
 TAAA 125

10 SEQ ID NO:783
 SEQUENCE LENGTH:103
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 15 CLONE:HUMGS00859
 SEQUENCE DESCRIPTION:
 GATCGAGGTG ACAAATANTC AGTCNTANG TCCCCACAAT GACCTCACCA NNATGGCTTT 60
 GGGGAGCTCT TCACCCTAA GATTCCGTCT GGTGCTAA TGN 103

20 SEQ ID NO:784
 SEQUENCE LENGTH:102
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 25 CLONE:HUMGS00860
 SEQUENCE DESCRIPTION:
 GATCTGGAGG CAAGATGCCA GGCCCCACAG GTGTTCTCAG GGCAGTTCTT GGTGTCTGCT 60
 TCTCAGATAC CAAGGACTGG AATTAACC TTTCTGGGA AA 102

30 SEQ ID NO:785
 SEQUENCE LENGTH:99
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 35 CLONE:HUMGS00861
 SEQUENCE DESCRIPTION:
 GATCACAGCC GAAGAGTGAA AGGTGCTGCA ATGAATGTTA GCTGTGGCCA CTGTGGATT 60
 TTCGCAAGAA CATTAATAAA CTAACAACTT CATGTGAAA 99

40 SEQ ID NO:786
 SEQUENCE LENGTH:94
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 45 CLONE:HUMGS00862
 SEQUENCE DESCRIPTION:
 GATCAAGTTA TTTTNAATT GGTTCACA TTGAAACAA GTCAGTCATT CAGATATGAT 60
 TCAAATGTCT ATAAACCGAA CTGATGTAAG TAAA 94

50 SEQ ID NO:787
 SEQUENCE LENGTH:102

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SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
5 CLONE:HUMGS00863
SEQUENCE DESCRIPTION:
GATCTCTTCT TCTCCCTGTG GCCCCTGCGC TGTGCCCCG TCCCGTCAC CCCGCCGNN 60
ACTGAAATNT ATAATCTGAC TTCCTGTACA GAAACCTGCA AA 102

10 SEQ ID NO:788
SEQUENCE LENGTH:93
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
15 CLONE:HUMGS00864
SEQUENCE DESCRIPTION:
GATCTTGTTA GCAATGCTGT TTTNCTGTT AGTCGGGTGA GAGTTGGCTC TACGCGAGGT 60
TTGTTAATAA AAGTTTGTTA AAAGTTTAAT AAA 93

20 SEQ ID NO:789
SEQUENCE LENGTH:100
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
25 CLONE:HUMGS00865
SEQUENCE DESCRIPTION:
GATCTTCAAG TGAACATCTC TTGCCATCAC CTAGCTGCCT GCACCTGCCC TTCAGGGAGA 60
TGGGGGTCAT TAAAGGAAAC TGAACATTGA ACCCTTTAAA 100

30 SEQ ID NO:790
SEQUENCE LENGTH:92
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
35 CLONE:HUMGS00866
SEQUENCE DESCRIPTION:
GATCAGAATT TAAATGTGT GATTCTTTT CTTTCTGTAA GTATGTATTG CTATGATAAA 60
TAAAAAATGG CAGGACCATT NTTTTATNA AA 92

40 SEQ ID NO:791
SEQUENCE LENGTH:93
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
45 CLONE:HUMGS00867
SEQUENCE DESCRIPTION:
GATCTCCAAC CAGGCCAGAG AAGATTCTCA CAGAAGGTTT TGAACCTAA GAAATAAATT 60
GGTTTGGTAA TAAATGGCTT CTGGTCAGAT AAA 93

50 SEQ ID NO:792
SEQUENCE LENGTH:114

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SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00868
 5 SEQUENCE DESCRIPTION:
 GATCTTGAT CTTGTATAA CGGATGTNAT TTGTACGAAG GGCAGTTCGT AAACAGCACT 60
 TGTNCTTTTA ATAAAAGAAT GTTTGCAAA AAAAAAAAAA AAANCCCNAG GAAA 114

10 SEQ ID NO:793
 SEQUENCE LENGTH:90
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00869
 15 SEQUENCE DESCRIPTION:
 GATCTGTTTT GTACTTTTAA TACTGTTGGA TACTTATAAT CAAACTTTT ACTAGGGTAT 60
 TGAATAAATC TAGTCTTACT AGAAAAATAA 90

20 SEQ ID NO:794
 SEQUENCE LENGTH:88
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00870
 25 SEQUENCE DESCRIPTION:
 GATCCATTTT ATAAAGTATG ATTTGCCCAA ACCTGTACCA TTTCCGTATT TCTCCTGTAG 60
 AAGTAAGAAA TAAATTCCT TAAATAAA 88

30 SEQ ID NO:795
 SEQUENCE LENGTH:89
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00871
 35 SEQUENCE DESCRIPTION:
 GATCTGGCGC TTGGGGGTAA GTGGNATGAT TTGCTAATAT TGAGNATCTG TTGTATCAAA 60
 CATAATAAAC TTTTTTTGA GATGTGAAA 89

40 SEQ ID NO:796
 SEQUENCE LENGTH:89
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00872
 45 SEQUENCE DESCRIPTION:
 GATCAGGGTG TCTCCTTGTC CTTCTNAGAT GTGGAGAAGA GGCTGCTGGC TACCCTAAAA 60
 NTTGAAATAA AAGATTTTTG CCTTTGAAA 89

50 SEQ ID NO:797
 SEQUENCE LENGTH:86

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SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00873
SEQUENCE DESCRIPTION:
GATCCATTGA GCCCAGCAGT CCAACCTGGG CAAAATAAGT GAGAGACCCT GTATCTGAAA 60
GTAATAATAA AAATAAAAAA TATAAA 86

SEQ ID NO:798
SEQUENCE LENGTH:86
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00874
SEQUENCE DESCRIPTION:
GATCCTTTTIT GATAATCTCA TTCCTAGAAA TTAAACCTTA ATGAAATCCC TAATAAAACT 60
CAGTGCTGTG TTATTGTGC CTCAAA 86

SEQ ID NO:799
SEQUENCE LENGTH:87
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00875
SEQUENCE DESCRIPTION:
GATCGAACAT TTCACCTCTC ATATTAAGTC TGGCAATGAT GACTATATGT ATTCCTGCCT 60
AAATAAATCA TCTATTAATC ATTAATAA 87

SEQ ID NO:800
SEQUENCE LENGTH:86
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00876
SEQUENCE DESCRIPTION:
GATCTCCGAG TCAGGACGGT CGGCCAGACC CACGGGGTAA CGGGTCTAAT CGTGTAGGAA 60
TAAAGCTGTA TTCCAGTGCT TCCAAA 86

SEQ ID NO:801
SEQUENCE LENGTH:84
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00877
SEQUENCE DESCRIPTION:
GATCCCCGCG ATACTTCAAC GCCTTCTGAC TTCCAGGTGA TGA CTGGGCC CCAATAAAT 60
CCCGTCTTTG GGTCTCTCTG CAAA 84

SEQ ID NO:802
SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00878
 SEQUENCE DESCRIPTION:
 GATCCCTCAA AACCTCACTA ACTGGAAGGA TGATTTTGTC TCAGTTTGTA CTCCTAAATA 60
 AAAAGTAAAC ATGACACCTC TAAA 84

SEQ ID NO:803
 SEQUENCE LENGTH:88
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00879
 SEQUENCE DESCRIPTION:
 GATCTGTGAA GAAATGAAAT AAAATGGTAT TTAGTAAGAA ATCTCTATTT TAAGAAAAAA 60
 AGTAAACCT GTTATAACA CATGCAAA 88

SEQ ID NO:804
 SEQUENCE LENGTH:82
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00880
 SEQUENCE DESCRIPTION:
 GATCGTGCCA TTGTGATATG AATATGCCCTT ATATGCTGAT ATGAATATGC CTTAAATAA 60
 AGTGTTCCTCC ACCCCTGCCA AA 82

SEQ ID NO:805
 SEQUENCE LENGTH:81
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00882
 SEQUENCE DESCRIPTION:
 GATCTTAAGT CATACTTN AATTGNTAG AGGTTGTTCA ACTGAAGGAA TAAATGTCTA 60
 TNAANCTAAA ACAAATGGAA A 81

SEQ ID NO:806
 SEQUENCE LENGTH:78
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00883
 SEQUENCE DESCRIPTION:
 GATCAAGTTT GTACATAACA CTAGTGGCAT TTCTTATCAA AAGGATTGGA TAATAAAAAAT 60
 AAGTTTCTAC TGGGTAAA 78

SEQ ID NO:807
 SEQUENCE LENGTH:78

SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00884
 5 SEQUENCE DESCRIPTION:
 GATCCCCCA GCAAGGATAN CATTCAAAGG AGCTCACATT TATGGAATGG ATGAATCAAT 60
 AAATTAATTC ACTTTAAA 78

10 SEQ ID NO:808
 SEQUENCE LENGTH:77
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00885
 15 SEQUENCE DESCRIPTION:
 GATCCCATTT CTGATGGATG TGTCACACCT TTTCTGTCAA AATAAAATGT CTTGGAGGTT 60
 ATGACTCCTT GGTGAAA 77

20 SEQ ID NO:809
 SEQUENCE LENGTH:77
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00886
 25 SEQUENCE DESCRIPTION:
 GATCTGTGTT AATCTGAGTA ACTTATTGCC TAGCCTATAA ATAAATTCCA AAATATCCAA 60
 TTCATTCTT CTTGAAA 77

30 SEQ ID NO:810
 SEQUENCE LENGTH:75
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00887
 35 SEQUENCE DESCRIPTION:
 GATCATCCTT CCTGGCAAAT AAATCCCGT TTCTATCCAA AAGAGCAATA AAAAGTTTTT 60
 AGTGAAATGT GCAAA 75

40 SEQ ID NO:811
 SEQUENCE LENGTH:76
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00889
 45 SEQUENCE DESCRIPTION:
 GATCTGAAAG CCTGAGTGTG TGTACGTGCG CGCGTGCGTG AAGGCCCTGC CACGATTAAA 60
 GACTGANACC GGCAAA 76

50 SEQ ID NO:812
 SEQUENCE LENGTH:129

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SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00890
 5 SEQUENCE DESCRIPTION:
 GATCTTTAAT ACAATATAGA AATTGTGTAA TAGTTATTAT AAATGTTAAT ACACAACTTT 60
 CAGGTAATTT TAACTGATTA TTTCTTTTGC TCTTTTAACT TAAGTTATTA AAGTTTAAAA 120
 GTTCGTAAA 129

10 SEQ ID NO:813
 SEQUENCE LENGTH:74
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 15 CLONE:HUMGS00891
 SEQUENCE DESCRIPTION:
 GATCTGGTCT CGGTGGTCCT TCCCCGCAGG CAGGTGTCAG GACCGGCCTA ATAAACATGT 60
 GTGGCCTCCT CAAA 74

20 SEQ ID NO:814
 SEQUENCE LENGTH:82
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 25 CLONE:HUMGS00892
 SEQUENCE DESCRIPTION:
 GATCCAAATC CCATTACAGT TGTATAAAGA AATAAAATTT TGTACTNATA TTATTAAAAA 60
 TCACATTTTT AATATTGTA AA 82

30 SEQ ID NO:815
 SEQUENCE LENGTH:72
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 35 CLONE:HUMGS00894
 SEQUENCE DESCRIPTION:
 GATCCCCAGA GACCCCATTT GCCTCTCAAC ACTCAGACCT TCAACTGTTT TTNAATAAAT 60
 CTACTTTTAA AA 72

40 SEQ ID NO:816
 SEQUENCE LENGTH:72
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 45 CLONE:HUMGS00895
 SEQUENCE DESCRIPTION:
 GATCCTACAC CCNGAGCCTC AGAGCACTGC TACTTTTTAA AATACTTCTT TCTCTTAAAA 60
 GTCTTTACCA AA 72

50 SEQ ID NO:817

55

SEQUENCE LENGTH:71
SEQUENCE TYPE:nucleic acid
5 TOPOLOGY:linear
CLONE:HUMGS00896
SEQUENCE DESCRIPTION:
GATCAGATGT TAAGACTGAC ATTTCCAAGG TTGGCTACTA TGTAATAA AAATTACACA 60
AATTGTGCAA A 71
10

SEQ ID NO:818
SEQUENCE LENGTH:71
SEQUENCE TYPE:nucleic acid
15 TOPOLOGY:linear
CLONE:HUMGS00897
SEQUENCE DESCRIPTION:
GATCTGAAGT AATTGTGCTG TATTTATGTT TATTCACCAG TCITTGATTA AATAAAAAGG 60
AAAACCAGAA A 71
20

SEQ ID NO:819
SEQUENCE LENGTH:84
SEQUENCE TYPE:nucleic acid
25 TOPOLOGY:linear
CLONE:HUMGS00898
SEQUENCE DESCRIPTION:
GATCTAGCTC TCTGATTCCA TACATTCCAG ACTTCTCAGT GGATTGTAA TAAACTATAA 60
ATAAAAATAG CTCTCATTTA TAAA 84
30

SEQ ID NO:820
SEQUENCE LENGTH:73
SEQUENCE TYPE:nucleic acid
35 TOPOLOGY:linear
CLONE:HUMGS00900
SEQUENCE DESCRIPTION:
GATCATGTCT TTTCCATGTG TACCTGTAAT ATTTTCCAT CATATCTCAA AGTAAAGTCA 60
TTAACATCAG AAA 73
40

SEQ ID NO:821
SEQUENCE LENGTH:69
SEQUENCE TYPE:nucleic acid
45 TOPOLOGY:linear
CLONE:HUMGS00903
SEQUENCE DESCRIPTION:
GATCTGATTA TTTACTTTGT TTATTGTCTA TATGCCTTTT AAAAAAATAA ACTTGTTATG 60
CAAAATAAA 69
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SEQ ID NO:822
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SEQUENCE LENGTH:69
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00904
 SEQUENCE DESCRIPTION:
 GATCCAGTTG TAGCTGCCAT CAGATGCCGG AGACTCGCCC NTCAATAAAA AAATCTCTTC 60
 TAGCTGAAA 69

SEQ ID NO:823
 SEQUENCE LENGTH:72
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00905
 SEQUENCE DESCRIPTION:
 GATCACTGTA AATGGTAATC AGTTGGAATT CTCCTAAATG TCTTCCAGAC ACTAGTAAAA 60
 AACGACCTGA AA 72

SEQ ID NO:824
 SEQUENCE LENGTH:68
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00906
 SEQUENCE DESCRIPTION:
 GATCTTTCTA CCTGCCTTTC CATGTCATGA GAGGAAGAAA CAAGAATGAC AAGTGTATGA 60
 CTNCCAAA 68

SEQ ID NO:825
 SEQUENCE LENGTH:67
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00908
 SEQUENCE DESCRIPTION:
 GATCACGTAC CTGTGCAGAA ACCGCCTCTG TGGCTGCATT TGAATAAAA CCCGACCCAG 60
 CAGCAAA 67

SEQ ID NO:826
 SEQUENCE LENGTH:342
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00910
 SEQUENCE DESCRIPTION:
 GATCATATTT TATGAACAGA AAGACTCAGG ACATATTAAA AAATAAACTG AACTAAAACA 60
 ACTTTTGCCC CTGACTGATA GCATTTGATA ATGTGTCTTT TGAAGGGCTA TGATACCATT 120
 TATTAATAAG TGTTTTATTT TAAAAACAAA ATAATTCCAA GAAGTTTTTA TAGTTATTCA 180
 GGGCACTATA TTACAAATAT TACTNNGTTA TTACACAAAA AGTGATAAGA GTAACATTG 240

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CTATACTGAT GNTTGTNTAC TCAAAAACCT CNGNTNAAACN GTATGTAATC TNAGTTCAC 300
GCACCTTAAGT TCACCNAACA TNNATNAATG TCAATGNAGA AA 342

5

SEQ ID NO:827
SEQUENCE LENGTH:72
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

10

CLONE:HUMGS00911
SEQUENCE DESCRIPTION:
GATCTAAGAA GTTGTGAATG TTGTTAATCA TTTAGCCGTT GCAATAAATG TAGAGGAAAT 60
GCAGTGTGCA AA 72

15

SEQ ID NO:828
SEQUENCE LENGTH:65
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

20

CLONE:HUMGS00912
SEQUENCE DESCRIPTION:
GATCACCTGA GGCCATGAGT TTNAGACCAG TCCTGGTAAC ATAGCAAGAC CTCCATCTCT 60
ACAAA 65

25

SEQ ID NO:829
SEQUENCE LENGTH:65
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

30

CLONE:HUMGS00913
SEQUENCE DESCRIPTION:
GATCCTAGAC AGCGCCTTAT CTATGATTGA GTGTCCGTGT AAATAAATTC CTACTTAGAC 60
TTAAA 65

35

SEQ ID NO:830
SEQUENCE LENGTH:65
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

40

CLONE:HUMGS00914
SEQUENCE DESCRIPTION:
GATCTGGGAA CTTTTNCTG TACAAATCTG TTTAAAAAAA AAAAAAGGNA CCNCATTGAT 60
TTAAA 65

45

SEQ ID NO:831
SEQUENCE LENGTH:63
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

50

CLONE:HUMGS00915
SEQUENCE DESCRIPTION:

55

EP 0 679 716 A1

GATCCAAATT AAAACCTGGT AGAATCTAAT ACATTGACTG CAATTAAAAAT GTTGCCTGG 60
AAA 63

5 SEQ ID NO:832
SEQUENCE LENGTH:68
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00917

10 SEQUENCE DESCRIPTION:
GATCCAGTTC TAAGTGTCTAT CTTTATNAT NAAGACAATA AAATCTTGAG TTTATGCTTC 60
ACTTNAAA 68

15 SEQ ID NO:833
SEQUENCE LENGTH:63
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00918

20 SEQUENCE DESCRIPTION:
GATCCACGGT TGTNACCATG TATTACCACA AATTTAACAA TAAAAAATTG TTTTAAGAGT 60
AAA 63

25 SEQ ID NO:834
SEQUENCE LENGTH:109
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00919

30 SEQUENCE DESCRIPTION:
GATCTACTGT CATTGNATG CAATTCCTG TTACCTTGAA AAAATAAAAA TGTTAACAGG 60
AATGCAGTGT GCTCATTCTC CCNAAATAGT AAANCCCACT GTATACAAA 109

35 SEQ ID NO:835
SEQUENCE LENGTH:62
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00920

40 SEQUENCE DESCRIPTION:
GATCCAATTA CACACATTCTG TTCACAACCTC AACACAAATT CCTATTAAAT ATTAAAAGTA 60
AA 62

45 SEQ ID NO:836
SEQUENCE LENGTH:61
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00922

50 SEQUENCE DESCRIPTION:

55

GATCTTAAAC ATAGGAAAAC CATACGTGTT CATGATAATA AAATGCTTTC TATGAAATAA 60
A 61

5 SEQ ID NO:837
SEQUENCE LENGTH:56
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
10 CLONE:HUMGS00924
SEQUENCE DESCRIPTION:
GATCATACCA CTGCTCTCCA GCCTGGCTAT CAGAGTGAGA CTCTGTCTCA CAGAAA 56

15 SEQ ID NO:838
SEQUENCE LENGTH:56
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00925
20 SEQUENCE DESCRIPTION:
GATCAGACAC TTAACCCCTTA TAANTTAAAG TCAATAAAGC ACCTTTTAA AGGAAA 56

25 SEQ ID NO:839
SEQUENCE LENGTH:57
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00926
SEQUENCE DESCRIPTION:
30 GATCAAAGTG AAACAATGTT TGGATGCAAC GCAGAATAAA AGAATATAAG AAATAAA 57

35 SEQ ID NO:840
SEQUENCE LENGTH:52
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00929
SEQUENCE DESCRIPTION:
GATCTAATTA AAAGACCTTC TGCACAGCAA AAGAACTAA CAACAGAGTA AA 52

40 SEQ ID NO:841
SEQUENCE LENGTH:52
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
45 CLONE:HUMGS00930
SEQUENCE DESCRIPTION:
GATCCCGGCA GAAGCTATGA AAGGGAATAA AGAGAAAAGA AGTACCCAGA AA 52

50 SEQ ID NO:842
SEQUENCE LENGTH:52

55

SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00931
 SEQUENCE DESCRIPTION:
 GATCTTTTAG TTCAACTCA GCTTTTACAA TAAAANGGAT TTGTATTGCA AA 52

SEQ ID NO:843
 SEQUENCE LENGTH:58
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00932
 SEQUENCE DESCRIPTION:
 GATCTCTTTT CAGAAGTGTC TATAGAACAA TAAAAATCTT TNACTTCTGA CCTTGAAA 58

SEQ ID NO:844
 SEQUENCE LENGTH:53
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00934
 SEQUENCE DESCRIPTION:
 GATCCTAAAT CATGACTTAC CTGCTAATAA AACTCATTG GAAAAGTGAG AAA 53

SEQ ID NO:845
 SEQUENCE LENGTH:52
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00935
 SEQUENCE DESCRIPTION:
 GATCAAGCTG TAAAAAACN AAAAAATTAA TAAAAATTC GAGAAATANA AA 52

SEQ ID NO:846
 SEQUENCE LENGTH:51
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00936
 SEQUENCE DESCRIPTION:
 GATCAGCATT GTGACTTGA GATAATAAAA TTTAGACTAT AACTTGGA A 51

SEQ ID NO:847
 SEQUENCE LENGTH:62
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00937
 SEQUENCE DESCRIPTION:
 GATCTGAGGT AACTTTGAA GTAAAAATAA AGCTGTGTTT GAGCATCATT TGTATTTTGA 60

AA

62

5 SEQ ID NO:848
 SEQUENCE LENGTH:59
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00938
 10 SEQUENCE DESCRIPTION:
 GATCCTCCCT CCCCTAATTA AAGTCTCTTT TTGCCCTTT GGGCTGNCAT GAGGTCAAA 59

15 SEQ ID NO:849
 SEQUENCE LENGTH:71
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00955
 SEQUENCE DESCRIPTION:
 20 GATCAGAATT TTAAATNAAA GGTTTTTTCT TTAAATNATT TGTATTACTT TATTAAAACT 60
 CTGATATTAA A 71

25 SEQ ID NO:850
 SEQUENCE LENGTH:661
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00972
 SEQUENCE DESCRIPTION:
 30 GATCCGGTTC TGGGACAGCA GGGGGCCCCA CTGCACCCAG GTCATCCCTG TGCAGGGCCG 60
 GGTACCTCC CTGAGCCTCA GCCACGACCA ACTGCACCTG CTCAGCTGTT CCCGAGACAA 120
 CACACTCAAG GTCATCGACC TGC GTGTCAG CAACATCCGC CAGGTGTTC GGGCCGATGG 180
 CTTCAAGTGT GGTTCGACT GGACCAAAGC TGTGTTGAG CCGGACAGAA GCTATGCACT 240
 GGCAGGCTCC TGTNATGGG CCCTTTACAT CTGGGATGTG GACACCGGGA AACTGGAGAG 300
 35 CAGACTACAG GGACCCCAT GCGCTGCCGT CAACGCCGTG GCCTGGTGCT ACTCCGGGAG 360
 CCACATGGTG AGCGTGGACC AGGGCAAGGA AGGTTGTGCT TTTGGCAGTA GGGCCACGAC 420
 CTGCCTGCTT GGGNTGGAGN TTTTNNCCG AAGCTNAAAG TTTCTNNNGG GGCAATGAAG 480
 GGGTTGGGG TTTGGGATTN GAGNTTNGNC TTGGGATTTA ATTGGGNAAG AAGGCTTGA 540
 40 AAGACCTTGN CTTTTTTNTT TAAAANTNAA GTATTGGTTT GGGGGNTTAA GGTAATTTT 600
 TTTTNGAATT TTAANTTNAT NTCTAAATTT TTTCCAAAT TTGAAAAAT TTTTTTTNAA 660
 A 661

45 SEQ ID NO:851
 SEQUENCE LENGTH:641
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00973
 50 SEQUENCE DESCRIPTION:
 GATCTTGGAT GTCTATTATA GGAGAAGTAT GTCCTGCCAA TGTACAAGAA GGCAGCATTG 60

55

EP 0 679 716 A1

5 TAGGATTAAC ATTCTTGCT ACTGTATATT ATCTTGAAG GCTCTTGTTA ATATGTTACA 120
 CTTAATATTC TCCACAGTTA CCTTTAGAGA GAATTTATGA GAAGTTAGTT TCTGATGCAG 180
 AGGTTTTTAG GCTGTGATTT CATCAAAAGT CCTAATAGCA TTCTACCTCA AAGGGACACT 240
 TAGNATGCCT AAAATTTATT CACTTAGTTT TCCTTTTTTA TTGAAAAAA TACATGACAT 300
 GTAATCTTTT TTTCTTGAAT TCTTCTCAG ATTTAAAGT ACTATATTAA AGAAAAAAT 360
 TAATGTCTAA AGGCCTAGCA TTCCTTGCAG GACCCCTATA CTAACCATGG TAATGGGGGA 420
 GAGGGGTGGG GCAGNTNNGT AGGGGNACCA GGTTCAGGC CTCAAGCTTC CCAAAGCCAT 480
 TTTTNTAAA TGGGAAATCC NTNAANTTNT GGAACCCGCT TTGNTATNGG NGCCCCTTTT 540
 TTTAAATTC CNGGCCTTTT TTTNNTTGGT AATGGGGGTT NCTGTTTNGG GTTTAAACCT 600
 NANCCTGGNC CGGGGGGGTT TAAAGGAATG CTGNCTGCAA A 641

15 SEQ ID NO:852
 SEQUENCE LENGTH:627
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00974
 SEQUENCE DESCRIPTION:
 20 GATCTGCTNC AGTGCTCTGA GCCCTAGGAT TCATCTNTCT TTTCACCGTA GNGCGCNGGA 60
 CTGGCATTGT ATTAGCAAAC TCATCACTAG ACATCGTACT ACACGACACG TACTACGTTG 120
 TAGNTCACTT CCACTATGTC CTATCAATAG GAGCTGTATT TGCCATCATA GGAGGCAACA 180
 TTCCTGATT TCCCTATTTC TCAGGCTACA CCCTAGACCA AACCTACGNC AAAATCCATT 240
 25 TCACTATCAT ATTCATCGGC GTAAATCTAA CTTTNTTCCC ACAACACTTT CTCGGCCTAT 300
 CCGGAATGCC CCGACGTTAC TCGGACTACC CCGATGCATA CACCACATGA AACATCCTAT 360
 CATCTGTAGG CTCATTCAAT TCTCTAACAG CAGTAATATT ANATAATTTT CATGATTTGA 420
 GAAGCCTTCG GTTTCGAAGC GAAAAGTCCT AAATAGGTAG GANGAACCTT TCCATTAAAC 480
 CTGGAGTGAC TATATGGNTT GCCCNATCCC TTACCANACA TTCNGAGGAN CCCGTATACA 540
 30 TAAATNTN GNAAAAAAN GGANGGNTTC GNACCCCCCA AAGGTTGGTT TNANGNCAAC 600
 CCCCNATGGC TCNATGGTTT TTTTAAA 627

35 SEQ ID NO:853
 SEQUENCE LENGTH:617
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00976
 SEQUENCE DESCRIPTION:
 40 GATCAGANTG CCCCTCCACT CATGAGACTC TTCATTTTGT CCACTTTGAC AGGAAAAGTG 60
 GGAATGTATG CAGAGCTCTC AAAAGAAACA AAAAAGGCCA AAACGGTGCC TTCAGCCACA 120
 TCCTCTGAAT TGGCCCTGAC TTGGACTAAA NCCNCTAATG CAAAATCCCT TGACAAAAGC 180
 GCATAGGTTA TTTCAAACCA GCATTGTTTT TTATGTAACC TGTTTTACCG CATCTTCTCA 240
 45 GCAGCTTCTG ACCACTGCTC AATTTTTTCC TTTACAGCCA TTGTTCTGGT GGACAAATAA 300
 CCTAGGTACT CCAAATCCTG GCAGGAAAAA TATACAGCAT TATGAAACAG CACTCAGTAA 360
 TCCTAAAATG GATTTTCCAA AGCTGGTTAC ACATGNCCTG CAAAGTCTTA TTTAAATTTA 420
 AAAGGCCTTT CTCATTTACC AGGGGTTTAG GTCAACGNNG GCAAACCCCT GGGGGAATTT 480
 AAATTGGGAA GGTANTTNC CTTTNGTAAA TTCATAGGNN CCAAANGGCN GGGNAGTTAA 540
 50 TTTTCCATN GGGTTGGTGG CNCCCGGNT TCATTGGTNT TNGCCCCAN GGAATTTAAT 600

55

TTTTTTAAAN CCTTAAA

617

SEQ ID NO:854

SEQUENCE LENGTH:602

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00977

SEQUENCE DESCRIPTION:

5 GATCCCGTGC GCGCGCTGC CCGAGGGGAG CAAGGACAGC TTTCAGTTC TCCTGGAGTT 60
 CGCTGAGGAG CAGCTGCGAG CCGACCATGT CTTCAATTTGC TTCCACAAGA ACCGCGAGGA 120
 CAGAGCCGCC TTGCTCCGAA CCTTCAGCTT TTTGGGCTTT GAGATTGTNA GACCGGGGCA 180
 TCCCCTTGTC CCCAAGAGAC CCGACGCTTG CTTTCATGGCC TACACGTTTC AGAGAGAGTC 240
 15 TTCGGGAGAG GAGGAGGAGT AGGGCCGCCT CGGGGCTGGG CATCCGGCCC CTGGGGCCAC 300
 CCCTTTTNA GCGGGTGGGT AGGAACCGTA GACTCGCTCA TCTCGCCTGG NTTTGTCGCG 360
 ATGTGTGAAT CGTGCAAATA AACGNTCACT TCCGAATTAA GCGGTNTATT TTTGAANGT 420
 TTAATAATTG TGTTTTNTGA ATACTGAAGT ATTTGGCTTT AAATTCCTAA NTTAAAAATT 480
 TAATNTTTTA CTTTTTAAAT TGCTGGGTTT AAGATNGTTN AAGATTATCC TTGNAACCTT 540
 20 NNGGGGGGANG TTNTATTTT NGAGTCTTTT NGGAANAGNC TTNAGGCTTT TNNACTTNGA 600
 AN 602

SEQ ID NO:855

SEQUENCE LENGTH:595

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00978

SEQUENCE DESCRIPTION:

30 GATCCAGGG CTCCTGCCA TTTTAGTGTG TTGGTGTAGT GTAACCATTT AGTGGTTGGT 60
 GGCAACAATT TTATGTACAG GTGTATATAC CTCTATATTA TATATCGACA TACATATATA 120
 TTTTNGGGGG GGGGCGGACA GGAGATGGGT GCAACTCCCT CCCATCCTAC TCTCACAGAA 180
 GGGCCTGGAT GCAAGGTAC CCTTGAGCTG TGTGCCACAG TCTGGTGCCC AGTCTGGCAT 240
 35 GCAGCTACCC AGGCCACCC ATCAGTGTG ATTGACATGT AGGTACCCTG CCACGGCCTA 300
 TGCCACCTG CCCTGCTTCC TGGCTCCTTA TCAGTGCCAT GAGGGCAGAG GTGCTACCTG 360
 GCCTTCCTGC CAGGAGCTTT NCACCCACTN ACATTCCGTC CCCGCGGCTT AACTGNAGCA 420
 AGCGTGGNCC TAGGACAGNA GGAGCTTCGG GCCCNGTTN ACCTTGCGGT GGGGCTNANG 480
 GGTGGCATT TCTTGCTGG GGCCACTGGG TTNAATTTT GGGNTGATNA TTGGGGNGAG 540
 40 GGGTGGGGTA ACAAACCAN TTTTGGNAA GNTTGGGANG NTTTTGNCTT TAAA 595

SEQ ID NO:856

SEQUENCE LENGTH:581

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00979

SEQUENCE DESCRIPTION:

50 GATCTGGAAT TGCAGCCAC ATAAACATAA AGGAGGATGT CCCTGGTCTG TTCCATCCCC 60
 ACGGATGGTG TTGCTGCTGG GCAACAGTGT TGGCTTCTT NAAGTACCCC CTTTCTCCT 120

EP 0 679 716 A1

5 CACCCACCTC CAAACTGACT AGCACTCAGA GGGACTTATG ATAAAGGTTT AGCTCCAGGG 180
 GTAGTACCTG AGTGTGTGCC ATGCCCTTC AGACCAGCTG CTTCCATCAG AATTCAGGG 240
 TCACAGCCCC AACAGAAGCA GCAGTGCCTC TGTAGGAGGG GTGCTGGGCT CTGGNCTTCT 300
 NATGCAGAGA GGTCCGGGAC AGGGTCAGTA TCGTGGGCAT GTNTATAGCT TCCCAAGTTC 360
 TTTTACAAGT CCCNTGCTGG GACTCCCTGA NTTTACTTTT GGTNGGNTTC CTAGGTNCTA 420
 ATTGGTTTTA CAAACTTACA NTTTTNTAGG AATTGANTT ANGATTANCT TGNTTTAATT 480
 TAATTGTAGA NTTTNGGGGC CTTTTTGGGN CTCAAATTTT NCCATTACAA GGNNTTATTN 540
 10 GGGAAANAAA GNNGTTTNA TNAAAATCCT TGGCCAGGAA A 581

SEQ ID NO:857
 SEQUENCE LENGTH:569
 SEQUENCE TYPE:nucleic acid
 15 TOPOLOGY:linear
 CLONE:HUMGS00980
 SEQUENCE DESCRIPTION:
 GATCTAAATC AGACAGGAGT TGGTCTACAT AGTAGTAATC CATTGTTGGA ATGGAACCTT 60
 TGCTATAGTA GTGACAAAGT GAAAGGAAAT TTAGGAGGCA TAGGCCATTT CAGGCAGCAT 120
 20 AAGTAATCTC CTGTCTTTG GCAGAAGCTC CTTTAGATTG GGATAGATTC CAAATAAAGA 180
 ATCTAGAAAT AGGAGAAGAT TTAATTATGA GGCCTTGAAC ACGGATTATC CCCAAACCTT 240
 TGTCAATTCC CCCAGTGAGC TCTGATTCTT AGACTGCTTT GAAAATGCTG TATTCATTNN 300
 GCTAACTTAG TATTTGGGGT ACCCTGCTCT TNTGGCTGTN CTTTTTTTGG AGCCCTTCTC 360
 25 AGTCAAGTCT GCCGGATGTC TTTTTTACC TACCCCTCAG TTTTCTTAA AACGGGNACA 420
 CAANTCTAG NGNGGTGTTA NGANTAATNG TTACTNNGGT TANTGGGGTA NTTNNTGGGG 480
 TNTNGGTTTG GGGCTAGGCA TTGTGGTAGG TTTTNAANAA TTAGNNGGTT GGNCCCCNTT 540
 NGNTGGGGTG NTTTCANGGT NGAATNAAN 569

30 SEQ ID NO:858
 SEQUENCE LENGTH:566
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 35 CLONE:HUMGS00981
 SEQUENCE DESCRIPTION:
 GATCCCAACC NGGCCTCTCC TGGAACTCTG AACCTGCTGT GGAAGGAATT GGCCATGACC 60
 TTCACCTCTG GAGAGTAGGG TCTATGGCGA GGGAAAAGGG NNTTCACCAT GATAACCTAG 120
 TGCCTCCATA GAGGGGTTTG GAAAAATTC AGTCCGATTT CTTTGTGTGT CAGCTGACTT 180
 40 CCTTAGCTGA TTGTTCCAC TTGCACCTCT CCACCTTTGG CACTAGAACT CCTGAGACAC 240
 CACTTCTCAT GCTTCTCCCT CCCTACCAGC GGTCAAGGCT TTGGAGCCAC TCTTTTGTA 300
 CTCCAGATTA TTAAAGAGA AAAGTACAAG ACAGAAATCT TCTAGCACTT TGAAACACA 360
 GTTGATTAAC CCTCTTGGGN GTATTTTTTG GGCTTTATAT AAAANCANGG TTTTTTAATT 420
 45 NGTAAAGTNT AAGTGCCATT AGGAANATGC ACCAGGGCAT ATTTTGGTT NAAGGTGGTT 480
 TTTTCAATGG TTTTNCAGGN TTNCATTTTC AAAAAAANGG TTTTTTAAT GGAGGTGTT 540
 NTTNAAANNT TCNTGANTGG TGGAAA 566

50 SEQ ID NO:859
 SEQUENCE LENGTH:556

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00982

SEQUENCE DESCRIPTION:

GATCTACAAT TACTAATTAA AGCTGTGAAT CTNTTCCCTG CTGGAACAAA TTCAAGATGG 60
 GAAGTTATTG CTAATTACAT GAACATACAT TCTTCCTCTG GAGTCAAAAAG AACTGCCAAA 120
 GATGTTATTG GCAAAGCAAA GAGTCTCCAA AAAGTTGACC CTCATCAAAA AGATGACATA 180
 AATAAAAAGG CATTGTATA GTTCAAAAAA GAACATGGNG TGGTACCTCA AGCAGACAAC 240
 GCAACGCCCT CAGAACGATT TGANGGTCCA TATACAGACT TCACCCCTTN GACAACAGAA 300
 GNACAGAAGC TTTTNGAACA AGCTTTGAAT ACATACCCAG TAAATACANC TGAAAGATGG 360
 GNANAAATAG CAGTAGCGGT GCCTGGCAGG NCAAGGAGG GNCTGCATNN ANCCGGTTNC 420
 AGGGGACTTT GTCGNGTGG GTAAAGCCAA AGGAAGCTTG TTCCAGGTCN ANGTGCTGGA 480
 TGCAAGTTGG GGCNTGGNAT TNNCATT TTTTGGGGT GTTCTTTTT TTANTAAACC 540
 TGNANTTCTT TTAAA 556

SEQ ID NO:860

SEQUENCE LENGTH:555

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00983

SEQUENCE DESCRIPTION:

GATCTGGATT ATTTGTCTAA GTGAGAGATT GCGAATATCA AAATATCTGT CTCACTTCTT 60
 CTGTGAATNA CACAGAGTAG AAATAAATTC ACTTTAAAAA TATGACTGAA TTTTGAAAAT 120
 CAAGACTGAA TCTCACATAG CTGCAGACAG GAACTAAGCC AGCCTCTTTG TATGTGGTAA 180
 CAAGTACAGT ATAAGANTGA AAGATTTACC ATCCTTGAAA GCTCTAATGA AAATCAATC 240
 CAGCAATATA TATTCAACTG TGTACAGGAT TTAAGAACTT ATTTTATGAA GGAGTAATAG 300
 TGTGTAGATA TAGATTCTGA AGTCTTTAAA CGTGCCTTAA TAAATNAAGT TCNCTGGCAT 360
 TGAGNTGANN ACCAGGTGAC CNTTGGGGNC AAAAACCNC ACAAGTGATT NGCACACCAG 420
 TATACNTTCA CCANTATACT NTNTGCACAC ACANCNTTGT TTTNGGTTCA GGGTTTTGCA 480
 AATNGGTCN ATGTATTGGC ACTGGCGTCT TTGNATTGTG TAAGTGGNTA TTTNTGAGG 540
 NTAGCGTGGT NNCNN 555

SEQ ID NO:861

SEQUENCE LENGTH:554

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00984

SEQUENCE DESCRIPTION:

GATCCATGTC TCAGCCTCCA CCCCGCCACA CCTGTCTGTG CAGCCCACCG GCCTTACCTT 60
 CTACCCTGCC GTGGATGTCC AGGCCTTTGC CGTCCTCCCC AACTCCTCCC TGGCTTCCCT 120
 CTTCTGATT GGCATGGTAA GCAGTTCCTG GGTGGACAG ATGAGGAGCC CCAGACAGTC 180
 CCAACAGCAC TGTCTTTGGA GTCAGGAGAC CATGTGAATC CTGTCTGGAT TCAAACCTGG 240
 ACTGTGTCAC TCCGGAGCCT GAGGCTTGAG TCACTGTACT CAATGGTGCC GACTCCTGGA 300
 GGTATTCATT CACCCAGCCA TTCCTAGTG CGTTTGTTA CTTATTCATT CAATTATTCA 360
 TTCAGTCAAT TTCTCATTCA TTCANTTATT CATTCCATGT TGGCTTGAA TATGTGTACT 420

EP 0 679 716 A1

GTNCCAATTN ATCCATTTAT ATCTTTAGTC ATTCAATTAT GCATTNGTGG TATTTGTTCA 480
TTNATTCANT TTTTAATTTN ATTNAGTTAN TNNNTNGGTT GGTGNCTTGG NGTANNGTNA 540
TACATTGNG GAAA 554

5

SEQ ID NO:862
SEQUENCE LENGTH:549
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

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CLONE:HUMGS00985
SEQUENCE DESCRIPTION:
GATCCTATGG TTCAGGAGGC CAGAAATTTT CACCTCTAGG AGGTGGTGGT GGCATAGGTT 60
ATGAAGCTAA TCCTGGCGTT CCACCAGCAA CCATGAGTGG TTCCATGATG GGAAGTGACA 120
TGCGTACTGA GCGCTTTGGG CAGGGAGGTG CGGGNCTGTG GGTGGCAGGG TCCTAGAGGA 180
ATGGGNCTGG AACTCCANCA GGAATATGGT AGAGGGAGAT AAGAGTACGA AGNCCAAACA 240
AAAAACCCCG ATTTTAGATG TGATATTTAG GCTTTCATTC CAGTTTGTG TTGTTTTTTT 300
GTTTAGATAC CAATCTTTTA AATCNTTGCA TTTTAGNAAG AAGCTATCTT TTAATGGTTG 360
TAGCAGTTAT TGACCTAATA TTTGAAATGG CTGTTGGCAG TAAATTATGA ATCAGTTTTT 420
GACCAGNGA TTTTTTNCN TATTCCTT ANTTTCCTGT TNCTGATATN CCCCCAAGTA 480
TGCAGTTNCT NNNCNCTNAA TTCCANGGNN CCATTTTTTT TTCNGGGTTC AANAATNGAA 540
TNGNTTAAA 549

25

SEQ ID NO:863
SEQUENCE LENGTH:543
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00986

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SEQUENCE DESCRIPTION:
GATCAGCAGT CTTCTGCTGC CTTCTTAATG TTTCACCTAA GTTCCCATAG TTGCTCTCAA 60
AAAGTTTCTT GGCCCTCGTG GGCCAGNTG GAGGGGCTGT ATCATCATTC ATNAGGAGCG 120
TCACTTGGTG GTTTAGGGGG AAATAATCTA TTCTNAAGAT TGAAGAGAGT GCAGGATTG 180
GGGGGTGAC TCTACATCCT TCAGTATCAG GGCTTATCTC CTTGTNTTAC CTCCTAGGAG 240
ACCCTCCTGT TCTTAAGTGT GGGCGATGAG AAAGGTGGTG GACTCTTCTT ACTGGCAGGG 300
CCACCTGCGT CTGTGGAGAC CCTGGGGCCC AGGGTGGCTG AGGTCCTGGA AGGCAAAGGA 360
GCAGGGAAGA AAAGGCCGTT TTTCAGGGCA AGGCCACCAA GATGAGCCGG CGGATGGAGG 420
GCGCAGGCGG TTCTCCAGGN CTACATCAGC AACGNAGAGT NCTAAGNANT TANGGCTTTA 480
GGGCACTTAN CTNCTGGTTT CCACAGGAAT CTTTNGTCA ATNAAATTAG TTTGCCTCAG 540
AAA 543

45

SEQ ID NO:864
SEQUENCE LENGTH:538
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00987

50

SEQUENCE DESCRIPTION:
GATCATTTCT ATAAAAGAAA TGGTCATTTT ACTTAGATGC CAGTCTACTT TATAAAGACA 60

55

AATGGATTAT AGACTTAAAA ATAGTCATTT TTCTTATTCA TAAATCTGAC AGGCATAAAC 120
 CCAAATCAAA GATAATTTGG TGCCCATTTAT GAATTTGAAG TTAAGTGATA GCTCACTTGT 180
 AAAGTGACTA CCTTAATGTG TATAGAGACC CCAGTCTACT ATTATTGGG AAAATTGTTT 240
 AGGTTATATG GGAAGTAG CTCTTTAAAA ATCATATTGC CCAACAGAAA CCTTAGGCTG 300
 AATTTACAGG TATGATAATT TTTGTAATTA ATTTTCTTAG AATTGTGCAG GCTGGGATGG 360
 GGATAATGNC ATACTCTTTT AACTGTACC AGCAGCATTT ATTNCTNG GACCTTTTAA 420
 CCNTTTTAGG GGTAGGGTN CTNGGGAAC CAACCTTAAT TNGGNCATCC TCCATTNNC 480
 TTNTNTNCCN NNNNCCNNT TTTTTTTTG GNCCCNTTN GNCCCCTTA AACNACCN 538

SEQ ID NO:865
 SEQUENCE LENGTH:533
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00988

SEQUENCE DESCRIPTION:

GATCAAACT ATANGTGGCT ATGGCGGATA TGATTATACT GGGTATAACT ATGGGAACTA 60
 TGGATATGGA CAGGGATATG CAGACTACAG TGGCCAACAG AGCACTTATG GCAAGGCATC 120
 TCGAGGGGGT GGCAATCACC AAAACAATTC CCAGCCTTTC CACATTGGCT TTCCCATGTA 180
 GTCCTTAGTG TGTCTGCTNC TCCTCTCTCT CCTCATCACA GTTCCCAGCC CCCACCTTCA 240
 ACTGAAC TCAACAAATCTT CAACTTCATA CAGTAGTCAC ATTGTTAGTA ATAACACTGG 300
 GCATTTTAT TTTGATANAN TAGACCGTTT AAATTTTGA GATTCTACCT TATATTTTTT 360
 GAATTATATA CTAAGCANA TAAGTAGGTG NTGTAATGTC CATTGGGGNC CAAGNTTTTT 420
 AGGTGTAAAT GGNAAAAGGG TANCAAAATT NAANCTCAAG TAAACACCCT GTAGGCTTTC 480
 CCCATGGNTT GGGGNATNTC CGGATTAAGG NCAGGGTTTT CCNTTTTCTN AAA 533

SEQ ID NO:866
 SEQUENCE LENGTH:532
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00989

SEQUENCE DESCRIPTION:

GATCTGAAGT GGTGGATTCC TTGTTTTTGC TAGTATCTCA TTTAGAGTTG AGATGGACCT 60
 TAAACTCAT CTGTTTTAAC TCACTTTTTA ATAGATGAGT TAACTTAAT TTAATAAGG 120
 ANNNNCAGT AGAGCCTGGA ACTTCAACCA TTATTCATC CCCATGCCCT GTTCCCCCCC 180
 ACTTCGAAAT TAAATGCGGT TAGCATCATA TAGTTCATTT TCCCCTCCA TGCTGCTGTG 240
 TGATTCTTGA CCTTGGGTAT GAGTTTTTCA TCCTTCATGC AGGGTTCTGT CAGTTCATGG 300
 TATAGTGATT CAGTGTTAAA ATGGTGGTGT CTCAGCTGTG CTGTGCACAT TTCCAACCTT 360
 GTCAAAATTA TAGTCCTGAG CAAGCAAGAA AAAGAGGTAA TAACATACCC ATTTTCTTTT 420
 ATGGANTATA AGCTTAATAA TATTTTTTTC NATGNGCCTA TTTTACCT GNGCAAATTN 480
 GTATGGNCTC ACATGGTTAA CCCCAATNAA TTANTCTTGG NCAATTTTAA AA 532

SEQ ID NO:867
 SEQUENCE LENGTH:528
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

CLONE:HUMGS00990

SEQUENCE DESCRIPTION:

5 GATCGCAAAAT NCACCTAAAC AATACATTTA CAAAGCCATC TTTACATGCA TTAAACGAGG 60
 GCTACAACAA TATTGTTTTA CAAATACTAG CACTTTTTTC CTGTTATGTA CTTAGTGTTA 120
 GAGGGTCAAA ATAATCTTTC TGCTTAGCAT CTCCTAAACC ATACCTGCAA ATATAGCAGG 180
 ATTNTTACAT TTACAGTACT TTAATACTTG TATAANCTAT GCAGAAATTT TTAATAAAGT 240
 10 GTAATATATT TNATAAGCTA ATAAGACTGA ATGGGTAAAG GTTTTNGCA TGC GTTAGTA 300
 TACTTGCGA TACTGAAACA TTTTGGTAAT CTTTCTTACT AAAGGATGTG AATGTTTAAT 360
 GTACCTTCTC TGTTCCTACT CTGTAGTCCA ATGGGAATTC AGTAATGNCA TTTGNCATG 420
 TCAACCTGGG GACCATAAAN TTGGTCCTGG TCCAGGCCCT CATNTCCTAT ATCCAGTATG 480
 CAATNTTATN TNNTNTNCCT GGTNAATNAA CCCCTCCGGG NTTTTAAA 528

SEQ ID NO:868

SEQUENCE LENGTH:526

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00991

SEQUENCE DESCRIPTION:

GATCTTTCCT CAGTATGTGC TGATGTTTGG GTTGCTTGTG GAATCACAGA CACTCCTAGA 60
 GGAGAATGCT GTTCAAGGAA CAGAACGTAC TCTTGGATTA AATATAGCAC CTTNATTAA 120
 25 CCAGTTTCAG GTACCTATAC GTGTATTTT GGACCTATCC TCATTGCCCT GTATACCTTT 180
 AAGCAAGCCA GTGGAACCTCT TAAGACTAGA TTTAATGACT CCGTATTGA ACACCTCTAA 240
 CAGAGANGTA AAGGTATACG TTGTAAATC TGGAAGACTG ACTGCTATTC CATTTNGGTA 300
 TCATATGTAC CTTGATGAAG GGGATTAGGT TGGATACTTC ANGTGAGGCC TCCNCTGGA 360
 AACAAAGCTGC AGTTGTTTTA GNTANTCCCA TCCNGGTGA NATTGGGNGN GGNCTTGN 420
 30 CCTAGCATN CGCATCACNA AGGCAATGTC NGCNTACAG TTANGGCATT GNGGGGCCGT 480
 TTTNCCATGN GNACTGGGTT ATTGGGGNCT NACCAGGTCC AANTTN 526

SEQ ID NO:869

SEQUENCE LENGTH:526

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00992

SEQUENCE DESCRIPTION:

GATCCTGTTG CTTCTGCAGG CCATTTTCTG AAAACCCCTG TTAGGAAGGT TGGATTGCG 60
 GTGACTTGCT TGAGCAAGAG TCCTGGGGAG AGATTTTNAG GTTTAATTTA ACGGTATATC 120
 CAGAGCTAAC AGTGACTCAA CTCGTCTAGT TCTGCAAGTC AGATGTACAC TTAGAGTCTC 180
 TCTGTGAAGG GTTTGGGTCT GAGCTGTATA GTATGTCAA CTGCCAGTAA GCCAGCCCT 240
 45 CACCNTCTGA TAGATATTCC TTTAATGCAC CAGACTTCAT GTTTGATAAA TGATTAATGG 300
 TTGAAATTGT TTCTCTTCTT TTGTGTTTC CCAGTTAATA GATGGTCACT GTTCCACAA 360
 TGTTTTATAC TTTCCAGCTT TTNGTAACN AACCTATAAT TACTTNAATT TTAATTTTTT 420
 TTAAAGCTTN GTTGGTGGNC CTAATGNGAA GGTNTTTTC CAGTGCATNA ATGGTTTTT 480
 NTGGNGCTTC TGNNAATGN CCNTCCCAAT TGTGGGTTGG GTTTTN 526

SEQ ID NO:870

EP 0 679 716 A1

SEQUENCE LENGTH:520

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00993

SEQUENCE DESCRIPTION:

GATCAGGACG GCTGGATTCA GGTGTCGTAC GAACAGTACC TGTCCATGGT CTTCAGTATC 60
GTATGACCCT GGCCTCTCGT GAAGAGCAGC ACAACATGGA AAGAGCCAAA ATGTCACAGT 120
TCCTATCTGT GAGGGAATGG AGCACAGGTG CAGTTAGATG CTGTTCTTCC TTTAGATTTT 180
GTCACGTGGG GACCCAGCTG TACATATGTG GATAAGCTGA TTAATGGTTT TGCAACTGTA 240
ATAGTAGCTG TATCGTTCTA ATGCAGACAT TGGATTTGGT GACTGTCTCA TTGTGCCATG 300
AGGTAAATGT AATGTTTCAG GCATTCTGCT TGCAAAAAAA TCTATCATGT GCTTTTCTAG 360
ATGTCTCTGG CTCTATAGTG CAAATGCTTT TATTAGCCAA TAGGAATNTT AAAATACCAT 420
GGACCTTACA CAAAAGGCTT TCATGNCCTT ACTTNTNAA AAGGGGTTAT TGTATTCATT 480
GGATATGTGC CGTAGCAATN NNGGNTGTT AGCGGNTAAA 520

SEQ ID NO:871

SEQUENCE LENGTH:517

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00994

SEQUENCE DESCRIPTION:

GATCTCCGTG GCTTTGGGTT AAAAGACACA CTTGTCCACA TAGGTTTAGA GATAAGAGTT 60
GGCTGGTCAA CTTGAGCATG TTACTGACAG AGGGGGTATT GGGGTTATTT TCTGGTAGGA 120
ATAGCATGTC ACTAAAGCAG GCCTTTTGAT ATTAAATTTT TNAAAAAGCA AAATTATAGA 180
AGTTTAGATT TTAATCAAAT TTGTAGGGTT TCTAGGTAAT TTTTACAGAN TTGCTTGTTT 240
GCTTCAACTG TCTCCTACCT CTGCTCTTGG AGGAGATGGG NACAGGGCTG GAGTCAAAAC 300
ACTTGNANTT TTGTATCTTG ATGTCTTTGT TAAGACTGCT GAAGATTAT TTTTTCCNN 360
TTATAATANG GGGNTAANCC CCACCTTNAT TCCTTCAATT CANCCTACCA TTTTCNNGGG 420
TTCTTNGTGT TGGGCTTGTG GCAGGNCCAG CTTNTGGGTT TTCCTTTTTN CCATGCCAAN 480
NTTNTNAATT NCCCATGTAC CAGTTTGNTN CAAAGGN 517

SEQ ID NO:872

SEQUENCE LENGTH:517

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00995

SEQUENCE DESCRIPTION:

GATCAGAAAT ACAGATTTTG ATAGCAAAGC GACGTTAGNT NGANGCTCTT GTGAGGAAAG 60
TCATTGGCTT TATCCTCTTT AGAGTTAGAC TGTGGGGTG GGTATAAAAG ATGGGGTCTG 120
TAAATCTTT CTTTCTTAGA AATTTATTTT CTAGTTCTGT AGAAATGGTT GTATTAGATG 180
TTCTCTATCA TTTAATAATA TACTTGTTGA CTAAGAGATA TAAGTNCTGT ATAAANNCNN 240
CCAATTATGT TAAACTAGCA TATCTGCCTT TATTGTGTTT GTCATTAGCC TGAGTAGAAA 300
GGCCTTTAAA ATTTTTTTAG AAAGCATTTG AATGCATTTT GTTTGGTATT GTATTTATTC 360
AATAAAGTAT TTAATTAGTG CTAAGTGTGA ACTGGACCCT GTTGCTAAGC CCCAGCAAGC 420
AATCCTAGGT AGGGTTTAAAT CCCCAGTAAA ATTGCCATAT TGCACATGGT CTTAATGGAN 480

GTTTGAATCT TAAATAAATT GGATATTCAC TTTTAAA

517

SEQ ID NO:873

SEQUENCE LENGTH:515

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00996

SEQUENCE DESCRIPTION:

GATCTGCGAA AGACCAACTT TTAGGCAGTG ATACTTTTCT CCCATTCCCT GGGGTGGGGG 60
 GAGTATGCAG TTGGTGCTTT CTGTAATTCC CTTGTNCTGT TTTGTTTCTG TAAGCTTTTC 120
 CCCTGGTGTC ATGGAAAGGA CTTCTTAAAT AACCACATTG TGGGTGGCTG TATCCAAAGT 180
 TTAATAAATT GGCCAGAAGT GCAGAGTATC CTTTCCTGGA TTCGTGTCAG AAAAGGGCTC 240
 CTTGCCACAA CTGAACCTAC TGTATAAAAA CCTGGCTAGG GAGATTTAAT TTTACTAAAA 300
 TTACAGTTTA ATGTTACCGT CTAGCCACAA ATCAAGCAGC AAAAGCTATT TTGATGATGA 360
 AAGGGGGTCC CGTTGAGCTG GCCATCTAGT GCAGTGTGCT CTCAGATNCC ATGTTTGTGTG 420
 ATTGTGTGCT TCACAAGNCC NTCTCTGGTG CTTGAATTGG ATTTGAATTC TTGGTNAGAA 480
 GNCTCAGCAT CTCCTTGGGG TNGGCTTGGG CCAA 515

SEQ ID NO:874

SEQUENCE LENGTH:514

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00997

SEQUENCE DESCRIPTION:

GATCAGNNA TNAAGTGCAG CAATATCATG AATTCTCAGA AGCCCTTTCA GGGAGCCAGT 60
 NAGTCATACA GTATCCACAG TTGAGTCACT TAAAGATGTC AGTATACGAA ACATTATTCA 120
 CAATCCTTGG GCAATCTCAT TTTTTTTTCC TTCTCCCTC CTCCCTGCC CCCCATACAT 180
 TTNTATCCTT GAGTTAGTTT TGGNGGGGCA GGAAGTACTT AACATCTCAG AAGCTAGATT 240
 GGGAAACATG CTCAGCTATA AGAAGTGAAG TTTAAATTTT GAGTTTAAAA ATGTACATCA 300
 GGAGCAGNTG GGGAGGGTCT TTTTTTTNAA AAAAATCTTT CCAATTTTGG GTTTTCTNTG 360
 CCATATGGCC GTTTTGTAAG TNCTTTNGGG GTTTTNTATT NTTTTNGAAA GTGGNTGAAA 420
 TCTTGTNTG GGNTTTTTTT CCCCAGAAACA TTTNNAATAT AACCCNGTTT ATTTTNNAT 480
 GNAAATTAAG CCTTNTTGG GTAAAAAGGT TAAA 514

SEQ ID NO:875

SEQUENCE LENGTH:513

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00998

SEQUENCE DESCRIPTION:

GATCTTCTAT TAAANTGATT CCTCTTATT AGAGAAGGAA AATTTAGTTG CTATACATCT 60
 TATATTTNCA CAGTTTATTA AAGTCAGTNC CCTAAAGGTA CCTNCTTNC TTTGTGGCAT 120
 ATATGGCATC TNCTGTCTTC AGATTNCTT AACTTTTGT GATTTATAAT GTTAGTGATT 180
 GGTGCCTTAT TCTCTGAGGA AAGATGGAGG GTTCATAAAG CAATGCCTTA TCCACAGCAG 240
 ATTTNCTTGT ATATTAAGTT AAACAGAATT CTGTAAATTA TTATGAAGGG TTCAAGCTCT 300

EP 0 679 716 A1

5 TTAGGGGGAG TTTTTTTTC TTGTTGGTA ACAAATTGGT TGCAATCTNT TATATTCGC 360
AATTGGNTTA GATATTACAG TCTACTTATT TTTNCANGNG TAAATTAATT GTNTAAGGTT 420
TGGGTNNGT ATAAATGGNT AAAATATTAA TATNGTGGGG GGTAAATTT GATTNGGNGT 480
TTTTTTTTT NAAGGCCNNN GGNTTANGG AAN 513

SEQ ID NO:876
SEQUENCE LENGTH:510
10 SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00999
SEQUENCE DESCRIPTION:
15 GATCAGTATG AGANGCAATA CCTAATCCTA TGITGCTATT GTATTTTNC CTAGTTGGTG 60
TGCTTGCTCA GAAAAACATA TACTGTATGT GTATACATAC CTGTGTATAT ATAAAAGGTC 120
AATTTATATA TNTNCCTATA GGGAAATGGA GTAACAAGTT CCCTATCTCC CATATTTATT 180
TGCCCATAGT AAAATGGCCA CATTGATGAT AATTCTAGA ACTAGTTTCT GAGATTGTCA 240
GCCTTTGTC TAAAAAATG GCAGTATTAA TGATTGACTT CTGCACTGC CATAGTTACC 300
20 TGGATTGTCA GCCTNGGTAG CCTTGTCTA AAGTCCTAAA GAGTCCAAA AAAATGTGT 360
TGAAATAATT GCTAAATAGT GGTGGGTGAT TCTNCAGTA GGNATTGTA ATAATTCNT 420
GGCAANAAG GTTATTNCCT GCTATTGGTA TTGGATNATT NGNCTTNTAT NCNGGTATTT 480
TNAAAAGGC AGGNTATAN GGNTNNCCN 510

25 SEQ ID NO:877
SEQUENCE LENGTH:504
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
30 CLONE:HUMGS01000
SEQUENCE DESCRIPTION:
GATCTTCCAT CCTCAAATGA CTCTTTTTC TTTATATGTT AACATATATA AAATGGCAAC 60
TGATAGTCAA TTTTGATTTT TATTCAGGAA CTATCTGAAA TCTGCTCAGA GCCTATGTGC 120
35 ATAGATGAAA CTTTTTTTA AAAAAAGTTA TTTAACAGTA ATCTATTAC TAATTATAGT 180
ACCTATCTTT AAAGTATAGT ACATTTTACA TATGTAATG GTATGTTTCA ATAATTTAAG 240
ACCTCTGAAA CANTCTACAT ATACTTATTA CCCAGTACAG TTTTTTCCC CCTGAAAAGC 300
TGTGTATAAN ATTTATGGTG GATAACCTTT TATGGTTTCC CTTCCAAAG GCCCAGGGTG 360
GGAGGGGGGA TTAAGGGGGC CTAAGGTNTA TGCCTCCNNG GTTTTAAANT TAAATNCCCT 420
40 CNNGGTATTT AAATTANNTT TTCCNANGG TTTNTNGGGG GANTGGGGGG GTTTANANTT 480
GCCTTNTTN GGGGTTTGGG GAAA 504

45 SEQ ID NO:878
SEQUENCE LENGTH:500
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01001
SEQUENCE DESCRIPTION:
50 GATCTGGGCT CTGAGCACAA GTCAGGAAAC ACCAACATAT TCACACTCTC CCAGTAGGTT 60
CCTCAGTCCG ATGGTGAATG GCTATTGTA AATGGCTGGT CTGGCTCTTT GGTGTTGGAG 120

55

EP 0 679 716 A1

5 CCTTTCCAAT AGCCCATGA AAAGAAGCAT CACCCAAGGA TATTGTAAAA AGGATGTAAC 180
 AAGGAGATAG GGTAGACATT GTACTCAGTG GGCCTTGGGG CCTAGCCCAG CTCTGAGCAG 240
 AGGACTGTGG CATTCACTGT CCTTGAAGTGT TTCACCTTCT TGGATAACAC ACGGGCCTTC 300
 TCTTCTGGAT TTCATCAGAG ATTACAGCCA GATGGGGGCT GAAGACCATC CTCTTTGACC 360
 ACAGAGGGTG TGAAGTGGG GAATTCCTCC CAATTTATGG TTTCCNAGGA AAATCTTAGT 420
 TCCTTTTATT TATAGGAATG CATGNCNTT TGGTGTTAAG GAAACCCAAG GGGNANTTAA 480
 NGGGACCANT CCTANTNAAA 500

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SEQ ID NO:879
 SEQUENCE LENGTH:500
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

15

CLONE:HUMGS01002

SEQUENCE DESCRIPTION:

20

GATCTCCAGC CTCCAGAAG CCTGCTGTGC TTTCGTCCA CAGCTTCTG CCCATTGTTT 60
 CTTACTAGTT TCTTGAATTG TNCTTGTGGA CTTTNCCTCA GGGATACATT GGCCTGCAGG 120
 TCCAGTTCA CATGTAGTCC CCTGCTCACC ATTGGAGAAT CAGCTCACTG CTCTCTAGAA 180
 ACGTGGCGTT GGTGAACGGA CCATGCTTCC GTAGCTCTGA CCTGGGCAGC TTGGACCTGG 240
 TCATCCTCTA CTGCCATACC TTTCCCTGGG GGCTTGAACA CAGAACAGGG AGATGGACAA 300
 CCACTTCAAA GAAAGACCCA CCGAATGCAG TTTCTGCTTG ANTGACTGGG NCTGCAGTTC 360
 CNTTNTCTG GGAAGTAGAG GTGGNCAGAT NTANGGCCCC TTTACTCATC CANCTTNGTN 420
 TTCAACTGGN ACTNCCNAAT NANTNAAAGA GCCTNAAATT TAAACTNGN TGTGGATNGG 480
 GNATATGGGA NTAGGGTTGN 500

25

SEQ ID NO:880
 SEQUENCE LENGTH:500
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01003

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SEQUENCE DESCRIPTION:

35

GATCGTCAGC AAGTACTGTA NCTGTAAAGG AAAATCTCTC TCTCTGGAGA ACCCACACAA 60
 ACCATTGACC TGAGTGCAGC TGACAGCCAC TGGNNATNTT TTCTATGATT GAAAATCTGC 120
 CATCGCTGAC TGTGGGCCAG TTTCAAAGGG ACCCATTGTA TACAGGGTGC AAATGTATTA 180
 TACGGATGTT TCCTTTTGT CACTTCATTT TTACAAGTTT TGCTACTCAC AAGCTTTATG 240
 TAGTGGAGGA TAGAGGTATT TTTGGTCTTT AGAAGCTTGT CGGGGTGAGG GCTGCTAACT 300
 TACACTTCAG AGGCCTGTGT CCCAAAGGCC TGGCTGCGTT TGCCGTGCTG TCGAGGACC 360
 TGTGTACACA GGCAGGTGTT CGCCTGCCCG AGCGCGAGTA GCTCTTTGTG TAGTNGGTGA 420
 AAATGCTTGC AGGCATCTGT TTAATTAATA ATTNCCTGCT GTTAAAGNCA GGGGTTAAAA 480
 ATNTCCACAA TTTANGGAAA 500

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SEQ ID NO:881
 SEQUENCE LENGTH:498
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01004

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SEQUENCE DESCRIPTION:

5 GATCAGGATT CAGANGTGA CATCTTCCCC GCAGACTNCC CTACTGAGCC ACCTAGCACT 60
 GCCACGAACC GGTGCGGCTA GGAAAGAAGT AAAATATTTT GCAGAGTCTG ATGAAGAAGA 120
 AGATGATGTT GATTTTGCAA TGNNTAATT AAGTGCCCAA AGAGCACAAA CATTTTTCOA 180
 CAAATATCTT GTGTTGTCCT TTTGTCTTCT CTGTCTCAGA CTTTGTGACA TCTGGCTTAT 240
 TTTAATGTGA TGATGTAATT GACGGTTTTT TATTATTGTG GTAGGGCCTT TTAACATTTT 300
 GTTCTTACAC ATACAGTTTT ATGCTCTTTT TTTACTCATT GAAAATGTCA CGTACTGTCT 360
 GATTTGGCTT NGTAGGAATT GTTATAGGN CTGCCCCTGC ATTAGGCACA GGATTTTAA 420
 10 ATTGTCCATG GGTNCCANC CTACCAGACC CTGCTTTTTT NGNNAATNGG AATTTTNAAC 480
 CATTNANAAA TNGGGAAA 498

SEQ ID NO:882

15 SEQUENCE LENGTH:494
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01005

SEQUENCE DESCRIPTION:

20 GATCTTACTC CACGNATACT TTTTGGTNTG TGAAGGCATC GGTTAAGGGC ACAAAGACAG 60
 CCATGGGGAC ATTTATGTAA ATACGTCTCT AATTGCCACA CTGCAGCTGA ACAGTGTGTA 120
 GTATTTTCCC AGTCAGCTTT GCCATACTGA CGTCAATCAT TTGAGAGAAA TTATTCAGAT 180
 TTNATTTTGG TATCTGTGGT AACAAAACAT TAACCAAAG ATTTNTGTC CAGAAGCCTC 240
 25 CCCGNCCTCC CAAGCTATTT GCTCACATTA ACANATTAAA GTGCCTGAAG CATAATTCAT 300
 TCTTTACCTG TATACTAAAA ACCCTGTTGT ATTGGTTTTT TTTNTAATAA GCCTTTTAC 360
 CTCTGTGTAA ANANATATAT ATACCAGGTG TATGATGGTN CATTTTGGGT CTNNANCTTT 420
 TTTTAAATGG TTTCTAATNT GTNTGNCNA ATGTTGCCNT TGNTTTTANA NTTGTNCCGG 480
 30 GGTNNATTTT TANN 494

SEQ ID NO:883

35 SEQUENCE LENGTH:493
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01006

SEQUENCE DESCRIPTION:

40 GATCTTGATG CTGTGGAAGT AGTTTGAGGA ACATCCTATG AGTTTNCTTA GAATGTATAA 60
 AGGTTGTAGC CCATCCAAC TCAAAGAAAA AAATGACCAC ATACTTTGCA ATCAGGCTGA 120
 AATGTGGCAT GCTTTTCTAA TTCCAACCTT ATAACTAGC AAAAAAGTGT TTGCTTATTC 180
 CACCAGTTCT ACTGTGACAT ACTCGAGTAT AAAGACATGT AGCAATAACG GGGAGTGGGG 240
 GGGGAGTCTC ACAGTGCCCT TGAAGGGGCC CGAAGTTGCC TTAATCTTC CTCAACCAAA 300
 TAAGTATTTT ATTAGTGCTT GAGAGAATCT GGAATGTAGG NTGGGTTCAA CTGCACAAAN 360
 45 GGAAAANGNT TTTTACCACT NTTTTATAT AGNTATAAAG TGNAGCAACC GCCTTAGTGC 420
 CTGAATATGT AGTCCATGAN TATGCCTTGT NTAATTTCCA GAAATTCAN ACCTTGACT 480
 GTTTTTTTTC CCN 493

SEQ ID NO:884

50 SEQUENCE LENGTH:492

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01007

SEQUENCE DESCRIPTION:

GATCAGCACT GCCAGTGGAG ATGGGCGTCA CTA CTGCTAC CCTCATTTC CCTGCGCTGT 60
 GGACACTGAG AACATCCGCC GTGTGTTCAA CGACTGCCGT GACATCATT AGCGCATGCA 120
 CCNNNGTCAG TACGAGCTGN NCTAAGAAGG GAACCCCAA ATTTANTTAA AGCCTTAAGC 180
 ACAATTAATT AAAAGTGAAA CGTAATTGTA CAAGCAGTTA ATCACCACC ATAGGGCATG 240
 ATTAACAANG CAACCTTTCC CTTCCCCGA GTGATTTTGC GAAACCCNCT TTTCCCTTC 300
 AGCTTGCTTA GGATGTTCCA ATTTAGGAA AGCTTAAGGC GGCCTACAGA AAAGGGANAA 360
 ANGGGCCACA AAAGTTTCTT TTTAACTTTT NAGTAAAAAT TAANTTAAAN CAGCAGCAGC 420
 AACCANTTTA AATTGGATTT AANGGTCNN AATTGGAATT NAATTTTTTG GNTTNNNCG 480
 GGNTTTNAAA AN 492

SEQ ID NO:885

SEQUENCE LENGTH:490

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01009

SEQUENCE DESCRIPTION:

GATCGAGTTT NATGCATCAC AGTTAACATG TCAGCTGGCC CTCCAGGCC CCGCCCCCAT 60
 CCCGTCCACG TTGCTGTGTC GTGAGGTGCA GCGGGTCACC CTGTGGCCCG TCCTGTGACC 120
 CATATTTAGC CGTGTGTTGG ACTCCGTGTC TTCAATGGTT TGTTAGTTGC CATTACAAC 180
 TTGTCTGGGT AGAGTTTTTG AGTTTTNCA GTTCAGTATC CCTCTGTCTA TTCACACTTC 240
 GTGTTAGTGG TAACTCAGTT TGTCTTTAA TAGTTACAGA AGGGATACGT CATTTGTNAA 300
 TGCTTTTGTG AAGTGAGTTA AACGAGCTTT CTGTATTTA ATGCTTTAGT GTTTCAGTTT 360
 TATAAGTGAA GATTTTATTT TAAAAACCAG TGGGAAAGAG TGGGGGGTTT CTTTTATGT 420
 CTGGGTCAAT CAGGCAGTAC ATCTGNTTTA AAGCTGAATG TAGGACANTT AATGAAATCC 480
 ANATCTGAAA 490

SEQ ID NO:886

SEQUENCE LENGTH:487

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01010

SEQUENCE DESCRIPTION:

GATCAGCTAT ATACTATTIA TATACAAGTN ATAATACAGA TTTGTAACAT TAGTTTTAAA 60
 AAGGGAAAGT TTTGTCTGT ATATTNNTT ACCTTTTACA GAATAAAAGA NTTACATATG 120
 AAAAACCTC TAANCCATGG CACTTGATGT GATGTGGCAG GAGGGCAGTG GTGGAGCTGG 180
 ACCTGCCTGC TGCAGTCACG TGTAACAGG ATTATTATTA GTGTTTTATG CATGTAATGG 240
 ACTATGCACA CTTTTAATT TGTCAGATTC ACACATGCCA CTATGAGCTT TCAGACTCCA 300
 GCTGTGAAGA GACTCTGTTT GCTTGTGTTT GTTTGTTTGC AGTCTCTCTC TGCCATGGCC 360
 TTGGCAGGCT GCTGGAAGGC AGCTTGTGNN NGGCCGTTGG NTCCGNCCAC TCANTNCTTC 420
 TGGNGCACTG GTTNTNCTT TANAGTTANG GTNCCATGNN NCAAGGGGGG TTCCNANGNG 480
 GAGGN CN 487

SEQ ID NO:887

SEQUENCE LENGTH:485

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01011

SEQUENCE DESCRIPTION:

GATCGCAAAT AACTAAATG TGGAGTGTAG GAACCAAAT GAAACCTGCT GTATGGAAAC 60
 TACTTTCACT TATGGTTCAT TGGTTTTTGT ACCAATATTT TTTATGCACT TCAGTGCAAG 120
 TTTTGTCACT TAACCTTACT TTATGAGTAA GCTAAATAAC CCAAATTACA TTTNTTTAAA 180
 CCTGTTTTAC TACTATGGCA CTTTGATAAA ATGGTCAGGA ACCAACTTTA CTGGCAAAAG 240
 GGTCCATGTA CCACCATGTG CTGGAGCATC TGTCTACAT GTGGATATCT ATGANTGGTA 300
 ATGTTTTCTT TCATGTAAGT GCCTATTCAG AGTTTCAGAA TTTTAAATG CCAAATATTT 360
 TCATGGGTCA TTTGCATGTA GTAAGCCAGA AAATATTCAA NGGGATTTTG GAAAACCAAT 420
 TGGTATTTAA CCAGCCTCAA ATTGTGCAAC CATGGTTGTA TAATAANGGA TTTGGAACCC 480
 GGAAA 485

SEQ ID NO:888

SEQUENCE LENGTH:485

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01012

SEQUENCE DESCRIPTION:

GATCTAATGN CATATTCAA AAGCTCAACA GCAACACCCA GGTAGTTTGT CTGTCAGCCA 60
 CAATGCCTTC TGATGTGCTT GAGGTGACCA AGAAGTTCAT GAGGGACCCC ATTCGGATTC 120
 TTGTCAAGAA GGAAGAGTTG ACCCTGGAGG GTATCCGCCA GTTCTACATC AACGTGGAAC 180
 GAGAGGAGTG GAAGCTGGAC ACACTATGTN ACTTGTATGA AACCCTGACC ATCACCAGG 240
 CAGTCATCTT CATCAACACC CGGAGGNAGG TGGACTGGCT CACCGAGAAG ATGCATGCTC 300
 GAGATTTCAC TGTATCCGCC ATGCATGGAG ATATGGACCA AANGGAACGA GACGTGATTN 360
 TNTGGNANTT TCGTTCTNGC TCTAGCAGAG TTTTGATTTC CANTGACCTT TTGGNCAGAG 420
 GAATTNTTGT TTNNGAAGGT TTTTTTTTAG TCATCANNCT NTTGTCCTTT CAACTATCAG 480
 GGGTN 485

SEQ ID NO:889

SEQUENCE LENGTH:492

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01013

SEQUENCE DESCRIPTION:

GATCGCAACG CCAAAGGTGA AGAACCANCT CAAGGAGACC ACTGAGGCAG CCTGCAGATA 60
 CGGAGCCTTT GGCCTGCCCA TNACCGTGGC CCATGTGGAT GGCCAAACCC ACATGTAATT 120
 TGGNTCTAAC CGGATGGAGC TGCTGGCGCA CCTNCTGGNA GANAAGTGA TGGNCCCTAT 180
 ACCTCCAGCC GTGAATGCNA GATTTTAAGA TTGCCCGGAG GAAGCAAACCT TTTCGTATAA 240
 AAAAAGCAGG CCATCTGCTT AACNTTGGN TCCACCATAA GGCACCTGGA CTNGGATTTT 300
 TNTATCTGAT AGAGGTATTT NTTGTGGCCC TGGGAGCTGT CTGNTTTTCC CCTACCCCCA 360

AGGNTGCCAG GAAGACGTCC ACCATTAGCC ATGTGGNAAC CTTTACTTCT ATGCTTACAA 420
 GTGCCTTTNA GNGAGCCCCA ATTCTGGTTT TNCCACAAAA TAAACCTAAT GCNNTCAGGG 480
 AAAACNNTTA AA 492

SEQ ID NO:890
 SEQUENCE LENGTH:478
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01015
 SEQUENCE DESCRIPTION:

GATCTTGCTT CCAGGCAGCA GCTTGAATTC CCGAATCTNC CTGCAAGCNG CATACAAATG 60
 CAGCGTGAGA ATCCATACAC GTAATCCATA TTCACCTTCC CATCCATCCC GCAGAAGAGG 120
 CATGGTGACA CCCAGGCTAC TGTCATGCT TGAGAGGACG TATTTGAAGG TTCTGTTACT 180
 ACAAGTTGGG AATATTCACG GGCCATGCCT GAATACCCGG NCTGTANCTC ACACNGTGGT 240
 CTGTGTAAGG GGNTACCCTN GGGGCGGCCT GGTTTAATCN TGATTAATAT CTGAAAGCNT 300
 GGGTTNNNTG GGAATGTNA GGGTTTTCTT AATGCCATTA AATTTTTTTT TAGGCNGTAA 360
 AAATTAATAA NCATTTTNTT ATCCAGCAGG CCTCTTTTAT ACCTTTATNG GGAATCTNC 420
 CATACTTACT TTCCGGCCAN NTTTTCAATA ATNAAATTTA TTTTGGAAAN TTTTAA 478

SEQ ID NO:891
 SEQUENCE LENGTH:474
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01016
 SEQUENCE DESCRIPTION:

GATCTTACAC TCTGCTTTTG TCCAAATAAA ATGCAATAGT ATCAATATCA ATTCAGAAA 60
 AATGGACTGA ATATGCTTTT TTGGTGATGA AATCTCATGT ACGATATTTA TAGTGATGTG 120
 CTTTTATTN CTCATGAGAT ACTAAATATT AATTGTGTTG TACATTTGTN CTTAGCATAT 180
 ATTAAGTTT TGAACCAAAT GTGTAAAGC TTACGCTTTG CCATGTAAAT TTCCAGAAG 240
 TTGTTGAGCT CAAATGTATC CTACATCCAG CTGTAGAAAT TTGTCAGAAA TTGTTTAAAT 300
 TTTGTATATA ATTGTACTGT TTAATTCTAG CCATTGCGCT GAACAGTATT TGAGTTACCA 360
 TATAATATGG CTTTACACAA NGGNAATGTG TGGCTTTTGT TTTGGTATTT TTTCCAGTAT 420
 AGGAAGTTCC CTGTGGCCTT ATTTAAATA AAGGTTATTA GGTAAACTG GAAA 474

SEQ ID NO:892
 SEQUENCE LENGTH:473
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01017
 SEQUENCE DESCRIPTION:

GATCACAGCT CACTGCAGGT TCAGCCTTCT GAGTTCAAGC AATCCTTCTG TCTCAGTCTC 60
 CTCAGTAGCT GGGGCTTTAG GTGGGCACTG CCACACCGTA CTAATTTTNG TATTTTTTGT 120
 AGAGACGAGG TCCCACCATG TTGCCAGGC TGGTGTCAAA CTCCTGGGCT CAGTCAGTCC 180
 CCCCATCTCA CCCTCCCCAA GTGCTGGAAT TACAGGCGTG ANTTACTGTG CCCAGCCTTA 240
 CGGACATCCT TTTGAATTAT CTTTTTCACT CATAGAATAT GAATACATTT ATTTAGACTT 300

GCATTCATCG TGAGGGGTCT TTGTCCTCTG TACTGTCTCT CTCCTTGCCC CTAACCCAAA 360
 AAGCTTCATT TTTCTGTGTA GGCTGCACAA GAGCCTTGAT TTGAAGATAT ATTCTTTCTG 420
 ACCAGTATTT AAGGGTTTCC AATAAAATGT ACACCNTCA AA 462

SEQ ID NO:896
 SEQUENCE LENGTH:462
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01021

SEQUENCE DESCRIPTION:
 GATCTAAATC CTCATTTATC TCTNCTATGT CTAGTATTTT ACTGTCACTG GAGGCTCTGT 60
 GGGCTGTCAT AGTTAATTGA CCATAATTAG CAATATACTT TTAAAGTGGG AAAGCTGAAT 120
 GACACTNTTT AAGACAATGA ACATTATCAA AACAAAATGT ATAATTNCTT AATTTGAATA 180
 ATAAATTAGG CGTTAAATG CTATTGTAG TCTTGATATA CAGAAATAAA ATAATTAGGG 240
 TTGGTCTTTT TTATTTTAGG TTGTTTATG TTGAATGTTC TATATCTTAT TAGTTAATTN 300
 GTATATTINA TTAGTATTTN GGGAAATAGC ATATCTGAGA CTGAAGGGGA AATTGGCCAA 360
 TTCACCTATT TGTGGTTTTT TTCTCAGCT ATTCTGAGCT TATTATTAA TTGNATGGCC 420
 TAATGGCTAA CCATTTACAT TAAATGGTT TTTNCCCCA AA 462

SEQ ID NO:897
 SEQUENCE LENGTH:459
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01023

SEQUENCE DESCRIPTION:
 GATCTNCTCT TTCCTCTCCT TTTCTCATT TATTCCTAAA GGAATCTGAC CATTAAAACG 60
 NCTCTACGGC CCAAAAAAAG ACAAAAAATAA AAATTCCTTT TTATTCCTGT CAACTGGATG 120
 GAAACACAAA TTTCATGGAG CTGTGTACCA TCGAAGAAAC CTGGTGTCTG GCATGAAATT 180
 ACTGTAAAGA ACTTCCTGTA AAACACGTTT TTTAACAAC TGAATGAAA AGCATTGGAG 240
 CGTCTGANTG AAAGACGTGA CCTCCTGCTG GGAATCTGAT GGTCTTCAGC ATTCACCTTC 300
 GTGTGTCTTC AGTGTCTCAT TGTATCCCT NGCTTCTGGN TTGGNCCTTA GGAGTNGTTT 360
 GGGATATAAC CTNAAATTGT NGGATGGGTA AANGGGAAT TTNNATGNNG TTTTTTGGT 420
 TTTTAAAAAT NATTTTNAAN NCGGGGTCAN TTTTTTAAA 459

SEQ ID NO:898
 SEQUENCE LENGTH:457
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01024

SEQUENCE DESCRIPTION:
 GATCCACCTG AGCGACCTCC GGGAGTACAG GCGCTTTGAG AAGGAGAAGC TCAAGTCCCA 60
 GTGGAACAAT GATAATCCCC TTTTCAAGAG CGCCACCACG ACGGTCATGA ACCCCAAGTT 120
 TGCTGAGAGT TAGGAGCACT TGGTGAAGAC AAGGCCGTC AAGGCCACCA TGTCTGCCCC 180
 ATCAGCGCGC CGAGACATGG CTTGCCACAG CTCTTGAGGA TGTACCAAT TAACCAGAAA 240
 TCCAGTTATT TTCCACCTC AAAATGACAG CCATGGCCGG CCGGGTGCTT CTGGGGGCTC 300

TTTCTAGAAC TTTCTGTTT TCATGTCTTT GNTTCACCTG GAATTGGGTT TAACACCCTT 360
 TTATAAGTT TGTGGTTTGN AAAATTTCCA TTGGGGCCAT CAATACGGAA ATATATTTGG 420
 TAANATTNGG GGGTTTCNATT TTTTAATTAA AATGGCAAAT GANNGGCAGG AAA 473

SEQ ID NO:893

SEQUENCE LENGTH:473

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01018

SEQUENCE DESCRIPTION:

GATCGGGTTG AGGATTGGGG CTAGCTCGAT NACANTAAGG CCCCAACATC GNGGGACCTG 60
 CTGTGGCGCG GATTCTTAGG AACGCTGTTC TAGCCGGCCC CCTCTCCAGG GGTGCGCGTG 120
 GCCGGCATT A TTTCTAGTT CTCTTGTA CCCTGAGGTG CCAGCGCGGG GAGTGAGGAG 180
 GGGTCAGGGG GCTAAGGATG CAACCTCTGA CGTCTGCGC CTTCTAGGA GAGTCTTACA 240
 TGTNTTGAGA TTTCACAAGC AATGCGAGTT GTAAAATACC AGCTCTACAN GAAGCTAGGC 300
 TCTGTGACGG CATAGTTTTC AGTAGCNTA TCACAATATT CACAATGGAG AATTATATGA 360
 CATGGTAAGC AGAAATAGGC CCCTTTTAAT GNGNTGCTTC TATTTTACCT CANATTGGTG 420
 GNTNTAGGNT AATCANTAAA AATCNATCCA NNGCNTTCA CAACACTNNN AAA 473

SEQ ID NO:894

SEQUENCE LENGTH:468

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01019

SEQUENCE DESCRIPTION:

GATCAGGGGG CCAGGCCAGC AGCTCGGGGG CCACAAGGAG ATGGATAATG TGCCTGTTTT 60
 TTAACACAAC AAAAAAGCCT ACCTCCAAAA TCCCCTTTT GTTCTTCCTG GACCTGGGCA 120
 TTCAGCCTCC TGCTCTTAAC TGAATTGGGA GCCTCTGCCA CTTGCCCGT GTATCCTGGC 180
 TCTCAGCTCA TGGGGAAGCC ACATAGACAT CCCTTTCTTC CTTGCACGC TCGCTAGCAG 240
 CTGGTAAGGT CTTACACCC TGATTCCTCA AGTTTTCTGC TTAGTGGCAC TGACATTAAG 300
 TAGTGGGGGG ACAGTCCATG CCAGGACACC CTGGAGTAGC CTTCCCCTT GGCCGTGGGG 360
 CAGGNCCTAA CTCACTGTCG CTTTGGAGTT GAGGGTGTCT TTTCTTNTT TTTCTTTAGT 420
 TCCTGTATTC TAAACATTAG TAAAAATAAA TGTTTTTTAC ACAGGAAA 468

SEQ ID NO:895

SEQUENCE LENGTH:462

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01020

SEQUENCE DESCRIPTION:

GATCCTGCAG GACTACAAAT CCCTCCAGGA TATCATTGCC ATCCTGGGTA TGGATGAACT 60
 TTCTGAGGAA GACAAGTTGA CCGTGTCCCG TGCACGAAA ATACAGCGTT TCTGTCTCA 120
 GCCATTCCAG GTTGCTGAGG TCTTCACAGG TCATATGGGG AAGCTGGTAC CCCTGAAGGA 180
 GACCATCAAA GGATTCCAGC AGATTTTGGC AGGTGAATAT GACCATCTCC CAGAACAGGC 240
 CTTCTATATG GTGGGACCCA TTGAAGAAGC TGTGGCAAAA GCTGATAAGC TGGCTGAAGA 300

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5 GTCGGGGGGA CAGCTNCACT CTGACTGGCA CAGTCTTTGC ATGGGAGACT TGAGGAGGGG 360
AGGGGNTTNA GGTGGGTGAG GTTAAGGTGC GTGTTTCCTG GTGCAAGTCA AGACCATCAG 420
TCTTATTA AAA AGGTGGGTGC CAATTTTTTT TACNAAA 457

10 SEQ ID NO:899
SEQUENCE LENGTH:457
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01025
SEQUENCE DESCRIPTION:
15 GATCCAGTAT CTTCTCGGC TTTTAGGGA GCAGGAAAAA TCGCTCTNAN AGCAACTTTT 60
TTTAAAAACC TGCCCTGTTG TATATAACTG TGTCTGTTT ACCGNGTGNC CTCCAAGGG 120
GGTGGGA ACT TGATATAAAC GTTTAAAGGG GCCACGATT GCCCGAGGGT TACTCCTTTG 180
CTCTCACCTT GTATGGATGA GGAGATGAAG CCATTCTTA TCCTGTAGAT GTGAAGCACT 240
TTCAGTTTTC AGCGATGTTG GAATGTAGCA TCAGAAGCTC GTTCCTTCAC ACTCAGTGGC 300
20 GTCTGTGCTT GTCCACATGC GGTGGGCGTC TTGGGACCTT GAATGCCTGC CCTGGTTGTG 360
TGGACTCCTT TAATGCCAAT NATTTCTTCA NTTTCTCTTG GGACCCNAG GGNTGCCNGT 420
TNGACAAAGT TTTGGNGAAC NTCCTAATT AAAATGN 457

25 SEQ ID NO:900
SEQUENCE LENGTH:454
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01026
SEQUENCE DESCRIPTION:
30 GATCCGANGA CCACATCAAT GGGCGCGTGC TCTACTATGC CACCTGCAAG TAATGCTACA 60
GCTTCCAGCC CGTTGCCCA CTCATCTGCC GCCTTTGCTT TTGGTTGGGG GCAGATTGGG 120
TTGGAATGCT TTCCATCTCC AGGAGACTTT CATGTAGCCT AAAGTACAGC CTGGACCACC 180
CCTGGTGTGT AGCTAGTAAG ATTACCCTGA GCTGCAGCTG AGCCTGAGCC AATGGGACAG 240
35 TTCACTTGA CAGACAAAGA TGGTGGAGAT TGGCATGCCA TTGAACTAA GAGCTCTCAA 300
GTCAAGGAAG CTGGGCTGGG CAGTATCCCC CGCCTTTAGT TCTCCACTGG GGAGGAATCC 360
TGGACCAAGC ACAAAAATT AACAAAAGTG ATGTAAAANT GAAAAGCCAN ATAAAAATCT 420
TTGGAAAAGA GCCTGGGAGG TTCAACGGGG GAAA 454

40 SEQ ID NO:901
SEQUENCE LENGTH:453
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
45 CLONE:HUMGS01027
SEQUENCE DESCRIPTION:
GATCTTNCTT NTTAAGTGA TAAGACAGTC CCACAGTCCA GCCTAACTAT GGGACAGCTT 60
TACGAGAAGG AAAAAGATGA AGATGGATTG TNATATGTGG CCTACAGCGG AGAGAACT 120
TTTNNANCT GAGGGCCATT GCTGGGCTAG GTGCACCGTA ACTGCTTGTG TATCTTGTA 180
50 ATAGCCAGCC ATTTNCAGT ATTATACCAG AACCTCTTCA CATAGACCTA TTAGTGCATT 240
TGTAAGTGGN TTTATTTCTT AATATATTGG AAGGTTTGT TCCTTAGNCT AGTAAATTAT 300

55

CATACAGNGT TTTATTTTGA GGTTCCTT NNNTGTGCAT TNCCTCATG GCCTGTAAAC 360
 CNCCAGGAAA CCTTTTCCTT CTNGGAAATC ATATTTGAAA TGATAATCN TATATCCGAN 420
 GTGAGGNTAG GNNCCGGGTC CTCCCAATAA ANN 453

SEQ ID NO:902
 SEQUENCE LENGTH:452
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01028
 SEQUENCE DESCRIPTION:

GATCTTAAGT GAAGAAGGAA GACTTGGCCT TTTGTATTGC TTGAATATTA ACTGTCTTGG 60
 AAGGAAGTGA TGCTACAAGA AGTCATACTT TCATAAAATT ATTTGCATCT GTGTCAAATG 120
 CAGTTTAGTC AGAACGTAAG ACATAATAGG TGTGGACATG AACTCTGGAG TGTGAAATAA 180
 AATCCACAGT TACTTAAGCA GTCTGTTTTG ATGGAAAGTA TCTTGGGATA ATACTTTCCT 240
 CTGTGGGATT TTGTTCATTT TAGATGGTGC ANGGNAGTAT CAGTCTTTAA TTTTTTGT 300
 GTTGTTTTGA TCANTCATTT GCTCTGATGG TATGATGCAT GGGCTTCAGG ACTCCAGCTG 360
 CACCACTGTA TAAAACTCAG TTCAGGTTTN CTAGCGGTCN TTGGNTAATT TTCGGGGCNT 420
 ANCCCGATNC CAATTNTTTT TAATGTGNTA AA 452

SEQ ID NO:903
 SEQUENCE LENGTH:448
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01029
 SEQUENCE DESCRIPTION:

GATCAGGGAC CCTCCNGCT TTCCTGGGCC TCTNAGTTGA ACAAAGCAGC AAAACAAAGG 60
 CAGTTTTATA TGAAAGATTA GAAGCCTGGA ATAATCAGGC TTTTNAATG ATGTAATTCC 120
 CACTGTAATA GCATAGGGAT TTTGGAAGCA GCTGCTGGTG GCTTGGGACA TCAGTGGGGC 180
 CAAGGGTTCT CTGTCCNGG TTCAACTGTG ATTTGGCTTT CCCGTGTCTT TCCNGGTGAT 240
 GCCTTGTGTTG GGGTTCTGTG GGTTCGGTG GGAAGGAGGG CCATCTGCCT GANTGTAACC 300
 NGCTAGCTCT CCGANGCCCT ACGGGCCTGN CTNGTGTGAG CGTGTGGACA GTGGTGGCCG 360
 GCGCTGTGCC TNCTCGTGTG GCCTACANTG TNCNTGGCTG TTGAGGCGCT GCTTCANGCC 420
 TGCAACNCGT CCNTNGTCTC ANTACAAA 448

SEQ ID NO:904
 SEQUENCE LENGTH:461
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01030
 SEQUENCE DESCRIPTION:

GATCGGTTTA CAGATGAGGA AGTGGATGAG CTGTACAGAG AAGCACCTAT TGATAAAAAG 60
 GGGAATTTCA ATTACATCGA GTTCACACGC ATCCTGAAAC ATGGAGCCAA AGACAAAGAT 120
 GACTGAAATA ACTTCAAATT CCAGCCAAAC GTTCCTTGTT GCCACTTTGG GTATTCTGAG 180
 ATTTTCTCTT GCATGCCCTT AGCTTTACAG CTTTTCATT TCCTGTTGTA TTTATTCTCA 240
 GCCATTTTGG GCATATGTAT CTTTATAATC AGACTGGAAA CGGGACTTTC TATTAATATC 300

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ATTTTTCAGA ATAAAAATA GGGTAATTTA ACCTACCAGC CCTTCTCCCC CAATAACTGT 360
GGGCCTATAC AGNGTCAATA TATTTTNC AGNGAAAGGT TTATTCGGCT CGATTTTTTT 420
CTGGAANTCC ATAAITTAAC CTTTATGGG TTAAANTTAA A 461

SEQ ID NO:905
SEQUENCE LENGTH:453
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01032

SEQUENCE DESCRIPTION:
GATCAGGGAC CATGAAAAGA AACTTGTGCT TCACCGAAGA AAAATATCTA AACATCGAAA 60
AACTTAAATA TTATGGAAAA AAAACATTGC AAAATATAAA ATAAATAAAA AAAGGAAAGG 120
AAACTTTGAA CCTTATGTAC CGAGCAATG CCAGGTCTAG CAAACATAAT GCTAGTCCTA 180
GATTACTTAT TGATTAAAA NCAAAAAAAC ACANAAAAAT AGTAAATAT AAANCCAAAT 240
TAATGTTTTA TAGACCCTGG GAAAAAGAAT TTTCAGCANN GTACAAAAAT TTANCGCATT 300
CCTTCTTTA ATTTTGTANT TCTTACTGT GGGAATAGCT CAGAAATGCA GTTCTGTTTT 360
ANGTAACAGN NTTGGATAAC TGAGCAGGGN ANCGNAATTT TGGNTTTNTA AAATTCCTTG 420
CTTTNANTAN ANNTTCCCTT NNCCCGGTGG AAA 453

SEQ ID NO:906
SEQUENCE LENGTH:445
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01033

SEQUENCE DESCRIPTION:
GATCCGATGG AGAAGGGGGG ACCCAGGCCA GCAGGAGACA GGACCCCGA AGCTGAGGCC 60
TTGGGATGGA GCAGAAGCCG GAGTGGCGGG GCACGCTGCC GNCTTCCCA TCACGGAGGG 120
TCCAGACTGT CCACTCGGGG GTGGAGTGAG ACTGACTGCA AGCCCCACCC TCCTTGAGAC 180
TGGAGCTGGC GTNTGCATAC GAGAGACTTG GTTNAACTTG GTTGGTCCTT GTNTGCACCC 240
TCGACAAGAC CACACTTTGG GACTTGGGAG CTGGGNTGA AGTTGNTCTG TACCCNTGAA 300
CTCCCAGTTT GCGAATTATA GAGACAATCT ATTTTGTAC TTGCACTGT TATTCGACCA 360
CTGAGAGCGA GATNGGGAAG CATAGATATC TATATTTTA ATTTCNCTAT NGAGGGCCTN 420
GTAAATAAAT TTCTAAAAGC CTAAA 445

SEQ ID NO:907
SEQUENCE LENGTH:444
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01034

SEQUENCE DESCRIPTION:
GATCTCAATG AAATTAAATT AATAACTATA TCTAGAAAAA CTCCCAATAT GTGAATATTA 60
AGCAACATAC TTATAAAAAA TTCATAGTTC ATGGATGAAA TCAAAAGAGA ATTCAAAATA 120
TTTCAAAATA AATTATGATG ATTATATAAN ATGTAGAAAT GTGTGGGATG CCACTACACC 180
AGTTCTTAGA GTGAAATGCA CAGCTTTCAA GGCTTCTGTT AAAAGAGTTG GGAATTACAA 240
AACAAGGAGC AGCGACTGCC AATGGGTGTG GAGTCTTTT TGGGGTGATG ATGAAAATGT 300

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TCAAAAATTG ATTTTATTGA TGGTTACACA CGTCTATAAA TATATTTNAN CGGNAGAATT 360
ATATGGATAT ATATGTGATA TATGGAGGTA TATCCTCTGT AAAATTCCTA NGGGTTTAAN 420
GGAGGATTGG GTATCCACAC CAAA 444

SEQ ID NO:908
SEQUENCE LENGTH:440
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01035

SEQUENCE DESCRIPTION:
GATCCCAGTG TTGCCTTAAC AGGGTGTCTG TCGTGCCGCA GTAGAGCACT GCTGCTTCCT 60
CCAACCCCAA AATTATGTT CCTAAGTAAG TCAGGTCCCT AAGCCCCGTC CCAAGAAGTG 120
ACACAAGTGG CCAACATCCA CACTGTAGGC TTGCAGGCTA CCCGCCCTGA GATTTGGTAA 180
AGAACACTGC CTTGTTCCCC ATCAGTAAAC AAGGTTACCT ACCTCAGGAG GCTGCTTGTTG 240
AGAGAGCAAA TGCAGTATCT TCAGANTGAT TTATTTTTTT ANTAAATTGT AAAGACTTGT 300
GCCATTGGCT GCTCTTTCTA GTCCCTAAN TTTCTGTTCT AGTTTAAANT TTCTCTAGAN 360
CTTGCAATNG TTGGGGGGTT TTTATANTGG TGTTTTTNCA ATGNTTTGTT TCNTTANNNT 420
AAANCCTTAA AAGTTCCAAA 440

SEQ ID NO:909
SEQUENCE LENGTH:439
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01036

SEQUENCE DESCRIPTION:
GATCGGCGTG GGGGTGCTGC TCATCTTCCT TGTCAAGTAC GACCTTAACA ACCNGGACAA 60
GCACGCCAAG CTGGACTTCC TCAACAACCT GGCCACGGGN CTGGTGTTC TCATCGTGGT 120
AGTCAACATC TTCATCACGG CTTTCGGGGT CCAGAAGCCC TTGATGGACA TGGCACCCCA 180
GCAGTAGGAC ACCCAGGACC NTGGATGCTG CTTGCCNNTG CAACTCAGCT GCGCGACCCC 240
AGGAGTCGCC ATACCTGTNA GGTGTCCACC TCCCTGCACA TGGCACTACC CAGANTGCCA 300
GAGCCCAGGC TGGNCTCATC TGCACCATGT CCCCGGACCA GCCCTTGCTC TGANTGCCGG 360
CCAAGNACCA NGTAGGAGGN CACTNTTGT TTNAGCAGN TTTTCCAGG NGGGNAGTTN 420
NNTTCTGGGA AATTGGGGN 439

SEQ ID NO:910
SEQUENCE LENGTH:435
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01037

SEQUENCE DESCRIPTION:
GATCCAAGGA CCCACACTTT GTCACCTCAT ATCTCTCTCT CTCTCCCACT TTCGCTTTCT 60
CTGTCTCTTC TTAGTTCTGC TTTCCTCCAC TGTGCCCTCG CTCTCAGAGA GAGCTCTCCC 120
CTGGCAGTGA CAAGATGGCT GCAGCAGCTC CAGCAACCTC AGAGGACTCC CCCATCCAGG 180
GTCCTTGTA GCTCCTCATC TGTAGGATGT GCAGTAAACA CTCACGTGTC CTTTCCTGAG 240
GAGCCCAGTG GCTGGGGTGG GGGCTGAGGG GCAGCCCCTA TGCCCTCACA GTGCAGCAAC 300

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CTTGGTTAGC TCACCCATCA GGGCAGACTT GGGCAGAAAT CATGTCTTGG CATATTGTTT 360
TGTAATCTGC TTTTAAATT GTCATATAT ATTATGAGCA TTTCCCTATA ATATACAATA 420
TTCTTCCACA TTAAT 435

SEQ ID NO:911
SEQUENCE LENGTH:433
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01038
SEQUENCE DESCRIPTION:

GATCATATGA AAAAGTAACA AGCTGTTCCN TGTTTCTGAT ACATAAAATN ATTTTAAGCA 60
TTTTATCAAT CATTAAAATT TACTGCCAGT TGTGAGTGGC TTTTAAATTA ACTTGCTTTT 120
CATTGCACTT CACTCTGCCT GTTTTCAAGG GGAGTAAGAT TGGTAACATT TGGGGAGACT 180
GTATCTGTCT ACTTAGCGTG GCTGTTTTGA GGGACTGTCC CATCAGTGAA CAAACTGCAT 240
GGCCTTGGAG AGAGACTCTG GGCCTTTGGC TCAGATGTGT TCATCAAATA CTCCTTTCAG 300
AGCTGTTGTG GGTGTAAGTG ACATGATGTG GCCAAAAAT CCAAACTGTG CAGTTGCGNT 360
TGTGACAACC ATGCAATGTG NCTGTAAAAA TTNANTTCA GTTTAAATTN ANATNNTTAA 420
TATTNNGTGG AAA 433

SEQ ID NO:912
SEQUENCE LENGTH:431
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01039
SEQUENCE DESCRIPTION:

GATCTTTCTA ATTCGAAAGC TGTGTTCTTT TTGAATACCG TGCATGGGGG TTAAGCTGAT 60
GTTAAACAG TTTGCAATAA AAAAAAATGA ATNAGCTTAA GTCATTAAAT CATTCAAGT 120
GCATTCTGCA TCCTTTAAAA ATAAGTTTAA GAAATTTAAG AGAATTGTGT TTTCAATTAAG 180
TTTTGCATAT CTTTGTGTTAT GCCATGTAAA TNCCCTTTT CGTATGATTA AAGGAAGGTT 240
ATGATAAAAT GATTAGTTCA TTTACATTCA CTTGTAGCAA TTACATGAGA ATTTGAATTT 300
NGTCGTGTTT GGGTTTGTNC ATTCCTGTGA ATGATGGTNC AGTTAGGTGA GATTNCTGT 360
TATGGNACCC CAACTACCA TTTGGNCCTC TTTAATCTTT GGGGGGTTC AATAAAAAAT 420
GGTCACTNAA A 431

SEQ ID NO:913
SEQUENCE LENGTH:431
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01040
SEQUENCE DESCRIPTION:

GATCCAAANT TTAAGGGATA TTGCCTATTT TGGAAGAATA AAATAAAAT GTTAAACTG 60
TTGAATTACA GAGAACAGAT GACTCTGAG ACATAATTTT AAACAAATAT TAAAAATANG 120
GCAGGTAAAC ATTTGCGTTT AGGCACAATA AATCTGTATT AAAGGGAAGC ACATCAAGGA 180
AATATATACA TGTTGANTAA TGTAACCTNAA AAATATTTTT TAAANCCAC TAAAAATGA 240
NAAATAATTT GATGGGTACT TTAAGCATTG TAGATAGAAA TTAATGTATA ATAGTGCCT 300

EP 0 679 716 A1

CCCNGTCTTT GTATGAAAAN TTAANAANCTC TCTAGTCCTT TAATGAGCAT GANTTTTATA 360
CTTCTACATT TTGTTGCCTA GGNAAAATTN TCCTCNGTA CCTTTGAGGT NATTCGGAT 420
TTTATGGTTT N 431

SEQ ID NO:914

SEQUENCE LENGTH:430

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01041

SEQUENCE DESCRIPTION:

GATCTATAGA GAGAGATATA TACACTTTTG ATTGTTTCT AGATGTCTAC CAATAAATGC 60
AATTTGTGAC CTGTATTAAT GATTAAAGT GGGGAACTA GATTAAATA TTTGTTTTTT 120
AACTAGTTTA TTAGTTTCTN TGGAATCTGC CTGTGTCCT GGGTTGGGT TTTGCTCTTG 180
GCAGCAGCAG GTGCCTCTTG GGTGCTCCTC CTGCTCCTGC CTGCAGCCCT AAGAGCAGGT 240
GGGTGCCGAG TGTCTGGCAC AGCTTGGATG CCGCCCACTG AAGACAGCAG AGGGGGGTTG 300
TNTTGAAGCT CCCGNGACAC AGTCAAGCAT CTTCTGAGNC TTCGATGTCT TCGGNAAGTA 360
AAAAATGGGN TTAGTAAAA CCCTGCCCN GTTTNTCACA GGGGGTTNTT TTGCAAGNNA 420
AANTGATAAA 430

SEQ ID NO:915

SEQUENCE LENGTH:428

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01042

SEQUENCE DESCRIPTION:

GATCAGATTC TAATTTGACA GGCAACCACT CAATGAAACA GACACACCTG CACAGTTGGA 60
AATGGAGGAT GAAGATACAA TTGATGTGTT TCAGCANCAG ACAAGAAGTG TCTACTGNAA 120
AAGGANCCCTG CTTCTTACT CTAGAACTTT GTTCTTATAG ACCAAGATTA CATTCTCAAT 180
TAGAAAACTG CAATTTGGTT CCACCACATC ATGACTATTA CTATAGTATA GTTTTCTCTA 240
TTCTTTTATT TTTCCCTTA CCCATTCCCT TATTGTGACA TAAAATAATG GGTGTATGTT 300
CACAAGCATT TTGCTGGTTT TNAATATTA ANTGGCCAAT GACATCCACT TGATGTCANT 360
CAANACNATA TCTGTGGGGG NAAANTACCG NTTCTNGAA ATTNCTCC NNTTTTCCA 420
TNAGTGGN 428

SEQ ID NO:916

SEQUENCE LENGTH:428

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01043

SEQUENCE DESCRIPTION:

GATCGCCAGG TTCTACAAGC TGCACGAGCG GAGGNTGAG CCCATTGCCA TGACAGTNCC 60
TCGAAAGTCG GACCTGTTCC AGGAGGACCT GTACCCACCC ACCGCAGGGC CCGACCNCTC 120
CCTCAGGCT GAGGAGTGGC TGGGGGGTCG GGATGCTGGG CCCCTCCTCA TCTCCCTCAA 180
GGATGGCTAC GTACCCCAA AGAGCCGGA GCTGAGGTC AACCGGGGCC TGGACACCGG 240
GCGCAGGAGG GCAGCACCAG AGGCCANTNG CACTCCAGC TCGGATGCCG TGTNTCGGCT 300

NNGAGGAGGA GATGCGGGAA GTTCCAGGCC ACGGTGCAGG ANCTCCAGAA GNGGTTNGGA 360
 CAAGGNTTGG AGGAGACAAG TCCAAGNNCA AGTAGNAGCC CCTGAAGGNN TTTNCATCAN 420
 GGTTCAN 428

SEQ ID NO:917

SEQUENCE LENGTH:424

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01044

SEQUENCE DESCRIPTION:

GATCCAATAT TCAATTCATT TGTGTACTCC CACATGCAAA ATGCTAAATT ACAATGCAGA 60
 CATTAGAAA AAGTATTGAC TGGAGGGGTT GAATTCCTTG AGAATTTATT TTATAGTCTA 120
 AATCACAAAT ACTTTACTCA ATTTAGTTTT TAAAATAGTA AACTGAATAT TTTTGTTGTA 180
 AGCCTATCAG AGTCAATCCT TCGTTTGGAA TTGTTTTCTT GTTTNCCTT ACTATAAATC 240
 ATTTAAAAAC TGAATTCATT TTCTTAGATG GCATAAGTCT GTCTCTTGAG AAATAAGTAA 300
 AATACTCCTA TTTTCAGTAT CTGTAGCACC TGAAATAGGT CTTTGTATAG CCAGAANCAA 360
 GTTATGNTTG AAGTTAGCTT TTCTTTGTCA CCAGTTTGG NCAATAAAAA TCTGAANGTT 420
 TAAA 424

SEQ ID NO:918

SEQUENCE LENGTH:422

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01045

SEQUENCE DESCRIPTION:

GATCAACATA ATGGACCACT CCTGAATGAG ACTTAATTTT GTCTTTCAAA TTTACTGTCT 60
 TAAATCAGTT TATTAAATCT GAATTTTAAA ACATGCTGTT TATGACACAA TGACACATTT 120
 GTNGCACCAA TTAAGTGTG AAAAATATCT TTGCATCATA GAACAGAAAT ATATAAAANT 180
 ATATGTNGAA TGTTAACAGG TATTTTCACA GGTITGTTTC TTGATAGTTA CTCAGACACT 240
 AGGGAAAGGT AAATACANGT GANCAAAATA NGCAACTAAA TGAGNCCTAA TAATTGGCCT 300
 TCGATTTTAN ATATTNGTTC TTATAAACCT TGTCAATAAA AATAAATCTA AATCAAAAAA 360
 AANTTGGTTC CACCTNTGCA GGTITTTATA ANTGGTGCCA ATTAAGGTT TTTGTTTTTA 420
 AA 422

SEQ ID NO:919

SEQUENCE LENGTH:422

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01046

SEQUENCE DESCRIPTION:

GATCCTTACT AAGNTTTTCA TGGGAGACTT CCTTCATCAC ATCTTATGTT GAAATCACTT 60
 TCTGTAGTCA AAGTATACCA AAACCAATTT ATCTGAACTA AATTCTAAAG TATGGTTATA 120
 CAAACCATAT ACATCTGGTT ACCAAACATA AATGCTGAAC ATTCCATATT ATTATAGTTA 180
 ATGTCTTAAT CCAGCTTGCA AGTGAATGGA AAAAACNNNC AAGCTTCAAA CTAGGTATTC 240
 TGGGAATGAT GTAATGCTCT GAATTTAGTA TGATATAANG AAAACTTTTT TGTGCTAAAA 300

ATACTTTTTA AAATCAATTT CNTTGATTGT AGGTAATTC TATTGCACT GGGCCTTTCA 360
 ACTCCAGAAA CATTCTGANG GTGGTACTTG GGGTTAANT TAAAAAGGTC CACTTTGGTA 420
 AA 422

SEQ ID NO:920
 SEQUENCE LENGTH:410
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01047
 SEQUENCE DESCRIPTION:

GATCGCTGTT TCCAGAACGG GGAGGAGTAT CTCATTGTGA AACAGACTCT AGAGTGGTTC 60
 TATTGGTCT TCAGTGTITT AGCCTCATTG GTTCATATTT GGCATGCAGC TTGTGGTGAG 120
 TACTGTTCTA GGAAGTGGCA AAAATGGGCA AAATGTATCA CTCCAAACAC TACTGATTCA 180
 GCATTGTTTT CATGTCTTAA AATTGCCACC TGCACITTTGT TTCTGCACTA TTATGTAGTG 240
 CATTTTAACT TAAATTTTTT CCAGCAACAT GTTACTTATT TANGATACAT TACTGATATT 300
 TCATTATAAT TANGTTCATC TTCCCTGTGA AACAAGAGAA TTGTAAAATG TTGTGGGAAA 360
 ATGATACATA TGTGGGATGC TAATGNAAT CATAGGTATT TTTGTGTAAA 410

SEQ ID NO:921
 SEQUENCE LENGTH:409
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01048
 SEQUENCE DESCRIPTION:

GATCACANTT GANCTGGCAG CGGGATGGCG AGGACCAAAC TCAGGACACC GAGCTTGTGG 60
 AGACCAGACC AGCAGGAGAT AGAACCTTCC AGAAGTGGGC AGCTGTGGTG GTGCCTTCTG 120
 GAGAAGAGCA GNGATACACA TGNCATGTAC AGCANGAGGG GCTGCCAAAG CCCCTCACCC 180
 TGAGATGGGA GCCATCTTCC CAATCCNCCN CCCCATCGT GGGCATTGTT GCTGGCCTGG 240
 NTGTCTAGC AGTTGTGGTC ATCGGAGCTG TGGTCGCTGC TGTAATGTGT AGGAGGAAGA 300
 GCTCAGGTGG AAAAGGAGGG AGCTACTCTN AGGCTGCGTG CAGCGACAGT NCCCAGGGCT 360
 CTTAATGTGT CTTNACAGN TTGAAANGCC TGAGACAGCT TGTTTTGTN 409

SEQ ID NO:922
 SEQUENCE LENGTH:407
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01049
 SEQUENCE DESCRIPTION:

GATCCAGGCT GTCATGTGAT TTATGGTGGC ATGTGTTGTG TATTGTTGG CTAATTGTGT 60
 CTTGAAATCT AGAATTATTT CACGCAGAAT TGTCAGTGTG TGTCAGGAAG AGAAAATGGG 120
 CTAGTGGAAG CCCAGTCTTG AGTTCTTGTG TTGTTACCAT TAAAAATTGA CATTTAATTT 180
 TCAAATCACT GTTGGTGCCT AATCACTNAA GTTATTAATT TATTCTGTTG TATTCTTTTT 240
 TTTNAAATNG TAACATATTT ATCCGGTGGG TGGGACAGGA GTGTGTTCAA GTGGGTCATG 300
 TTTTNTCTGT GGTGACACAT GGTACAGGCT TGGAGCTTGC AGGTCCCTTT CTAATTGTTG 360
 TTTGGAGCAG GNCAATTAAA GTCCACTANG AAATNCACCN CTTTAAA 407

SEQ ID NO:923

SEQUENCE LENGTH:411

5 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01051

SEQUENCE DESCRIPTION:

10 GATCCAGGTT CCTCCAGAAA TAAGATATAC AGATTACTTT GTNATTGTAA GTGGAAGTTC 60
TACCCGACAC TTACATGCCA TGGCCTTCTA CGTTGTGAAA ATGTACAAAC ACCTGAAATG 120
TAAACGTGAC CCTCATGTTA AGATAGAAGG GAAGGACACT GATGACTGGC TGTGCGTGGA 180
TTTTGGCAGC ATGGTGATTC ATTTGATGCT TCCAGAAACC ANAGAAATCT ATGAATTAGA 240
GAAATTATGG ACCCTACGTT CTTATGATGA CCAGTTAGCT CAGATAGCAC CTGAGACAGT 300
15 ACCTGAAGAC TTTCATTCTT GGAATAGAAG GTGATACTTN ATCTGTNACT NCANTGGGNG 360
TTAAAATGTG GATTAAATTN TTTTANTGCA NTGNGGTAG TCATTTTCAA A 411

SEQ ID NO:924

SEQUENCE LENGTH:109

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01052

SEQUENCE DESCRIPTION:

25 GATCAGAGCN TATNTTATGA TTGTTGATAA CTAACCAAAG TAGNTGCCTG CAGAGACTTT 60
AAAATGTAAT AAAGATGT ATGCTGCCTG TCAGCTATTC TCATTTAAA 109

SEQ ID NO:925

SEQUENCE LENGTH:405

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01053

SEQUENCE DESCRIPTION:

35 GATCCGAGGC TGGGAAGAAG GGGTTGCCA GATGAGTGTG GGTGAGAGAG CCAAAGTAC 60
TATATCTCCA GATTATGCCT ATGGTGCCAC TGGGCACCCA GGCATCATCC CACCACATGC 120
CACTCTCGTN TTCGATGTGG AGCTTCTAAA ACTGGAATGA CAGGAATGGC CTCCTCCCTT 180
AGCTCCCTGT TCTTGGGTAA GGAAATGGAA TACTGAAGGG CCCTTCACTG CCTTGCTCC 240
TCCCATGTTA TGCCAGCGT TTGATGGGTA GCAGAGAGGA CANANATCAC CACATGGCTA 300
40 TTTTCCCNC TGAATNCTGT CTNGNATTGN GTACCTNTCA AGTGTATTAT GTGNATGCTT 360
TNGAAATGAA AAATTTGGGC NACCTTATGG GNAGGGNGTN GGAAA 405

SEQ ID NO:926

SEQUENCE LENGTH:405

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01054

SEQUENCE DESCRIPTION:

50 GATCTTAAGC AGTAATCTGT CAGTGTGTTGT ATTTGTATTC TCTGCAATTT TACTGTGAAA 60

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EP 0 679 716 A1

AAAAATTGT TTTCAACAAT TGGTGTCAAT TTCTTGATGT CACTATTTGT NGGAGAGTTA 120
AATGGTCTCT NCCCTTTGTG TATCTTACCT AGTGTCTTACT CCTGGGCACC CTTAATCTTC 180
AGAGGTGCTA AATTGTCTGC CATTACACCA GAAGGATGCC TCTGATAGGA GGACAACCAT 240
GCAAATTGTG AAATAGTCCT GANGTTCTTG GATTACTTTA CACCTCAGTA TTGATTTGTC 300
CCAGAATTTN CTGGCCTTNC ATGGCANTGA AANTNTTNGG GGGAAAGATT TAANGTATTT 360
NANTTTTAAN GAGTGTGTTA TAANNATANT TGTACTGNNT NCTNN 405

SEQ ID NO:927
SEQUENCE LENGTH:404
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01055

SEQUENCE DESCRIPTION:
GATCTATGTT ACATTTACCA CACTGAAGTT TTTTTGTG TTTTTGTTT GTTTTAAAG 60
AATCACCTC ATTGTTGAAA GTAAATGTAC TCTTAGGGTG CGAATATTAG TGTTCCAATA 120
AGCATGTGAT TATATTAAGG TGGTGTAGC GGAAGATAA TTCTGATTCC ATTGGGAATC 180
TTAGGTTTTT GTAAATTAT TGGGAAAATA GTTTTCCTG TACTGCTGAA GTTTCTTTTT 240
GGTAAACAGT ATCTTTCTAA AAGAAAAAG CATGAAGGGA GAAATTGAGG TGTGTATACA 300
TTTCTCTCAA TGACCAGCAT TGTATTCGTG AATACTGTGT ATCTTGCACT GAACAGTGTG 360
GAAGCTGTTT ATTTTCAAT CTGAAGTAAA ATACTTTCAA GAAA 404

SEQ ID NO:928
SEQUENCE LENGTH:399
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01057

SEQUENCE DESCRIPTION:
GATCANGTGT AAATGTGACC TTGTACAGTT TACTAAAATT ACTGATATTT TTTACTACAT 60
TGAGACAGTT ACTGTGAGAA TAGGACACAA ACACCAGCTA TTGCCTGCAT CTGGGAAATT 120
GCTGAATCGC ACAGCAGTCA TGTACATAATC AGAAAATTAC TGCCAAATAA TTGTAAATT 180
TGTAAGTAT AAAGTATATA AAGTAGATAC TAAATACAGN CACTTCANTA TTTTGTGAA 240
GCTATTGACT GTACANTTAG ACATTTTCAN ANGGGTGTAA TTTATTTANN GTTGTCTCAT 300
TTTGGTAAAA TTTATGTGAA CTTTAAAGC TAANTATTAA NCCTTAATAT GCTATGTAAA 360
TNTTTCCNT NTATACCATT TNCTGGTGGT NTTTTTTN 399

SEQ ID NO:929
SEQUENCE LENGTH:397
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01061

SEQUENCE DESCRIPTION:
GATCTGCAGA AGGTATCTGG TGATGCAGAG ACTCTTTCCC CGCATCCNTC ACATGAAAGA 60
CCCCATCGGT GACAGCTTCC AAAACGACAA GCTGGTGGTC TGGGAGGCGG GCAAAGCCGG 120
CCTGGAGGAG TGTCTGGTGA CTGAAGTACA GGTCGTGCAG AAAACTTGAG ACTGGGGTTC 180
AGGGCTTGTG GGGGTCTGCC TCAATCTCCC TGGCCGGGCC AGGCGCCTGC ACAGACTGGC 240

EP 0 679 716 A1

5 TGCTGGACCT GCGCACGAGC CCAGGAATGG ACATTCCTAA TGGGTGGTGG GCATGGGAGA 300
 TGCCTGTTTA ATTTGTCCTG AAGCTGCCAA GGAAGAAGAC CAGAACTTTG TGTGTTTATT 360
 TCATGATAAA GTGATTTTTT TTTTTTTTNA ACCTAAA 397

SEQ ID NO:930
 SEQUENCE LENGTH:402
 SEQUENCE TYPE:nucleic acid
 10 TOPOLOGY:linear
 CLONE:HUMGS01062
 SEQUENCE DESCRIPTION:
 GATCCCCAAC AATGTCAAGA CAGCCGTCTG TGACATCCCA CCTCGTGGCC TCAAGATGGC 60
 15 AGTCACCTTC ATTGGCAATA GCACAGCCAT CCAGGAGCTC TTCAAGCGCA TCTCGGAGCA 120
 GTTCACTGCC ATGTTCCGCC GGAAGGCTTC CTCCACTGGT ACACAGGCGA GGGCATGGAC 180
 GAGATGGAGT TCACCGAGGC TGAGAGCAAC ATGAACGACC TCGTCTCTGA GTATCAGCAG 240
 TACCAGGATG CCACCGCAGA AGAGGAGGAG GATTTCCGGT AGGAGGCCGA AGAGGAGGCC 300
 20 TAAGGCAGAG CCCCATCAC CTCAGGCTTC TCAGTCCCT TAGCCGTCTT ACTTCAACTG 360
 CCCCTTTNCT NGTCNCNTCAA GAATTTNGTG TTTTGCTTGC CN 402

SEQ ID NO:931
 SEQUENCE LENGTH:396
 25 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01063
 SEQUENCE DESCRIPTION:
 GATCTGCCGA CCTTGCTATA GATGCCATGT TACCAATGAT TTCCTGTGGT GGGGGCTTGC 60
 30 CATTNTTTAC TCTCTATTT ACCAACTTCT GGCCTAGGCA TGACAGTGGG CACCTTCCCC 120
 CAGCCCTGGN TGGGCCCAGC GCCTNTTTC TGTGTTAGAA AGGTTTATA TATATATAAA 180
 ATTACATATA TATGTAGAAA TATATGTAAT NTTGGGGGCC CTGTTCCCTG CACATTTTAC 240
 AGTTACCTCA TTTTNNCCA TGTATGTATT TGAGAAAATG CTAATATATA GNGAAAAAAA 300
 35 TGGGTCTTAA AAGCTNAAAT GTGNGGTTT TNCCATTCCA GGGGNTCACA TTNGGTTTGN 360
 GGCATNGACN ATACCTNGTA TGTCGNNTA TAAANN 396

SEQ ID NO:932
 SEQUENCE LENGTH:394
 40 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01064
 SEQUENCE DESCRIPTION:
 GATCCGTGGA TTTTGGTGC AATTCCTT TTATTCTTG TCTGAAGAAA GCCTACTGCC 60
 45 TTCTGTTGGG ACCAAAGAGG CCATAGTGCC CATGGAGGT TGGACTTAAG AGATATTCAT 120
 TGGCAGCTCA AAGACTTCCA CCCTGGAGAC CACACTGCAC ACAGTGACTT CCTGGGGATG 180
 TCATAGCCAA AGCCAGGCCT GACGCATTCT CGTATCCAAC CCAAGGACCT TTTGGAATGA 240
 CTGGGGAGGN CTGCAGTCAC ATTGATGTAA GGNCTGTAAA CATCAGCAAG NCTTTATAAT 300
 50 TCCTTNTGCC TAANTTGTA AANGGGGNC TGCATTCTTG TTGGAAGNAT GNACTNTNTT 360
 TNNGGAAAAC CACATTTTAA AAANTTCCCG TAAA 394

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SEQ ID NO:933

SEQUENCE LENGTH:393

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01065

SEQUENCE DESCRIPTION:

GATCCACAGG CTTTGTACT CAACGCTGAC AACAAACCTA AGAGGTAGGT ATCATTATAT 60
 CAACCATTTT ATGAATAAGA AAACAACAGC ACAGAGAGAT GCAGTCACTT GCCCAAGGTC 120
 ACACAGGGCC AGGGGTTGGG CCAGGATTCG AAGCAGGCAG GCTGTCTCCT GGGTCTGAAC 180
 TCTCAACTAC TACACCCTAA TCAAACAATC CCTCTGGTCA AATGTGAGTG ATAATAATAG 240
 TACCCACCTC GTGGGTGTTG AGGGTGAGCC CAAGTTAGCA TTCAGCGTGG GCATGTGAAC 300
 AATTATAGTC AATATTGANT GGAGACCTAT GATGCTTTTA TGAAGGTTTC TATTTTGGGT 360
 TAAAAAATGC ATAAAATTTC TCCTGACCAG AAA 393

SEQ ID NO:934

SEQUENCE LENGTH:393

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01066

SEQUENCE DESCRIPTION:

GATCACCTTA AGTGAAATNA TTTNCCTTTA ATCTTTNATG TATTTATTCA CTTTGGGAAG 60
 CTAGGAATGA GCAACACAAA TTTTACTCTG AAGTCAGAAG AGCTCATATA TAATANTTCT 120
 AATGTCCAC CTATTTTCAC TTGTCCATTC CATGTACCAG CTTAGTTATG ATANNNGTC 180
 ACATAATTAT CTTTGATAAA GGTAGAGGCA CAAAGAGGCA AACTAAGCAA GTCAAATTCT 240
 AATGTGTGTA CTTCATAATA ATTTTATC CATTTTCATC TTTATATTCT GTAACATGAA 300
 NCTTACCTAA TCTTCAAATG TTAGCTTCCA TTTTTCACCT TTGAAATACT TAAATCTTTC 360
 TGGANTAAAT ATAATGGGGC CTNTAAAANT AAA 393

SEQ ID NO:935

SEQUENCE LENGTH:392

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01067

SEQUENCE DESCRIPTION:

GATCCTGTTC TTTCAGCAGG TGAAAAATAA AACGCANTCA AATTCATGG TTTTAATTTT 60
 NAACTCAGAA GCACTCAAAA ATGCAAAATG TGATAATGGG CACTTGTTTA AAAGANTTAG 120
 TGTATCCAGC CTTCACTCCA GCTGGTTAAA AATGTTGCAC TTATCAGCAA CCNNACCACT 180
 TTCATCTGCT GAAAGGNCAA ATGTGCTTGG TTTTACTATT ATGTAATCAC AACTTCTTTT 240
 TNTGCTTGTA GTTGCTTAAA ATTATGTATT TGGTCTNGGG CTGCAATTG GTTTNATGCT 300
 NTATNTGATT ATTACNGCAG TAGGTTGCCT NTCCNGTATG GGAAAAATAA AGTGAATNG 360
 CCCNAATTAA ACCNCCTCTN TCTTAAGGTA AA 392

SEQ ID NO:936

SEQUENCE LENGTH:391

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01068

SEQUENCE DESCRIPTION:

GATCAGGCAG CCTCCTGATG CCAGANCACC TCAGGCAGAG CCTACTCAGC TGTACCTGTN 60
 TGCCTGGACT GTCCCCTGTC CCCGCATCTC CCCTGGGACC AGCTGGAGGG CCACATGCAC 120
 ACACAGCCTA GCTGCCCCCA GGGAGCTCTG CTGCCCTTGC TGGCCCTGCC CTTCCACAG 180
 GTGAGAAGGG TCCTGTCCAC CAGCACACTC AGTTCTNTTC CCTGCAGTGT TTCATTTNAT 240
 TTTAGCAAAN ATTTTGCTG TTNNTGTTNA AACATGATAG TTGATATGAG CTGAACCCCT 300
 GGGTTNGGNG GGAATTGGTC AGAGTGGCAA CCTGGGACTG TGAGCCCTGT TCGGNACAGN 360
 NTATGGATAT GAAAANTCTG NCCNNNGCNA N 391

SEQ ID NO:937

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01069

SEQUENCE DESCRIPTION:

GATCTTTCCC AAGATTGTAA CTGAAAAC TGCTCTCTTG TTTTNTTCGT TTTGGGGGTG 60
 GTGGTGCTGG CTGGGCCATG CTTGTAAAGT GATGTGTGTC TCTGATTAA CGGATTCAC 120
 GTTTTCTCTG CTAATTGAGA GAGCGTTATT TACATTATTT ATTTGTTTGG ACACAAGTNC 180
 TTTCAGTGTT TTATCCTAGC TAATGGCTTC TTAAGGTAA TAAAACCTT CCAACGTAAT 240
 TGGTCAGATA AAACCTTTTT CCTTGATGC TTAATAAAG CAATTAGTGA AGCACTTCTA 300
 TCCAAATGA CTTTTTGTG CTTTTTAAA ACCAATTAC TGTTACTGGA AACTTTGTAC 360
 AATAAGCAA ATCACGCAGA TTAANGGAAA 390

SEQ ID NO:938

SEQUENCE LENGTH:389

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01070

SEQUENCE DESCRIPTION:

GATCAGAGGG AAAGAATGAC CAACCNNGCA ATAAGTGAC TAACTCTAC GCTCTGGTTA 60
 ATGTAATGTA CTCTCCTGGA CTGAATGCAG TGTATAATN CTGTCTACAG CTAGAAGCTG 120
 TGCCCCAGTT CCACATTGA TTACACATGT NAGATTTGCT GCTGTTGCAG TATAAACACT 180
 AGGTATAATA GGATTTGAAA TTGCATTACA GTTCATAAAA NTNGAAAATG AGGAATTAAA 240
 CCNGCAAGTG AACATTTGAA CGNTTATNCT NTCTACATAA GACATGGTTG GGACATCAGT 300
 ACTNACAAGA TGGTTTANGT ATGGTACTAG NGNANTTAAG NTTCTTTCT CTCTGGTTTA 360
 TNGATNGGGT TATTTCCATT ATGTATTNN 389

SEQ ID NO:939

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01071

SEQUENCE DESCRIPTION:

5 GATCTCACGC TGCCTCTGTG GTTCCCTCCC TCATTTTCC TGGACGTGAT AGCTCTGCCT 60
 ATTNCAGGAC AATAATGGCT ATTCTAAACG CTAAGGAAAA AAAACAAACA CAGAACTGTT 120
 TCAAGTACTC AAGACTGACT TACAGACCAA CCAACCACCT TGCTGGAACC CTTGCTAGCA 180
 GGCATTCTTA TAAAAGAAAC TTTCGAGCCT CCTTATATTG CTGGAACTC AGCTGTGCTC 240
 CAGACTAGAG CCTCCTTACC TATGCTATGG ATTTTAAATT TATTTCTCT TATTTATGT 300
 10 ACACTGCTTT TTTTGGTTAC AGTGTATGAT GGATGTGTAT GAAAAAATG TATCTTTGGG 360
 GAACCAATTA CAGTTTGTGTT AATTTGGAAA 390

SEQ ID NO:940

SEQUENCE LENGTH:543

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS01072

SEQUENCE DESCRIPTION:

20 GATCCACACA CGTTGGTCTT TTAACCGTGC TGAGCAGAAA AAAAAACAGG TTAAGAAGAG 60
 CCGGGTGGCA GCTGACAGAG GAAGCCGCTC AAATACCTTC ACAATAAATA GTGGCAATAT 120
 ATATATAGTT TAAGAAGGCT CTCCATTGG CATCGTTTAA TTTATATGTN ATGTTCTAAG 180
 CACAGCTCTC TTCTCCTATT TTCATCCTGC AAGCAACTCA AAATATTTAA AATAAAGTTT 240
 ACATTGTAGT TATTTTCAA TCTTTGCTTG ATAAGTATTA AGAAATATTG GACTTGCTGC 300
 CGTAATTTAA AGCTCTGTTG ATTTTGTTC TGTGTTGATT TTTGGGGGAG GGGAGCACTG 360
 25 TNGTTTATGC TGAATATGA AGTCTGAGNC CTTCCGGTGC TGGGGACCAC ACANGNGTTN 420
 GTTGNAAAGT TTGACCAAGN AGNCCTGCGC ATNNNCTCTG GATGCCTNTG GTATCCATTC 480
 TTNGANGCAA TCCGCTCGGG NCCCGTGGGC CCAATAAANC NGGTATTNT CCCAANGGGG 540
 AAA 543

30

SEQ ID NO:941

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS01073

SEQUENCE DESCRIPTION:

40 GATCTCAAGA TTTCTAAATT GTCAAGATTT ACATGGCATT GTGGTGAAC TAGTTAACAC 60
 TTAGAGCTTT TGGTATGTAA TAACTATTTG CTATGGACTG ATTAAATGTT TCAAAAGATT 120
 GTGTTCTTCA AA 132

45 SEQ ID NO:942

SEQUENCE LENGTH:387

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01074

SEQUENCE DESCRIPTION:

50 GATCAGCACT AAGTCCTGCA TTCCTGTAA AGCCACTTGG GTCATAAGAA GGGAGTAAAA 60
 AATGAAGTCT GACTAGNAAC CTATTGCAGA GGCCAAGTAC ATTTAGTATG GCATTGAGTT 120
 GTGATATAGT TTTACTTTGA TGTGCATTTT GAATTTTCAGC TACACCTAGA TAGACGTAAA 180

55

ATGATAATTA AAATGCTGTA ACCAACTTAT CTAATAAAAT TGGCAACCAG CCACTATTTT 240
 GTTGAATATG AGAAAGTTAA AAGTTTATGT TAATTTTNG GGTCTGATAG AATATTTTCAT 300
 GTGTATTACA GTGGTATTCA TATGCTATGT CTCTAAACTT TATTTTCAA AGCTTANGGC 360
 CCANATACAA NCTTCTCTGG GNNTAAA 387

SEQ ID NO:943

SEQUENCE LENGTH:386

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01075

SEQUENCE DESCRIPTION:

GATCAGANAA AAAGTCCATA TGGACTGTGG ATACCTATCT AAAAGAAGAA AACTGATGGC 60
 TAAGTTTGCA TGAAGTGC ACTTTATTGC AAGTNAGTGT TTCTAGCATT ATCCCATCCC 120
 TTTGAGCCAT TCAGGGGTAC TTGTGCATTT AAAACCAAC AAAAAAGAT GTAAATACTT 180
 AACACTCAA TATTAACATT TTAGGTTTCT CTTGCAGATA TGAGAGATAG CACAGATGGA 240
 CCAAAGGTTA TGCACAGGTG GGAGTCTTTT GTATATAGTT GTAAATATTG TCTTGGTTAT 300
 GTAAANTGG AATTTTTTAG ACACAGTAAT TGAAGTGTAT TCCTGTTTG TATATTTAAT 360
 AAATTTCTTG GTTTTCATTG TTAAA 386

SEQ ID NO:944

SEQUENCE LENGTH:383

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01076

SEQUENCE DESCRIPTION:

GATCTTCTAG CTACCATNCA TTTTCTTCAC TGTTCACAAA AGATGAGTGT GAAATTCAGT 60
 GAATGCTGTT ACTAATCCTG TTACGAGATG AATCTCATTT CACCAAAATT AAATTATGTT 120
 TTTCCGCTAA AATGATGATA CAAGTTGAAG ACACATCACT CTGAAATTGG AAGACCTCAC 180
 CACTTAAGGC TCCACAGTGG CTTACTCAGC TGAAGTCTAG GTTACTACTC TTTACTTTGT 240
 TCACCCATTG GGGGGTGCAG TTTTTTAAA ATGTTGGGAG ATGGCCATTG TAACTACTGT 300
 TGAATGTCTC TGTTTGGGA AGGTATAACA NGAANTAAAA ANGNNTATAT ATGANGGGAG 360
 AGNCTGGTTA TCTCCTCCCC AAA 383

SEQ ID NO:945

SEQUENCE LENGTH:382

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01077

SEQUENCE DESCRIPTION:

GATCTCTCCA TGTACCTGC AGGGGGCTTG GTACTGTGAA ATNAGTAACT TAATCCTGAC 60
 AACCCTAGTG CAAGGTATGG CCCATCTCCT GTACGCTTGG AGCGACCTTT GGCTACGTGG 120
 CTGGCCTTGT TATTTACCA CTCTGGATAT ACTGGAATAG AAAGCAACTT ACATACAAGA 180
 ACAATTAAGT GGAGCAAAGG GAGATATTTT TTTGTGCAGA TTCTGTAAGG GCTGGGCAGA 240
 AATGTGTATG GTCAAAGCCA AGCAGTTCCA TTTACAGCTC TGTTTTTTAC GTAGTTACAA 300
 CATGATGTGA TTGTAGCTTT TTAAGTATG AAACCCCTGA GAGATTGTAC CTTCTAGTT 360

GAAATAAAGT ATTTATAATA AA

382

SEQ ID NO:946

SEQUENCE LENGTH:381

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01078

SEQUENCE DESCRIPTION:

GATCCGAACA CCTCCAGATT CCGGCTTCTA CATGGNNCAG ACGGGGACGC ACAGGCCACC 60
 TTCCTTCTGG CAGGGACTCT TATTATTCC CATTGCTCTA GGGCTTTCNN TTTCCNTTC 120
 TTCCGGTAGG CCGCGTAGAG GCATGCACCG GGTAGGTTTC CGCGGTGACC CCGCGGCGGC 180
 CTGAGGGACG CTCCTGCC CATCCCGCT GTTGGGCTGG GCCGCTTTC CTCTGCTTCG 240
 NCCTGTGCTG TGTTCCTCAG CTTTGTAGCA GCAGCTTGAC AAACCCAGGC GCACTGTACC 300
 AAGGCAATGT AACTTTTAT TTTGGTCAA TTTAAGTTCT TTTTGTACC AAATATTAAT 360
 AAACCAGTTT TGGACTTAA A 381

SEQ ID NO:947

SEQUENCE LENGTH:380

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01079

SEQUENCE DESCRIPTION:

GATCTGAGTC CAGAGTTGGC CACTTTGTGT GGGTCCTCAC AAGCAAAGAG AGCACTAAAC 60
 TTGACATTGG GGGTCCACCA CTCCAACTTT NCTTTCTGAA GGTTTGGTG TACATTGAGC 120
 CCCAGAAGGA AAGGAGAGTA TCTGTGAGTG GGGGCCTCCC TTGACCCAG TACGAAGTCT 180
 ATGCCCTGAA TCCCAGAGT AGCCCTTCCT GTGCCCCAAC TGGCCTGGG ACAANCAGCG 240
 TCCACTACAT CTAGGCTGCC GGCTAAGTGG CACACTTCTT GACCTCCTAC CAGGACTTTG 300
 GTAAAAGCTA GCTTTGGGGA GGGGTGGGT AAATATGAGA GGTGGAGNG CCANTGCTAG 360
 AATAACATGG GTAGACTAAA 380

SEQ ID NO:948

SEQUENCE LENGTH:380

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01080

SEQUENCE DESCRIPTION:

GATCTGCATC AGTTGTAAAG GGAATTGGT ATATTCACAG ACTGTAGACT TTCAGCAGCA 60
 ATCTCAGAAG CTTACAAATA GATTCCATG AAGATATTN NNNCAGAAT TAAAACCTGCC 120
 CTAAATTTA ATATACCTTT CAATCGGCCA CTGGCCATTT TTTTCTAAGT ATTCAATTAA 180
 GTGGGAATTT TCTGGAAGAT GGTGAGTAT GAAGTAATAG AGTTTGCTTA ATCATTGTA 240
 ATTCAAACAT GCTATATTTT TAAAATCAA TGTGAAAACA TAGACTTATT TTTAAATTGT 300
 ACCAATCACA AGAAAATAAT GGCAATAATT ATCAAACCTT TAAAATAGN TGCTCATATT 360
 TTTAAAAATA AGGTTTTAAA 380

SEQ ID NO:949

EP 0 679 716 A1

SEQUENCE LENGTH:399

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01081

SEQUENCE DESCRIPTION:

GATCAAAGCA TGCAATAAGC AATACAAAT ACCAAGCCTT ATACTTAAAA GAAGTTTAAC 60
 ATATTGGTTA ATATACTGGT TAATATACTG GTTAAACATA TTGAATGTAT ATAAGTGGCA 120
 AAAC TAGATT TTTAAGGAAG TGTACATTAT AATATTGGAG CTCAGTACTG CATGANGAGA 180
 CTTCAATAAA ACTAAGAAAN CATTATTTTG GGGAGAAATT TTAGGCATTT AAGANCTTGT 240
 ATTTTCTAT TTTAAAAAGT TAAATTATTC CGTAATTTGG ANGGAAGTTT CGTTGAATGT 300
 AGGCCATAAC CGTTTGANGG GTTTTCCTTT GGANAAC TTG GTGNTTTNG GTGCCCTTAN 360
 TATTTTGGTC CTTTAAATAA AAATGCNCCT GNATTTTCN 399

SEQ ID NO:950

SEQUENCE LENGTH:379

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01082

SEQUENCE DESCRIPTION:

GATCAGGCCC TGGGCCCCC TGCATCTTTT ATAGCAGTGG GTGTCCAGTC CAGGACACTG 60
 GTGCTTTTTT ATACAAGAGA ACGAGCCAGA GTTCACTCCT TCCTCCTGGC TCTCTATATA 120
 CCTGTGAATA TGTGAAATAG TGTAATATG AAAGAACTTG TACCTATCAC TTCAACCCCT 180
 GCCTTGTAACA TAATACTATT CCATCCACAC AGTTTCCACC CTCACCTGCC CCNTCATACG 240
 GAGTTGGATG GGGGCCGAGT NAGGTAACCA GGTGGCATCT ACCNNATGTT TTATAAGGAA 300
 TTTTGTACAG TCTTNGTGAA ATAAATAAC GTGCTTCATT TGNAAAAATN NNGTTNNNTT 360
 TNTNTTNTNT NGNGGGTTN 379

SEQ ID NO:951

SEQUENCE LENGTH:376

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01083

SEQUENCE DESCRIPTION:

GATCTAGTAG AAATAAGGG ATGGGAAAAA CCTTTTCATT TTTCATCTNC TTTCCAACAA 60
 TATGAATTC TTAGTTTCA AACTATACTC AGGAAAGCTG GGCTTTAGGA TTTAACATGT 120
 AGTGATGAGT TCTGTGTGTA TTTAATATT TNACTCAGGA TTCCTATTAA TTGAAAAAAA 180
 TTTTAACTT TTTTATTATA AATCTTTTTT TCAGGGAGGN GATATCACCA AACATGATGG 240
 AACAGCGGGA CAGTCCATTT ATGGAGACAA ATTTGANGAT GAAAAATTTG ATGTGAACAT 300
 ACTGGTCCTG GTTACTATC CATGGCCANT CAAGGCCAGG ATTACCAATA ATTCNTCATT 360
 TTTGTTATAC CACTGN 376

SEQ ID NO:952

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01084

SEQUENCE DESCRIPTION:

5 GATCAAGCCA CCACGTGCCC TACGATGGCC TAACAGGAGT GCCCATTGGC AGATTACACA 60
 TGTAATATG ACCTCAGACA AAAAGGAACC AGAGGCCCAA GGGCAATAAT AAGGTGGAAT 120
 TTNCAGGTCA GCCCAGGAAT TGGCAGAGGA AGTAGGTGTC TGATAACCCT TTGTGGAGAA 180
 TGAGATTCCC CCCACCTGTG TGAGAAAAAT AAACAGCTCT GGAGTCTTGT NCCTGACTCC 240
 AGAGGAACGA GAGCATTCCA GGAAGAGAG ATTCCCTGGA AAATTGAAAA TGTGAATCCT 300
 10 AGGGGGAAAT TGGGGATTGT NTCTTCCCT GTTGAAAATG TTTNGNTGGG AATAAATATC 360
 TTCAGGAACC ATAAA 375

SEQ ID NO:953

SEQUENCE LENGTH:374

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01085

SEQUENCE DESCRIPTION:

20 GATCTTCTNC ACACACCCCA TCACCCAGAT AATTACAGT TCTGTTAACA GTGAGGTTGA 60
 TAAAGTATTA CTGATAAAAA ATTATCTAAG GAAAAAACA GAAATATT TGGTGTGGCC 120
 ATCTTACCTG CTTATGTCTC CTACACAAAG CTAAATATTC TAGCAGTGAT GTAATGAAAA 180
 ATTACATCTT ACTGTTGATA TATGTATGCN CTGGTACACA GATGTCATTT TNGTTGGTCA 240
 CAGCACTACA GTGAAATACA CAAAAATGA AATTCATATA ATGACTTAAA TGTATTATAT 300
 25 GTTAGANTTG ACAACATAAA CTACTGTNGC TTNGAAATGA TGTATGCTTC AGTAAATCA 360
 TATTCAAATN TAAA 374

SEQ ID NO:954

SEQUENCE LENGTH:376

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01086

SEQUENCE DESCRIPTION:

35 GATCAAAGCA AAGAGCGCCT TTCCATGTAT CTCATGAAAG CTGACCTGAT GCCTTTCCTG 60
 TATTGGAATA TNATGCTAAG GGGTTACTGG GGAGGACCAG CGTTTCTNCG CAAGTTGTTT 120
 CATCTAGGNA TGAGTTAAGN ATGGCTCAGC ACTTGCTCAT CTTGGATGGC TTCTGGGCCA 180
 AAAGTGCAGT CACTGAATGA CCAAGAGCAG CACGAAGGAC TTGGAACCTA TCCTTGTAAG 240
 40 GAGTTCCTTG ATGGGTAATG GTGACCAAAAT GCCTCCCTTT TCAGTACCTT TGAACAGCAA 300
 CCATGTGGGC TACTCATGAT GGGCTTGATT CTTGGGAAT ANTAAATTGA AATANTACTT 360
 TTNTTTTCTG AATAAA 376

SEQ ID NO:955

SEQUENCE LENGTH:371

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01087

SEQUENCE DESCRIPTION:

50 GATCAGAACC TCCAAATACT GCCATGAGAA ACTAGAGGGC AGGTCTTCAT AAAAGCCCTT 60

55

5 TGAACCCCT TCCTGCCCTG TGTTAGGAGA TAGGGATATT GGGCCCTCAC TGCAGCTGCC 120
 AGCACTTGGT CAGTCACTCT CAGCCATAGC ACTTTGTTCA CTGTCCTGTG TCAGAGCACT 180
 GAGCTCCACC CTTTCTGAG AGTTATTACA GCCAGAAAGT GTGGGCTGAA GATGGTTGGT 240
 TTCATGTTTT TGTATTATGT ATCTTTTGT ATGGTAAAGA CTATATTNG TACTTAACCA 300
 GATATATTTT TACCCAGAT GGGGATATTC TTTGTAAAA ATGAAATNA NAGGTTTTT 360
 NAANTGGNAA A 371

10 SEQ ID NO:956
 SEQUENCE LENGTH:368
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01088

15 SEQUENCE DESCRIPTION:
 GATCTGGGGA GGGCTAGCCC AAAACCTCCC GCATCGGGCA GGCACCCCT GAAGTACTTC 60
 CTTCAGGGT TCCCTTTGT NAGGGTGTG AGTAGCCTCA CCGGCCTGTN TGGAGGAGCA 120
 GCTGGCTCTG CTCTGAGAAA CTCTGGCAAG TGGACGCCAT TCTNTGCCC TTAGGATTCA 180
 20 CTGCTCTCTC CTACAGCCGC CAGNCCTGGG GTCCTGAAAG ACCTTGGGTG GTAAAGCTGT 240
 ACTTGGTGGG AGTNAGGGCG TGGGGAGGAA CCATGCAAAT CGCCTCCAT GGGTTTTAA 300
 NTGCAGTAAA TAACATTCT GGATGAGACT NGTTTCCAAA NTAAACCNG CTATTATCTG 360
 TTTTGAAA 368

25 SEQ ID NO:957
 SEQUENCE LENGTH:369
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01089

30 SEQUENCE DESCRIPTION:
 GATCCGAGCT CTGGAGCGTG GATACCGGAT GTCTCGCCA GAGAACTGCC CAGAGGAGCT 60
 CTACACATC ATGATGCGCT GCTGAAAAA CCGTCCGGAG GAGCGGCCA CCTTCAATA 120
 CATCCAGAGT GTGCTGGATG ACTTCTACAC GGCCACAGAG AGCCAGTACC AACAGCAGCC 180
 35 ATGATAGGGA GGACAGGGC AGGGCCAGGG GGTGCCAGG TGGTGGCTGC AAGGTGGCTC 240
 CAGCACCATN CGCCAGGGCC CACAACNCGN TTNCTACTT TCCNAGACAA CNACNTCGG 300
 TTTCAGGCCA CAGTTTTCTT CATCTGTCCA GTTGGGGTAG GTTGGGACT TGGNAAAATN 360
 TTTTTTTN 369

40 SEQ ID NO:958
 SEQUENCE LENGTH:366
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01090

45 SEQUENCE DESCRIPTION:
 GATCGAGCCA CTGCACTCCT GGGGCAACAG AGCAAGACTT CGTCTCAAAA TAAATAAATA 60
 AATAAAGTGG CTCTTGGGGA AAAGCAATTT AATGTACCAC GATGAATAGC TAACTGTTCC 120
 50 CAAGTGTTTG CTATGTGCAA CACACCGCGT GAGAGTGTTA CCTGCATTAT TACATTAGGC 180
 TGAGAGGTAA AATAATTGCG CCGAAGACAT ACAGCTAGTG ACGAATGGAC TGATGGTTG 240

55

AACTTAACGT CTATTTGACT TAAGGTCCTG CACCCTGCCA CTTGTAATTT TCAGANTCAC 300
 TGATAATCTG AAATAATGCA GCTTAAACCA TGTTTCTTA ATTAAAAGTA TAATTGGATG 360
 GTGAAA 366

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SEQ ID NO:959
 SEQUENCE LENGTH:364
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

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CLONE:HUMGS01091

SEQUENCE DESCRIPTION:

15

GATCCTGAAG GTGAAATGAA ACCAGGAAGA AAAGGTATTT CTTTAAATCC AGAACAATGG 60
 AGCCAGCTGA AGGAACAGAT TTCTGACATT GATGATGCAG TAAGAAAACCT GTAAAATTCG 120
 AGCCATATAA ATAAACCTG TACTGNTCTA GTTGTITTTAA TCTGTCTTTT TACATTGGCT 180
 TTTGTTTTCT AAATGTTCTC CAAGCTATTG TATGTTTGA TTGCAGAAGA ATTTGTAAGA 240
 TGAATACTTN CCTTTAATGT GCATTATTAA AAATATTGAG TGAAGCTAAT TGTCAACTTT 300
 ATTAAGGATT ACTTTGTCTG CCCACCACCT AGTGTAATAA AAANTCAAGT AATACANTCT 360
 TAAA 364

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SEQ ID NO:960
 SEQUENCE LENGTH:364
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

25

CLONE:HUMGS01092

SEQUENCE DESCRIPTION:

30

GATCTGGGGC CGNCCTTACG GGGCAGGGCT CAGTCCTGAC GCTTGCCACC TGCTCCTACC 60
 CGGCCAGGAT GGCTGAGGGC GGAGTCTATT TTACGCGTCG CCCAATGACA GGACCTGGAA 120
 TGTAAGTGGT GGGGTAGGCC TCANTNAGTC GGCCGGTCAG GGCCCGCAGC CTCGCCCCAT 180
 CCACTCCGGT GCCTCCATTT AGCTGGCCAA TCAGCCCAGG AGGGGCAGGT TNCCCGGGGC 240
 CGGCGTAGG NTTTGCATA ATGTTCTNT CCCNGCGGGT GGGNGCGGGG AAATTCATAT 300
 CCCCTGTTTC GTNTNATGTT GTGTCNNCG NNCCCAAATT TAAAAAGGNA ATTTNAAAAAN 360
 GGTN 364

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SEQ ID NO:961
 SEQUENCE LENGTH:362
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

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CLONE:HUMGS01093

SEQUENCE DESCRIPTION:

45

GATCGAGGGG CGGGGGTCAG CTATGCAGCC CATCACGTGT GTTTTTCATC TGGGATGAAA 60
 AAGCCTGGTT CTCTTTTGAA ATGCTTGATT GTACTTATTG AGCTAAACAA GNCTTGGTGA 120
 CTNNTTGTGA TTTGCCTCAA AAGTTTTAAG TCCTGGGTTT TCAGACTACT GTGTAGCAGC 180
 TGTGTGTTTA ACATACTGTA GCTTTTCTC CCTGGGGGC ACATACAAAT AGGATGTGTT 240
 GATGTGGACT CTAACTGTA ATTTTCCTGT AACTATTTTG GAATGATGCA TATTCTAAT 300
 GTTTGTATA CTGTACAGA GTATTTGCTG TTGGTTGCTT TTTTITTTN TTCANNGGGA 360
 AA 362

50

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SEQ ID NO:962

SEQUENCE LENGTH:360

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01094

SEQUENCE DESCRIPTION:

GATCCAGGCC AAGGCACTGG CTGTNAGTGG CAGAGTTTGG CTGTAACCTT TGCCCCTAAC 60
 ACGAGGAACT CGTTTNAAGG GGGCAGCGTA GATTGTNTNA TTTGCCACCT GGATGAAGGC 120
 AGACATCAAC ATGGGTCAGC ACGTTNAGTT ACGGGAGTGG GAAATTACAT GAGGCCTGGN 180
 CCTCTNCTTT CCCAAGCTGT GCGTTCTGGA CCAGCTACTG ANTTATTAAT CTCACCTAGC 240
 GAAAGTNACG GATGAGCAGT AAGTAAGTAA GTNTGGGGNT TTAACTTGA GGGGTTCCCT 300
 CCTGACTAGC CTNTNTTACA GGANTTGTGG NAATATTAAN TGCAAATTTA CAACTGCAAA 360

SEQ ID NO:963

SEQUENCE LENGTH:358

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01095

SEQUENCE DESCRIPTION:

GATCCAATTT GTAGCTTCCT GCCTGGCTTC AGAGAGCCCA GCAACCTTCT AGGCCTGCTT 60
 TCCAGACTTC TGAGATAGCC TGGGATGAGC AATCCTGTTA TAGTACATCT GGACCTTCCC 120
 TACCTGGGCT CTGGGGAGGC TGTGGGCTG GAGAGGGAAA AGGAGGGAGG GGGTGTCTGC 180
 ACCACCTGGG AAGATAGCAC AAGGCCTAAT GAGGTCACCC TGACTCCCCA CCCCAGCATT 240
 TCATTCATAC CAGATAATAG GTGCATTACT GCCANCTGAC CTTATAACCC TCTGCACCTT 300
 CAAAAGGTT CATGGTTTTT AATTGCTGCT TTTAATAAC ATTTTGTTNA AGNTTAAA 358

SEQ ID NO:964

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01096

SEQUENCE DESCRIPTION:

GATCGGCCCT ACTAAGATGC AGAGACCCCG NCAGAGCTNG CATTGACTAC CAGATTTATT 60
 TTTNAAACCA GAAAATNTTT TAAATTTATA ATTCCATATT TATAATGTTG GCCACAACAT 120
 TATGATTATT CCTGTCTGT ACTTTAGTAT TTTNACCAT TTGTGAAGAA ACATTAAAC 180
 AAGTTAAATG GTAAA 195

SEQ ID NO:965

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01097

SEQUENCE DESCRIPTION:

GATCCAAGAC TGGCTGACTT CATTTGAAAT GGTGAATCT GCTGTGTAAT AAAGTGGTTC 60

EP 0 679 716 A1

AACCATGATT AGGAACTGAA ATTTAGTAGA AGAGGGAAAA GGAGTTAATG TAACAAATTA 120
 TTTTAGCTAC AAACCCCGGT AATAGAGCAC TTGGGGGATG GGATGGGGTG GGTGGTGAG 180
 ACAATCAGAA TGGTAAATTG ATTAATGCT CCTAACCTG TAATTTGTG CATAGAGCAC 240
 CCTATGCTGT GGAAATAACT GTTCTTAGAT TTCATTGTAA CTGGACTGTT CAGGTTGCCC 300
 AGAGGGAAAG ACCATTCTTA ATTCTAATAA AATAACCTTT TATTTTGTTA TTCAAA 356

SEQ ID NO:966

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01098

SEQUENCE DESCRIPTION:

GATCTCCACC ACCATCTCCC CTCTACTTCT CATTCCCTAA CTCTCTGCTG AATATGGGGT 60
 TGGTGTCTC ATCTAATCAA TACCTACAAG TCATCATAAT TCAGCTCTTG AGAGCATNCT 120
 GCTCTNCTTT AGATGGCTGT AAATCTATTG GCCATCTGGG CTTACAGCT TGAGTTAACC 180
 TTGCTTTTCC GGAACAAAA TGATGTCATG TCAGCTCCGN CCCTGAACA TGACCGTGGC 240
 CCCAAATTTG CTATTCCTGT GCATTTTGTG TGTTCCTTCA CTTATCCTGT TCTCTGAAGA 300
 TGTTCCTTGA CCAGGTTTGT GNTTCTTAA AATAAAATGC AGNGACATGT TTAAAA 356

SEQ ID NO:967

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01099

SEQUENCE DESCRIPTION:

GATCTTCCAC AAAACATCTA GCCATCTAAA ATGGAGAGAT GAATCATTCT ACCTATACAA 60
 ACAAGCTAGC TATTAGAGGG TGGTTGGGGT ATGCTACTCA TAAGATTTC GGGTGTCTTC 120
 CAACTGAAAT CTCAATGTTT TCAGTACGAA AAACCTGAAA TCACATGCCCT ATGTAAGGAA 180
 AGTGCTATTC ACCCAGTAAA CCCAAAAAG CAAATGGATA ATGCTGGCCA TTTTGCCTTN 240
 CTGACATTTT CTTGGGAATC TGCAAGAACC TCCCCTTTCC CTTCCCCCAN TAGGNCCATT 300
 TAAGTGTGTG TTAAACANCT ACAGNATACT ANNTAANAAG TTTGGCCAN NCCAAA 356

SEQ ID NO:968

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01100

SEQUENCE DESCRIPTION:

GATCAGATTT TTGGGTCATG TCTGTTGTAT TTTCAGTAAT GTGATTTCAG ATGGTCATCT 60
 GGATTCTCCC ACTTCTCTAC TCCATTATTT CTCTACTTTT CCTTCCAGCA NACCTGANNC 120
 GTGAGGGAGA TGGATTAATG TGAGTAACAG GAATGTGTCT TAAAAAGCT AGAGTGGTTA 180
 CATTTAATCA GGCAGTAAGA TAATTTGGGT TCTTGAGTTG TTTTGGNGTA ATATCCACA 240
 ACTGGGGTAG GAAGCTCAGG ACTTTTTNT TTAAGCTAG TCATTTCAA AGCATATTGT 300
 ATTTTTTTGA NTGACTACAG TATGCCCAAN TTCAANANCC AAANCCCNCT TTGGGN 356

SEQ ID NO:969

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01101

SEQUENCE DESCRIPTION:

GATCCAACAA TTTTNAAGAG CTCTCTCTTA ATCTCTGACA TAATGAGTCT GAAACAAAGA 60
 AAAGTTACCT TACCGTGTCT TTACTTCCTT TCTTCTGGGC TGTGAACTCA AGTGCCTTGA 120
 GGGCCAGCTA AGAGCTTTTT GGGATATTG TCTAACTTAA TTGAACTGTT ACTGAAAGAT 180
 AAATTAACAA AATGGTTCAG AGTTTGGAT TAAGACCTTT GTAACCTAAT GACCGTCAGC 240
 ACAGGAGCTT CGGTTTCCTT CTCTGTAAAA CAGGGCTCCT CATTCCAATT CCACCTATCC 300
 TGTAGCCTTG TGGGAATAAA AGGAGGCACC ACGTGGAGGT GCTTGGCAGG NTGAAA 356

SEQ ID NO:970

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01102

SEQUENCE DESCRIPTION:

GATCATANAA NGGCCATCTG GGCCAGCTN GTGTACAGCG AGGGNGGGCA GCCCCCTCCA 60
 CTCCACTCTG CTCCACAAA GTCGGCTCCC GAGAGCTCGA GGCTGCTTCT TTTTATATGT 120
 GCAGGGCCCG GCGGGGTGAA GGGTCAGAGA GACGGACACA AGGAGCCGGC AGGAGNGCGG 180
 ANCGAGGATG TCCTTTCCCG GGAGACAAGT CGGAAAAGCC TGGCTGGACT GCCTCAGCCC 240
 CGNGTGANTC CTGNCNTNAA GGNTTCCCG TCCTGAGCTC GGGAGATNTT CAGAGTCACA 300
 CTGNCNCCT GTCTTGCCAC GGAGAGGTCA ACTTGCCACC GGNAGTNCNT GGTAN 355

SEQ ID NO:971

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01103

SEQUENCE DESCRIPTION:

GATCCAAACA ATATCTTCAA GGCATTCTTT GCGGGTCCTG GCGGCTTCAN CTTTGANGCA 60
 TCTGGTCCAG GGAATTNNTT TTNCAATTT GGCTAATGAA GGGCAACCAC CCAGAACCCA 120
 GAAATNCAG ATTCACTCAG TTTAATCTTG AATGTGGAAA CAGTTCACCT CCTCCCTTCA 180
 TCACGTCTCC GTGTGCTTAG AGCAGTTTCG TTTTCTCAGT TGGATGCCCT GTGTCTCTGT 240
 GAGTGGGGTG GAGCAAAGGG AACCAATGCC GAAGACCGAG GGCAGGGGAG GGGAGGCGGG 300
 GGTNGGACAG NGAGGCAGCT TGTGAATTTT TGTTTTACTG TTAACTTTA TTAATA 355

SEQ ID NO:972

SEQUENCE LENGTH:352

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01104

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

5 GATCNTAGGC TGGGGCCAAC TGAACCATT GGCAGCTGCA CGCTCATTAC TACCCTCCGC 60
 TCCTGCGCTC TGCCACTGTC CGGAAATTCA TGGTTGGCTA CGAAATGCTT GCTCAGGCTC 120
 AGAGGGACCT CACCCCTGAG CAGGCTGCAG AGAGACTAAG GGCACCTCCT GAGGTTTCATT 180
 ACCACCTGGG GCAGAAGGAC AGGGAGACAG CAACCATCGC CTGACCACGC CGACCACAGG 240
 GCCTTGAATC CTTTTTGT TTCAACAGTC TTGCTGAATT AAGCAGAAAG GGCCTTGAAT 300
 CCTGGCCTGG AATTGGGCA GATATAGCAT TAATAAACT GTGCATCTCA AA 352

10 SEQ ID NO:973
 SEQUENCE LENGTH:358
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01105
 15 SEQUENCE DESCRIPTION:

20 GATCAAGGGG GTTGGGAGGG GGGAAAGAGA CCAGCCTTGG TCCCTAAGCC TCCACNNAAC 60
 GTCTTCTTAA TCCNCACCTT TTCTTACTCC CAAAAAGAA TGAACACCCC TGACTCTGGA 120
 GTGGTGTATA CTGCCACATC AGTGTTTGAG TCAGTCCCCA GAGGAGAGGG GAACCCCTCT 180
 CCATCTTTTT TGCAACATCT CATTCTNCC TTTTGTCTTT GCTTCCCN CN TCACACACTT 240
 GGTTTTGTTC TATCCTACAT TTGAGATTC TAATTTATG TTGAACTTGC TGCTTTTNTT 300
 TCATATTNGA AAAGATGACA TCGGCCCAA GNGCCAAAA NTAAATGGG ANTTGAAA 358

25 SEQ ID NO:974
 SEQUENCE LENGTH:354
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01106
 30 SEQUENCE DESCRIPTION:

35 GATCTTAGGC AAAATACCAG NTGATGAAG CATCTGATGC CTTTCATCTGT TCAGTCATCT 60
 CCAAAAACAG TAAAAAATAC CACTTTTTGT TGGGCAATAT GAAATTNTTA AAGGAGTAGA 120
 ATACCAATG ATAGAAACAG ACTGCCGTGAA TTGAGAATTT TGATTCTTA AAGTGTGTTT 180
 CTTTCTAAAT TGCTGTTCTT TAATTTGATT AATTAAATC ATGTATTATG ATTAAATCTG 240
 AGGCAGATGA GCTTACAAGT ATTGAAATAA TTAATAATTA ATCACAATG TGAAGGTTAT 300
 GCATGATNGT AAAAAATACA AACATTCTAA ATTAAAGGCT TTTGCAACCA CAAA 354

40 SEQ ID NO:975
 SEQUENCE LENGTH:351
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01107
 45 SEQUENCE DESCRIPTION:

50 GATCAGAGCT TGAACACAGG CTTATTTTAA AAANNANAAA TATTTTAAAC ATGGGTTTCC 60
 TTATTGAAAA ATCAGTGTAT TAGTCATAAA ACACCATCAT TAAGAATAAT TGAACAATAA 120
 AGTTTGCTTT CAGATGCAGT TTTCAAATTA TAATCTCATT TCAATTTATA ACGTTCTCAG 180
 TCCTTTGTGA TAATTTTCTT TTTTCATGTA AGTTTAATTA TCTGCATTTA TCTTTTTTCC 240
 TAGTTTTTCT AATACTAATG TTATTCTTAA AAATTCAGTG AGATATAGGG NTAAAAAAT 300
 GCTTTGAGGA GNATGTTTAA TAGGAAATTA AAATACTTT TTCTGGCCAA A 351

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SEQ ID NO:976

SEQUENCE LENGTH:420

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01108

SEQUENCE DESCRIPTION:

GATCCAGAAC ACTTCAAGAA CTCGTCAAAC AGCTCGATAA GCCTTTTNA CTGTNTACAT 60
 CTGTACCGGG AATAACATTC CTAGGCTGAA ATTTCCACAA AGAATAGAAC CTGTACCCAG 120
 TTCTTCAGGC TGATTTCCCT GACCTCTTGG GCATTTGTAT TTGTAGTAAA GTATTGCAGA 180
 GATTCTAAG TTTTTATAG CAGCCATCAA ATTTGGACTT TGTATTGTTT ATTCATAAAA 240
 GACACTTGGT AATAGACTTC AGTGAACCTCT GTATGAATGC AGTAGTGTGC GTGCAAAATC 300
 CGCTTCCTGA GCGTAGGGTG CTGAGCTGGC GCTAGGGCTC GGTGTGTGAA ATACAGCGTA 360
 GGTGAGCCCT TGCCTNAGT GTAGAAACCC ACGGTCTTTA AGGTTCTGGC CTTGGTCCAN 420

SEQ ID NO:977

SEQUENCE LENGTH:349

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01109

SEQUENCE DESCRIPTION:

GATCCTCATG TACTCAGAGG CACTTCCCTC CTAAGTCAA GACCATCCTC ACTGACTATG 60
 TGCCAACGCC TCGTTTCAGG CTTGTNACTC AACAAAGGGC TTTCCATTG ATAGAAGCAG 120
 TTTGGGATTT GTAGTTGCGA CTTCTTCGAT AGTTACCTGC ACGTCCATTG CTGGCAACTG 180
 ACTTGTCAAT AAAACCTGGC TCTTTGGTTA AGGGAGCTAC GCTGTGGTTT ATTCTTAAGT 240
 TACGTGGATA AACTAACCTC TAACAGAAAT ATACTTTGGT TAATTTTGAA ATGTGTCATT 300
 TTTAAACAAT CTTAAAAGTA ATACAGAATT GTGATTTATT AATTTTAAA 349

SEQ ID NO:978

SEQUENCE LENGTH:349

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01110

SEQUENCE DESCRIPTION:

GATCAGAGTG GGTTAAGCTG ACCAGGAACA CCCATTAAAC CCCTTTTCTT TTTTGCTTTC 60
 ATTTTATAAA AGGAAAAGAG GACCTGTCAG ATAGGCAGCC CCATGCTACG TGATTCTTTA 120
 TGTGTGTGTT TTTTGTGTTG TAAATTGTAT AATTTTAAA TATCTGAGTT TTAATAAAAG 180
 AAAAAAGTAC AAAAAATCT TGTATGGCC TTAAGAAGGG NNTAGTGCAT CTTTCAGGGG 240
 TCACTCTGCC ATGGGGATAA AATAGCTGTT TCACAAACAG TTTTATTTAA AAAANCAANN 300
 ACCANNAAN ANTCAAAATN TCATGNAANN TNTTNAACCT TCATTTTNN 349

SEQ ID NO:979

SEQUENCE LENGTH:345

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS01111

SEQUENCE DESCRIPTION:

5 GATCACGTGG GTGTCAGTAT CTTAACGGC CTCATTCTT GGTGTNAGA TTTATTGA 60
 TATGCCCACT CACCCTCGAC GAATCTGCC GCTTTGGGCT GTGGTGCCTG TGTATCTTG 120
 CCCGTCTGGT CTCCAGTTGG TGAATNACC TTTTGTAC TGCCACTTCT CAGCATCTT 180
 NAAATTTGAC ATAATGTTGC TTCATTTCAG TTTTAAAGT TCTGTAATTT GTTGATTGTA 240
 10 TTTAACTATG TNAGTTCTGT TGTNATGTT ACTGTATTGT AAAGCACCTC ATTCATGTNA 300
 TGAGTGCTCT ATAAATCAAT AAATGATGAC TTAGAGGGCT GTAAA 345

SEQ ID NO:980

SEQUENCE LENGTH:344

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01112

SEQUENCE DESCRIPTION:

20 GATCTGCTTG GNGTTTCTN CCCCCACCC CAACTTCTG TCGAGGAGCA AGGCTTGCCA 60
 GCAAGTCAGA AGGATTTGAA CCGAGCAGCC AATCTTTCCA GCCCTCCNT ACCGACCTCT 120
 GTCTGGAGAC GCAGCAGCCT GTGCTCTCCA GGGCCTCTGG TTTGNGTAT TATAGTATAT 180
 TTNGCTGTGG AAAATGTCAC GTTAGTCAC CTTGGAGCCA CTCACCTGGT CCTGTTGTTT 240
 TANCCCATCC CTCTNTNGN GGGCTATTGA TTTNTTCTNA GGAGAGTACA NCGTCACTAT 300
 25 TGTAGNGTAA CCCTGTACTC AATATTACCA TAGNNGNTG NCGN 344

SEQ ID NO:981

SEQUENCE LENGTH:357

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01115

SEQUENCE DESCRIPTION:

35 GATCAGAAAC CAACCATGAA TGAACCCCTG GCTCCTTCAC CACCCCCACG ATTGGTATGA 60
 TGCTGCCGGC ACAGNTGGGA TACACACGGC TCCCCAGGC CTGAGCTGCT TACTAGGGA 120
 ATCTGCCCAC CACCCTGTCT TCCTCTGCAA GTGCTCAGGG AAATGGCCTT NCCGCCGGAG 180
 NCATNCTATC TGNCTGACAG GCTGTGACTC TTCTCTCAAC CTGGCCTTC TCCCCTCTTC 240
 TGAGCTAGTT GGTGAATNN NNGTTAATGC TTAAGATTG TTTTCTCTT TTCACAGCAA 300
 40 CATTTCTTG AATTTTTTC TGCACAGCTT TTCCAAAATA AAAACCTTC AAACAAA 357

SEQ ID NO:982

SEQUENCE LENGTH:340

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01116

SEQUENCE DESCRIPTION:

50 GATCAGAAAT AAGATTGACT TGGGTGTTAT ATTCATCTC TCTCCAGACT CTAGGTATAT 60
 TTCCAACCTT ATATATCACA GTATTTAAAA AGACATGTTT GCATTGAGAA ATTAACCCTA 120
 AAGGGTTTTT AATAGGGTGT AGACCTCCAG TACCTTTGTA ACTAAAGTCT GTCTAGTCAT 180
 NGTAAATATT TATCTGTCAG TTTTGACAGA TTGGGCCAG CTTGATGTTT TAAATCTTCA 240

55

GCCCCGTATG AAAACTTAAA GGTATATATT CANTTTTTTA CCATTTTATG GAAAATATTT 300
AAAAATCTGTT TTTACAGGGT TTTTTTTTTT TTTTTTTTTN 340

5 SEQ ID NO:983

SEQUENCE LENGTH:340

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01117

10 SEQUENCE DESCRIPTION:

GATCTGGTTC GGCTGCTGTC GGATGAGGAC GTAGCGCTCA TGGTGCGGCA GGCTCGTGGC 60
CTCCCCTCCC AGAAGCGCCT CTCCCCTGG AAGCTGCACA TCACGCAGAA GGACAACTAC 120
AGGGTCTACA ACACGATGCC ATGAGCTGAC GGTGTCCCTG GAGCAGTGAG GGGACACCAG 180
15 CAAAAACCTT CAGCTCTCAG AGGAGATTGG GACCAGGAAA ACCTGGGAGG ATGGGCAGAC 240
TTCCTGTNTT TGAGGCTAAT GGACCCGTGG GGCTTGTAAT CTGTCTCTTT CTACTATTTA 300
CATCTGATTT AAATAAACCA TTCCATCTGA AAGGGGCAAA 340

20 SEQ ID NO:984

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01118

25 SEQUENCE DESCRIPTION:

GATCTATGTA TTATTAGAAA AATGAAGTAT TTCTGACATG GAACAAAGAA AGTGGAAGT 60
GGTACTTAAT GGGGAAGCA AAATTAGCTG GGAATAAAC GGACATGTTT TGTTTGTGA 120
ATTCTACCTA AATGTCTCTC TATCCACAGA GAACTAGTA TTAATTGAAG ATGTGAAAGT 180
30 TCCTGTGGTA GCCATACCTT GAAGCACAGT GTTTGTACAT AAGTAAATAT CTTGATTCTA 240
AATTAAATCC AGATTATCT AATATATATN ATTTNATATC TTTGTTGTAT TAAANTGGTT 300
TAATANTCAC TANAANTANN ACATTTTGNA TGTTGGAAA 339

35 SEQ ID NO:985

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01119

40 SEQUENCE DESCRIPTION:

GATCTCAGGA ATTTTGTAG GGGATTGAAG CCAGANCTAG TTGCGTCCCA GGGACCAAGA 60
GAAAGAAGCA GATATCCAAA GGGTGCAGCC CCTTTGAAA GGGGTGTTTA CGAGCAGCTG 120
TGAGTNAGGG GACAAGGGGC AGGTCCCAGG AGCCACACAC TCCCTTCCTC ACTTTGGACT 180
GCTGCTTCTN TTAGCTCCTC TGCCTCTGAA AAGCTGCTCG GGGTTTTTNA TTTATAAAAC 240
45 CTCTCCCCAC CNCCACCCN CCAACTTCCT GGGTTTTCTC ATTGTCTTTT TGCATCAGTA 300
CTTTGTATTG GGATATTAAA GAGATTAAAC TTGGGTAAA 339

50 SEQ ID NO:986

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01120

SEQUENCE DESCRIPTION:

5 GATCCTTTCC GACACACATG TCTGAAGACT TATTTTCAAA GNCAGCACAT TTTTGGAAAC 60
 TAATCTCTTT TCCGTAATAT TTCCTTTATT TCAATGATTC TCAGAAGGCC AATTCAAACA 120
 AACCACATT TAAGGTTCTT TAGGATTATA GAATAAATTG GCTTCTGAGT GTTAGCTCAG 180
 TGAGCTAGGA AAGCACCAAT CGATATTTGT TTCCTTTAGG GATACTTTGT TCTCACCCT 240
 10 GTCCCTATGT CATCAAATTT GGGAGAGATT TTTTAAAATA CCACAATCAT TTGAAGAAAT 300
 GTATAAATAA ANTCTACTTT GAGGACTTTA CCAAGTAAA 339

SEQ ID NO:987

SEQUENCE LENGTH:337

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01122

SEQUENCE DESCRIPTION:

20 GATCCAAAGT GTTAAAAATG CTGAAGTCAT GTCAAGTACT GTCTGGAGGG TTTTTTTAAG 60
 AAAAGGCATT TGGCATTAA CTGTCTCTTG TTTTATTTT AAGTTTTTGG AAACCTTTTG 120
 ACATAAAATG CTGCCAAGTA TCTAAGAAAT GTATATACTG ACAGAAGATA TTTGAAAGTG 180
 GAAAATTGGA AATGAAATAT GTTGCTGGGN GCGTTAATCA CCTCCGCCCA GGATTTAGTC 240
 ACTTGCAGGA CCTCTTTATA GTCTAGGATG GCAGAGCAGA AGATTTTAAT ATGCTTTTAT 300
 25 TAAGTGATGT AAAATAAATG CTTTTTGGAT TATCAAA 337

SEQ ID NO:988

SEQUENCE LENGTH:371

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01123

SEQUENCE DESCRIPTION:

35 GATCGGGCAG CCCCCACCTA CAGCAACATG GAGGAGGTGG ATTAGCAGGT CCCTGGCTGA 60
 TGGGGGGGAC TGGGTTTGGG ACACCCACAC AGNGGGCCAG CTCCTTGCCG CTTCTCCTTC 120
 TCTAACCAG AGGACACTGG CTCTGTCACT GGGAAAGCTGA GGGGTATGAT TTGGGTGTGG 180
 AGACCTCTCA GGTTGGGACT TCTTGTCACT TTGGACCCCT GACCAAGTGG CTTTGGCTTC 240
 TCCAGCCGCC TCCAGTGCTG CGTGATTGA TTCTGTTGTA CCTTCAATTC TTCTGACCCG 300
 40 CATTATAAAC ATTATAATTN NATTCTAAAA ATTGTAATTT TTTTGGCAAT TTTGGAAGTG 360
 ACTGCTGCTG N 371

SEQ ID NO:989

SEQUENCE LENGTH:334

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01126

SEQUENCE DESCRIPTION:

50 GATCTTCTTT ATATTCTACT TGAGTGCTGT CTCCATGTTG ATGTATCTNA GCAGGTTGTC 60
 CACAGGTAGT CTAGGAGGGT GGCAACTTAG AGGTGGGGAG AGAGATTCTC TTATCCAACA 120

55

EP 0 679 716 A1

TCAACATCTT GGCAGATTG ACTCTCAATC TCTTCACTAA AGTTGTAAAG NTCNNCCGGT 180
GATAAGTACT TCAATTTCAA CTTGTAGNNT GGGGAAATTT AGAATTATGC AGNTTATGGA 240
ATTGTATATG ATGACATTG CAATAGGTCT ATTCTCTATC ATTGTAAGAA GNTGTGTGTA 300
CTGGTATTTG NCCCAAGTAA TAANCTAACT GAAA 334

SEQ ID NO:990

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01127

SEQUENCE DESCRIPTION:

GATCTGNCGT GCCCACC AAC TGGTGATGGA AGGTTACAAG TGGCACTTCA ATGAGACGGT 60
GCTCACTGTG TGGTCGGCAC CCAACNACTG CTACCGCTGT GGGCGTGTGG CAGCCATCTT 120
GGAGCTGGAC GCGCATCTCC AGAAAGATTT CATCATCTTT NAGGCTGCTC CCCAAGAGAC 180
ACGGGGCATC CCCTCCAAGA AGCCCGTGGC CGACTACTTC CTGTGACCCC GCCCGGCCCC 240
TGCCNNTTNC AACCCCTCTG GCCCTCGCAC CACTGTGACT CTGNCATCTT CCTNAGACGN 300
AGGNTGGGCG TGGGNGGGNN TGTNCTGGNT NTN 333

SEQ ID NO:991

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01128

SEQUENCE DESCRIPTION:

GATCGGACTG AACAGGAATC CTCGGGGGGT GAACAGCCAT TCCTTCGTGA CCTGTGCACG 60
NCTTCTGCAA CCCTGGAGCT CTGCTCGGCT AGTCTGACTC GAAAAGGGCG TGA CTCAAGC 120
TGACGGGACT CCAGTAGGGA CTTTGAGAGC ACATTTTGTA AAAATATTTA TCTAGACGCA 180
AATGCTTATC CATGAATGTC CTCTTAGACC ATTTGGGGAT GAAGCCATCT TAATAATTAG 240
TAATAATTAA TTAGTAATAA TTAGTAAGCA TTTTCTCAAT GCTCTGATTC CATCATGTTT 300
TCTTAACATG ATAAC TTAAA AAATTGAAA 329

SEQ ID NO:992

SEQUENCE LENGTH:332

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01129

SEQUENCE DESCRIPTION:

GATCCTCCTC AGAAACTACC GGACTTGT TT TCTGTATTGG TGTGTTTTGT ATCTTGCTTG 60
AACTTCCTGT TCTTCTTGGT ATACTTTAAC ATTATNATNA TGTGGGATTC CAAAAGTGGA 120
AGAAATCAGA AGAAATCAG CTAGCTGTAT TCCTAAACAA ATTGTTTCCT AAACAAATGT 180
GAAAATGTGA ACAGTGCTGA AAGGTTTTGT GAACTTTTTG CTATGTATAA NTGAAATTAC 240
CATTTTGAGA ACCATGGAAC CACAGGAAAG GAAATGGTGA AAAGTCATTG TTGTCTACAC 300
AAAATAATG TATATGGAGA CCAAGACCA AA 332

SEQ ID NO:993

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01130

SEQUENCE DESCRIPTION:

GATCAAGAAA TCAGGATGGC CATTATTTA ATATCCATTC ATTCATGTT AGTGGGACTA 60
TTAACTTGTC ACCAAGCAGG ACTCTATTTT AAACAAAATT TAAACTGTT TGTGGCCTAT 120
ATGTGTTTAA TCCTGGTTAA AGATAAAGCT TCATAATGCT GTTTTTATTC AACACATTAA 180
CCAGCTGTAA AACACAGACC TTTATCANGA GTNGGCAAAG TTTTCCAGGN TTCATATACA 240
GNTAGGCTAT NNGNCATGTA TTTTGAAACG CAGTGTTNCA TNATGAAAGN GCTCTCAAGT 300
NGCTTNAAG NTANTTTATT AAANGGGTNN 330

SEQ ID NO:994

SEQUENCE LENGTH:330

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01131

SEQUENCE DESCRIPTION:

GATCCGGGCC TTGCGTGCAG CCTCCCAACC ATGGGCTGGG TTTNGTGCTT ACTGTATGTT 60
GGCGACTTGG NNAGGGCAGG AGACGCAGCG TGGAGCCTAC CTCCCGACAT TCACGCTTCG 120
CCCACGNTGC TCCGACTGGC TGCAGCGGAC ACTGCCCAA GCAGAGGGGA GTCTCAGTGT 180
CCTGCNAGCC AGCCGAACAC TTCTCTCCGG AAGNAGGCTG GTTCGACTGT NAGGTGTTGA 240
CTAAACTGTT TCTCTGACTC GCCCANAGGT CGTGGCTAAA GGCACCTAGG CGNCTTAAAT 300
TTGTAAATAA AATGTTACTA CGGTTTTAAA 330

SEQ ID NO:995

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01132

SEQUENCE DESCRIPTION:

GATCTGAATG ATGATGGAAG CATGCAGACA GCCTCTCAGT CTTACTATTT AATGTTGTAG 60
CTGGGAAAAA ACCCAGAGAG GTTAACTGAT ATACTGGGT GGGACTAGGA TGTGGGTTTT 120
GTNACTCTNA ATCCCATGTC CTCAAACATAC GCTGCCTTCC GAAGTCTGGC ATTTGTNAGC 180
TCATGCTTCC TTGTAGTCCA GCTTCTTATG TGCCTGTAAT ATTCTCCAGT ANGATTGTAA 240
GCCCCTTAAG GGCAGGGACG TCTTTNCATC TCTAGCACTG CTATAGTGTT CTATCCTTAG 300
TTATGGACCT AGATAAATAA NTNGGTGGTG GCAACAAA 338

SEQ ID NO:996

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01133

SEQUENCE DESCRIPTION:

GATCTTTATA TTTNATACTC TAAANTCGTA CAAGCCAATC TNCATTTCNA CTAGTGGAAG 60

5 CTGTATAGCT GGTACATCTT CCAGGACCCT TTTATCAAGA AACAATGCAG CTTCTACATT 120
 TGTNCTGCTT CTACACCAAA ACAGCTGGAA TGTATATNGT ATGGTTCTGG ATGCTCTTGT 180
 ATACCTNACT CTTCAATTCT NACCTAACCC ATGTGCTATG ATTTGAATGT TTCTCCCCTG 240
 CAAAACATCAT GTTGAAATGT AATTGCCATG NTAACAGTAT TANTAGGTGG NNTATTTNAG 300
 NGGTGNTTAG GGTGGGATTG GTGNTGTN 328

10 SEQ ID NO:997
 SEQUENCE LENGTH:326
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01134

15 SEQUENCE DESCRIPTION:
 GATCTTGTGT CTTAGAGAAG CCCCCATACC TGGTAGAGCA TGTACCATCT TACATGCTTA 60
 AATAACTCCA CATTTATTTG TGTATTNAC TCTGTGTTAT AAATATACAT TTGTNGGTCT 120
 CTCTCTTGGA TTTTTFGTT TCTTTGTCCT GTAACACCA CTGAAAGGGT GCAATACAGC 180
 TTTCTTGAAA TGTGTATTGA ACGGATGAAT GTATAAATAA AANTTAAATT TTGTAAATT 240
 20 CTGCTTATNC TTAGAAAAAG AATCTAAATN GTGACAAATC AGAATTGAAA AANGTATTCT 300
 AATAAAGANA AACANGCTTT TATAAA 326

25 SEQ ID NO:998
 SEQUENCE LENGTH:325
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01135

30 SEQUENCE DESCRIPTION:
 GATCCCCAGT GTTGGAGGTG GGACCTAAGT GGCAGGTGTT TGGGNCATGG GGATGGATTG 60
 CTCACAAACG GCTCGGTGGC CTCCTGCAG TAACGAGTGA GTTCACACAC TATTAGCTCA 120
 CATGAAACCT GGTATTAAAA GAGTCTGGGA CCTCCCTCCA TGCTCTCTCT CTGCTCCTT 180
 TCTCTACCA CATCACACGT GGCTCCCCTT GCCTTCTGCC ATGAGTGAAA GCTTCCTGAG 240
 35 GGCCTACCA GACACAGATG CTGGTGTGAT GCTTTTGTG CAGTCTGCAG AACCCCGAGT 300
 CAAATAAACC TCTTTTCTTT ATAAA 325

40 SEQ ID NO:999
 SEQUENCE LENGTH:322
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01136

45 SEQUENCE DESCRIPTION:
 GATCACTTTC AATTGAAGTC AGGGTATTGT GCATAATAGA AAGTATTGGA CTGAGATATT 60
 TGGTTACCAT GGAGGCCAAT GCTTTTTTCA TCTTATTAAG TGTGATGTGA CTTTTNCTT 120
 TGTACAGAAG AGTACTGTAT TTTTGAATAG CCTACTCCA AGTAAGAGCA AATCTGTATG 180
 ATAACATTTT TNCNCTGGA CATAAGACAT AACAGTAACA CGATGTACAT TTACAAGCGG 240
 CCTTATGTAC ATTTCCCAAC ANTCTTTTGA AGGCAAAATT GTGACCATAT GTGTATAATT 300
 50 AAAATCGTTT TTAATCCNTA AA 322

55

SEQ ID NO:1000
 SEQUENCE LENGTH:322
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01137
 SEQUENCE DESCRIPTION:
 GATCTTAGAA ACCTCTGCAC AGAAGCTGCT TTGCTGGCTC TGCAAGAAAA TGGACTAGAC 60
 GCAACTACAG TNAACAAGA GCACTTTCTA AAATCACTTA AGACTGTAAA ACCGTCGTTA 120
 AGTTGCAAGG ACTTGGCTTT ATATGAAANC TTATTTAAGA AAGANGGATT TTCTAACGTG 180
 GAAGGTATTT AAAANTCACC TTAACCTCTT GTNCAGTTCA CATTAAATTGA AATGTGAAC 240
 TGCTGTGCTG TTGCAACTTC ACACCTTTAG AATTGTGTT TATATTTCTT GTANGTGAAT 300
 AAATANANCA NNNCAGNNCA AA 322

SEQ ID NO:1001
 SEQUENCE LENGTH:353
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01138
 SEQUENCE DESCRIPTION:
 GATCTCAGAA CAACCTTTCT TGTTAGTAAC ATATTTTGG CAATACATAN CAACCTGGGC 60
 CTGGTGGATA ACCAACAAGA TGGGGAAGAA AAGNATTGAG AACTTTAAGA GTGGTGTGGA 120
 TGCAGACTCT TCTTATTNA AAATCTTTAA GACAAAACAT GACTGAAAAG AGCACCTGTA 180
 CTTTCAAGC CACTGGAGGG AGAAATGGAA AACATGAAAA CAGCAATCTT CTTATGCTTC 240
 TGAATAATCA AAGACTAATT TGTGATTTTA CTTTTAATA GATATGACTT TGCTTCCAAC 300
 ATGGAATGAA ATAAAAATA AATAATAAAA GATTGCCATG GANTCTTTC AAA 353

SEQ ID NO:1002
 SEQUENCE LENGTH:320
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01139
 SEQUENCE DESCRIPTION:
 GATCTGACCT GGTGAGATTA TTTCTGATGA CCTCATCAA AAATAAACAA TTCCCAATGT 60
 TCCAGGTGAG GGCTTTGAAA GGCCTTCCAA ACAGCTCCGT CGCCCCTAGC AACTCCACCA 120
 TTGGGCACTG CCATGCAGAG ACGTGGCTGG CCCAGAATGG CCTGTTGCCA TAGCAACTGG 180
 AGGCGATGGG GCAGTNAACA GANTAACAAC AGCAACAATG CCTTTGCAGG CAGCCTGCTC 240
 CCCTGAGCGC TGGGCTGGTN ATGGCCGTTG GACTCTGTNA GATGGAGAGC CAATCTNACA 300
 TTCANGTNTT CACCAACNN 320

SEQ ID NO:1003
 SEQUENCE LENGTH:318
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01140
 SEQUENCE DESCRIPTION:

5 GATCCTNCNA GTTAGCCTAG TACTGCTGTA CTGGCCTGTA TGTACATGGG GTCCTTCAAC 60
 TGAGGCCCTTG CAAGTNAAGC TGGCTGTGCC ATGTTTGTAG ATGGGGCAGA GNCATCTAGA 120
 ACAATGGGAA ACTTAGCTAT TTATATTAGG TACAGCTATT AAAACAAGGT AGGAATGAGG 180
 CTAGACCTTT AACTTCCCTA AGGCATACTT TTCTAGCTAC CTTCTGCCCT GTGTCTGGCA 240
 CCTACATCCT TGATGATTGT CCTCTTACCC ATTCTGGAAT TTTTTTTTN GNNGATANNT 300
 ACAGAAAGCA TTTGAAA 318

10 SEQ ID NO:1004
 SEQUENCE LENGTH:320
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01141

15 SEQUENCE DESCRIPTION:
 GATCTTTCTG TCTTCTGGGT TCCATTTTNN AAATGTTTAA AAATATGTTG ACATGGTAGT 60
 TCAGTTCTTA ACCAATGACT TGGGGATGAT GCAAACAATT ACTGTCGTTG GGATTAGAG 120
 TGTATTAGTC ACGCATGTAT GGGGAAGTAG TCTCGGGTAT GCTGTTGTGA AATTGAAACT 180
 20 GTAAAAGTAG ATGGTTGAAA GTACTGGTAT TGTTGCTCTG TATGGTAAGA NCTAATTCTG 240
 TNNCGCCATG GTNCATAATT NCCTATNCAC CTTNCCTNCC CTTTNCAGC CCAATTAAAG 300
 GTTGGGGTCN TAACCTCAAA 320

25 SEQ ID NO:1005
 SEQUENCE LENGTH:315
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01142

30 SEQUENCE DESCRIPTION:
 GATCTGGGGG CTCGAGACTC TGAAGGCAGG GACCCTCTGA CCATCGCCAT GGAAACAGCC 60
 AACGCTGACA TCGTCACCCT GCTACGACTG GCAAAGATGA GGGAGGCTGA AGCGGCCCAG 120
 GGGCAGGCAG GAGATGAGAC GTATCTTGAC ATCTTCCGCG ACTTCTCCCT CATGGCGTCA 180
 35 GACGACCCCG AGAAGCTGAG CCGTCGNAGT CATGACCTCC ACACGCTGTN ACCCGAGGCC 240
 CACGGGGCCG CGCCTGCNTC CCTTCCCCGN NACCGNGCNN TCTGCCATTA AAGCCTCCGT 300
 GCTTCGNTCT TCAAA 315

40 SEQ ID NO:1006
 SEQUENCE LENGTH:315
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01143

45 SEQUENCE DESCRIPTION:
 GATCCCTTGC NTGCCCTCC CTGTGGCAGG GCTAACTGCC TGGCCCTCCT GGCTCGCAGC 60
 CAGCCAGNCC CTTGGCAGCA GGTTCCTCTC AGGGCTTGGN TCTTCAACCT GTGGCGACAG 120
 GAGGCAGGGC AGACTGTGGA GGACAGGATG CAGGTCAGGG AGAGGGAAGG CAGGGGTGGA 180
 CCGCCATGAG CATGAAAAGC CCGAAGCAAG TTGACTCTTN AATTGCAAC TGTATGNTC 240
 50 TGAAAATGAG AACGATGTAT CAANTTGATG CANTTTNGAT GTTGTACTTA CAATAANGTT 300
 TTAATGTGTN TTAAG 315

55

SEQ ID NO:1007

SEQUENCE LENGTH:315

SEQUENCE TYPE:nucleic acid

5

TOPOLOGY:linear

CLONE:HUMGS01144

SEQUENCE DESCRIPTION:

10

GATCTGAGGN CAGGANTTAA ACCACAGAAT GTATNTGCCT GTAAAGCACA GGGGAAGAAA 60
CGACTCATTA GAACTACACC TGTACATAC CATTGGGTAA ATGNTTTAAG NGGGGAATGG 120
TGTGACAAAC CTTCAAAAAA NATGAACACC TTAATGTTCA GGAAGTGAAGC TAACTCCCTA 180
TGNTTAGGCA CAGCTTGATA CGAGCGGAGA CTTGGCAGTC AATTCCANGT CTTTATACT 240
NATTACCTCA TCGTNACTGT NAGTGCAACT ATAGTCTGTT GTNGGAATT GGNCATCCCT 300
TAGTNTCNGA TGGTN 315

15

SEQ ID NO:1008

SEQUENCE LENGTH:314

SEQUENCE TYPE:nucleic acid

20

TOPOLOGY:linear

CLONE:HUMGS01145

SEQUENCE DESCRIPTION:

25

GATCAGAAAA AACAGAAGCC AAACCTCGGG TCATCTTTGT TTTTAAAGCT GAAGTGGGAC 60
TGTCTGGCAC TCTGTGTATT TATGCGTTCC AGCATCTGGA ACCTCCCATC CCTGCCCTCC 120
TCCTGTGTAG CTGCCACCTC CCCGCTGGGC CCAGCATGGC TCACCTGTCC CGTGGGCTGT 180
GTTTCTTGTT GTTTTCTCT TTGCAAAGAC ATAGCTAGGA AAGCGAATGA TAAGGGAAAA 240
GTTCTCAGGG AATTGAAGTG TTGTTGCTAT GGTGACGTCC TTTTGCTGTG AATAAAGGTG 300
CTCTTTGCAG CAAA 314

30

SEQ ID NO:1009

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

35

TOPOLOGY:linear

CLONE:HUMGS01147

SEQUENCE DESCRIPTION:

40

GATCCACAAT AGTGGCATGA GGCAGGCGAC TGTNTGTNAC CTCTATGTCC GCAGAGTCCA 60
GCACGCTAAC AGCTGGGAGA TAAAAGCAGT GGAGAGGGCT GTTGGGGGAC ATGCCATGGA 120
AACTACCTAG GACCTGTTCC CTGAGTTAAC ATTCTAGCCT CATCTACTTG TTTTGGCCCT 180
GCAGCTCATA TACANACTGG CCCACCATTT ACGNACCATC CCCTCAAGTA ATCTTAAAGG 240
TTCTCAGCCC ANACANATTA ACTGTTCTGA CCCACCTNC TTAATAAACA ATCCTGGGNT 300
CAGCCATNTG AAA 313

45

SEQ ID NO:1010

SEQUENCE LENGTH:311

SEQUENCE TYPE:nucleic acid

50

TOPOLOGY:linear

CLONE:HUMGS01148

55

SEQUENCE DESCRIPTION:

GATCTGGCAG TTGAAAATTG TGGGAAAGAG AATTTGTATG GGCAGTGTAT CTATGAAATA 60
 CCTCATAACT TACGTTTACA TGTTTTCTA ACTTTTNGTA TTTTCNTNGT ATAGCCACCT 120
 AGAGAATTCT TCATAGATTA AGAACTACAG TTTTNACCAC TTAACATAAG TAAACAAAAG 180
 TCCTTCATAA TTNAACCATT AGCATCTTTG GCCAAACCAA AATAAAGANA AGCATCTNCT 240
 CCTAGTTGTG TGTGGGCAAC AGANACANGT TAAGGNAACA NAAATACTTA TATATACACN 300
 GANCANANGT N 311

SEQ ID NO:1011

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01149

SEQUENCE DESCRIPTION:

GATCTCCCTT GGTCTTCCAT GGGATGGTTA GTGTGGAGGG GAGATATAGA TTGTCCGGCC 60
 GNTTTGTGAT TCCATGGGAT TGATTGAGTC TTCTGGATT TTTTNCNTGT ATATTNNGG 120
 TACTGGAGCT TTTAAAAATG CTTGGNTTCA GGTATTTTNA TTCATGTGAA GTGTATATGA 180
 TTCTNTGAG ATAAGGTTTT AAGCTAAAT GTNACTCCCT GNTTNAGCNT CTGAACCCTG 240
 ACAGATTNAC AGGGACTTTG CTGGTGTAGG CTTTTTAAAG GGNTTANTAN TCCACTTTGA 300
 GCCTNAAA 308

SEQ ID NO:1012

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01150

SEQUENCE DESCRIPTION:

GATCTGGAGT TACCTGAGGC CATAGCTGCC CTATTCATT CTAAGGGCCC TGTTTTGAGA 60
 TTGTTTGTTC TAATTTATTT TAAGCTAGGT AAGGCTGGGG GGAGGGTGGG GCCGTGGTCC 120
 CCTCAGCCTC CATGGGGAGG GAAGAAGGGG GAGCTCTTT TTNACGTTGA TTTTNTTTT 180
 TCTACTCTGT TTTCCCTTTN TCCTTCCGNT CCATTGGGG CCCNGGGGGT TTCAGTCATC 240
 TCCCCATNTG GNCCCCGGA CTGTCTTNGT TGATTCTAAC TNGNNNGGA AAGAAANTAT 300
 TATTCAAA 308

SEQ ID NO:1013

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01151

SEQUENCE DESCRIPTION:

GATCCATGGG GCCGCAATGA AGCTTGGAGA TACATGGGTG GCTTTGCAAA GAGTGTTC 60
 TTTTCTGATG TATTCTTTAA AGGATTCAAA TGGGGATTG CTGCATTTGT GGTAGCTGTA 120
 GGAGCTGAAT ATTACCTGGA GTCCTGAAT AAAGATAAGA AGCATCACTG AAGATAATAC 180
 CTGGAAGCAT CATAGTGGTT TCTTAACTCT CCAAATAAG ATTCTTCTC TGTAGCCTAC 240
 TTGTCTGGTT TATCCCTTAC AGAATATTAG TAAGATTAA TCAATTAAAA TATATATATA 300

TGCCAAA

307

SEQ ID NO:1014

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01152

SEQUENCE DESCRIPTION:

GATCGGTCCA CGAAAGTTAG CCCATATGTA TATCTTGAAT AGTATAGGGG AGGGTATTCA 60
 TAAAGTCCTT ATGTGGTTTT AACTAAGTGA AATTATGGAC AAGAGAANNN NTTGTAAAAT 120
 CGTCTTAAAG GCAAATTAA TTTNACTCC TGTTTATGGG ACATTCGTTC TATTAAGTGT 180
 CAGACACAAT TTCTGTTTTT ATCTGAGAGC CAGTTTTCTT TTATTTCTAC ATCTAAAATA 240
 AGANCATATT GTACACTATT ATATAATACA GAATTGTCTT AAACTTAAT AAATTCGCAT 300
 TTAAA 306

SEQ ID NO:1015

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01153

SEQUENCE DESCRIPTION:

GATCTCAGCA GTGGGGCAGG AGGGTGCCTG ATTCGGGGA GTCCTGACCC GAGCCTGTTG 60
 TCAGAGTTGG GAGGGGCTCT GAGCAGTGTG GGGCAGGCCG GGTCTCCCAT CCCGAGGCCA 120
 GCCTTCCTGT GCAGAGCCCC ATCCACTGGT TCTTGCCCTG AGCCACATAT GTCTGTNCCA 180
 TGGGCTGAGT GCCACGACAG GCGCGTGTGA CAGCTGCTGC CCACGCATNT NGAAGCTAGG 240
 TGGGACTCAT TCCTAATTCT GCGCTTGTA TGAAGCTGA TTAACACACC GCCACTTTTT 300
 TGCAAA 306

SEQ ID NO:1016

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01154

SEQUENCE DESCRIPTION:

GATCAACAAG AAATGTTATG AAATGGCCTC CCACCTTCGG CGTTCCAGT ACTGACCTCG 60
 TCTGTCCCTT CCCCTTCACC GCTCCCCACA GCTTTGCACC CCTTTCCTCC CCATACACAC 120
 ACAAAACATT TTATTTTTTG GGCCATTACC CCATACCCCT TATTGCTGCC AAAACCACAT 180
 GGGCTGGGGG CCAGGGCTGG ATGGACAGAC ACCTCCNNT ACCNATATCC CTCCCGTGTG 240
 TGGTTGAAA ACTTTTGTTT TTTGGGGTTT TTTTCTCTG AATAAAAAAG ATTCTACTAA 300
 CAAA 304

SEQ ID NO:1017

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01155

SEQUENCE DESCRIPTION:

5 GATCTAAAGC AGGTNGTGTT GTTTACATGT TTCTACACAT TTCATCCTTT AAAAAGTTGT 60
 TGAGAGAGGT TGTATTTACC TTCCAAGGT TGGAAAGCAG GGAATTTCC CAGTGTCTTA 120
 GTTTTCACC AGAGGAATAT GTGTAAGTAG CAAAGTATTT GCTGCTTACA TATAGTGTGT 180
 ATGTATGTAT ATATGTAAAT NGTGTGTAA AGAGCTGATA CTGATTTTCA TATGNCAATG 240
 TTAAGGCAAA GGCCTCCCTG CATTTGANGA GCAGGTNTTC ATTTATATGT ATTTTNGGGA 300
 10 TAAA 304

SEQ ID NO:1018

SEQUENCE LENGTH:304

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01156

SEQUENCE DESCRIPTION:

20 GATCAGAAAT NAAGTGCAGC AATATCATGA ATTCTNAGAA GNCTTTAAGG GAGCCAGTNA 60
 GTCATACAGT ATCCACAGTT GANTCACTTA AAGATGTCAG TATACGAACA TTATTCACAA 120
 TCCTTGGGCA ATCTCATTTT TTTTCCCTTC TCCCCTCCTC CCCTGCCCCC ATACATTTNT 180
 ATCCTTAANG TAGTTTTGGA GGGGCAGGAT GACTTAAACA TCTCANAAGC TAGATTGGGA 240
 ACATNTCANT ATAAGACTGA GTTTAAATTT ANGTTAAAA TGNCATCAGA ANANTTGGGN 300
 25 GGGN 304

SEQ ID NO:1019

SEQUENCE LENGTH:169

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01157

SEQUENCE DESCRIPTION:

35 GATCTAATAC TACTGTCAGT TTTAATGTGC ACTGTGTTTT ATACAGTATC TTTTTTGT 60
 CACTTNGGAA ATTTTACTA AAAATTGCAA AAAATAAAGT ATTGTGCAA GATGTAAGGN 120
 TTTTGANAC TTGNNGTGCA TTAATAANTA GACGATTAAN TCAAGGAAA 169

SEQ ID NO:1020

SEQUENCE LENGTH:303

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01158

SEQUENCE DESCRIPTION:

45 GATCCTCTAC CACAGACATT AATAGCTGAG CAGGAGCCAC ATGGATTGAT TGTATCCACT 60
 CACCATTGAC GATGGCATTG AGCGTANTAG CTTATTTCCA TCACTACGTG TTTTGGAGCT 120
 TGCTCTTACG TTTTAAGAGG TGCCAGGGGT ACATTTTGC ACTGAAATCT AAAGATGTTT 180
 TAAAAACAC TTTTCACAAA AATAGTCCTT TGTCATTACA TTATTTACTC ATGTGTTTGT 240
 ACATTTTGT ATGTTAATTT ATGAATGATT TTTTCAGTAA AAAATACATA TTCAAGAACC 300
 50 AAA 303

55

EP 0 679 716 A1

5 SEQ ID NO:1021
 SEQUENCE LENGTH:303
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01159
 SEQUENCE DESCRIPTION:
 GATCCTTNGG CTCAGAATCT CGAGAACCGC CTGCTCCTAA CAATTCAGCA AGTCAGGGGC 60
 TTCCTCTCTG TTAGTCCCCA AATCCTTACT TATTTTAAAA AGACTAGACC CTCTCTAAAG 120
 10 ACTGTTCCAT TTAAACATGT CCTGATTCTG CATCCGTGGG TTTTGTGAAA GAGAGCTAGC 180
 TGGCGGTTAG AGCCTGGAAG AAGGAGGGAA GTGGCACCTC ACTAGCATT ATCACTTTT 240
 TCCTTCTCTT TTTAAAAATA AAACCAGACT CTGTTCTGAA AATAAAAAAC TTGAGACTTG 300
 AAA 303

15 SEQ ID NO:1022
 SEQUENCE LENGTH:303
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 20 CLONE:HUMGS01160
 SEQUENCE DESCRIPTION:
 GATCTGNCTT ATCCGAGCTT GTTATTGGGG AGCCATAAGA GTCAGTTATC CAGAACACAG 60
 TTTTGCATAA GCTTGTATG GATTTCAGTAA TGCAGGTGAG AGTGTCTAGC AGTTCTTGGT 120
 25 AAGTACTCTT GGACATCTTT AAATTATTTA TCCTAATGGA TTCCATTCTG GTTTATGTAT 180
 AATCGTTTCA AGACTTTGGG AGTCTTTTAT GAACAAATGC TCATTGCACT ATATTATATG 240
 CAAATTGTNN NGCTGCTAGG TTTTCAAAT TTGAATAATA AAGCCTTTTC ATGTTCTTTT 300
 AAA 303

30 SEQ ID NO:1023
 SEQUENCE LENGTH:303
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 35 CLONE:HUMGS01161
 SEQUENCE DESCRIPTION:
 GATCAAAATC CTGTACAATA CTATAAATAT ATATTNATNT TTTCACAGTC ACCAAGTGTA 60
 TTGTAATGTA TACTTGAAAA ATGTTATAAC TTATGAAGTA AAGTTTCTNA TAGTAGTCTT 120
 TAAAGATAT AAGACTTAAT ATGTTTTATT CAGCTTCTAT AAGTGTGACC AGTTTTNATA 180
 40 TTTATTTATG CTAATATTTT TAACAAGTCA TTTCAAAATA TGTGTATCTC AAATCCTCCC 240
 NAAAGTGTG TGGCCTTAAC TGTTTCAGTAT TGCAATAAAA NATATATNTN NNTATGTGGT 300
 AAA 303

45 SEQ ID NO:1024
 SEQUENCE LENGTH:302
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 50 CLONE:HUMGS01162
 SEQUENCE DESCRIPTION:

55

EP 0 679 716 A1

5 GATCTATGGA AAAGCTGGGAA TGTAATGTAG GATTCTGTCA GAGCTCCTAC AGAGCACAGT 60
 TGCTTTAGT TTCCTTTAAA GATGTAAAAA TATTGTATAA TACAGTTTGG TCCCTACACA 120
 ATTGTATTTG CCAAGCTTAG TGCATTATGA TACCTTTATT TATTGTGTTT GGGCAGTATT 180
 ACTATATATA TATAANCATA CAGTTACTGT TTTATATATT CTTAGGTCAT TCAAAGCCAT 240
 GTATGCTGTA AATGTGCTAG TCTTTAGAAT GACACATAAT AAATAACTGA CAAGATATTA 300
 AA 302

10 SEQ ID NO:1025
 SEQUENCE LENGTH:435
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01163

15 SEQUENCE DESCRIPTION:
 GATCGAGCCA TTGAAAGCTC ATTACCAGTA GGACATAATT TTTGGCTCTC CCTATTACACA 60
 ACCAGTGCAC AGTTTGACAC AGTGGCCTCA GGTTCACAGT GCACCATGTC ACTGTGCTAT 120
 CCTACGAAAT CATTTGTTTC TAAGTTGTGT TTATTCCTGG AGTGACATGC CACCCCGAAT 180
 20 GGCTCACTTT CACTGAGGAT GCTGTCTCTT GATTTAGCTG CTGCCTCCAG CCTCTGGCTT 240
 GAGAACTTAC TAAAGGCACT TCCTTCCTGT TAAACCCCTG TAACTCTCC ATAAATTTGG 300
 TGATTCTCTG CTAGGCCTAA GATTTTGAGT TAACATCTCT TGAAGCCAAA CTCCACCTTC 360
 TGTGCTTTT TGCTTGGGGA TAATGGAGTT TTTCTTTTA GGAACCAGT GCCAAGGAAT 420
 25 GNCAAAGGTN TTAAG 435

30 SEQ ID NO:1026
 SEQUENCE LENGTH:298
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01164

35 SEQUENCE DESCRIPTION:
 GATCCACATC CTCTACAGGT CGGGGACCAA AGGCTGATTC TTGGAGATTT AACACCCAC 60
 AGGCAATGGG TTTATAGACA TTATGTGAGT TTCCTGCTAT ATTAACATCA TCTTAGACTT 120
 TGCAAGCAGA GAGTCGTGGA ATCAAATCTG TGCTCTTCA TTTGCTAAGT GTATGATGTC 180
 ACACAAGCTC CTTAACCTTC CATGTCTCCA TTTNCTTCTC TGTGAAGTAG GTATAAGAAG 240
 TCCTATCTCA TAGGGATGCT GTGAGCATTA AATAAAGGTA CACATGGAAA ACACCAAA 298

40 SEQ ID NO:1027
 SEQUENCE LENGTH:328
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01165

45 SEQUENCE DESCRIPTION:
 GATCCACTTT GTTGGTTGTT GTTGACAGAAG ACTGAACTGT TTTGGAATAN TTAACAATTA 60
 CAGAAACAGT CAAGTGTTTT CCAATGTGGT TGTCCGTTT CTATGGCCTT GCTGTGTACT 120
 TTCCCTCTTT TTGACAGTAA ACTTCTGCCT ATGGCTTACA GTTTGACATT TAATTTATTA 180
 50 GCGCTGCTCT GCACCCCTNC CTTGGGAGGG AGACTTCATG TGGTTTATTG CGAGTTTTTT 240
 TGTTTACTTT TCAGGGTTNG TACCTACAAA GGTTTAAATA ATAAAAANCA AAGNTTTTTT 300

55

NGGCNATTNG TCTTGTCTTN GTGGGAAA

328

5 SEQ ID NO:1028
SEQUENCE LENGTH:297
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01167
10 SEQUENCE DESCRIPTION:
GATCTACAGT GCTGATGAGA AGAGAGCCCT TGCATCCTTT AACCAAGAAG AGAGACGAAA 60
GAGAGAGAAC AAGATTCTGG CCAGTTTTCG AGAAATGGTT TACAGAAAAGA CCAAAGGGAA 120
GGATGACAAA TAAAGATTTT NTGATTGTCC AGAAGACATT TTTAACAACA AAAAAGAAAG 180
15 TCTGGGTTC ACACATACAT AGAAAAAGAT TATTATGTTC TGAGAAAGCT TTACAGTGCT 240
ACTGTGCCTT CTATTTAATT CTTTCAGTCC TTCAATAAAA AGCTGCTTAT TGATAAA 297

20 SEQ ID NO:1029
SEQUENCE LENGTH:297
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01168
SEQUENCE DESCRIPTION:
25 GATCCTGCTG AAATACATCT GCAGCTGACA ATGAGAGAAG AAACAGAAAA TGTCATGTGA 60
TGTCTCTCCC CAAAGTCATC ATGGGTTTTG GATTGTGTTT GAATATTTT TNCTTTTTTC 120
CTTTCCCTC CTTTATGACC TTTGGGACAT TGGGAATACC CAGCCAATC TCCACCATCA 180
ATGTAATCC ATGGACATTG CTGCTCTTGG TGGTGTATC TAATTTTGT GATAGGGAAA 240
30 CAAATCTTT TGAATAAAAA TAAATAACAA AACAATAAAA GTTTATTGAG CCACAAA 297

SEQ ID NO:1030
SEQUENCE LENGTH:296
SEQUENCE TYPE:nucleic acid
35 TOPOLOGY:linear
CLONE:HUMGS01169
SEQUENCE DESCRIPTION:
GATCCAGAAC ATGGGAAGTT AGGGAAAATG TGTGATTTTG TGTTTTGAAT TACTGTCAGA 60
ATTACATACA CAATTACAAC AAACTTTTT TAAAAGACAT TTCATTGTAC TGCAAAAATC 120
40 TGAATATTTA TATTTCTNGT TTTTTCTTT ATATGTTTTG CATTNTANTA TGTTGAGCCA 180
CTGGAAAATT TGTAACAGNT TANTTTGTTA TNGGCGTTA ANTGTGTTGT CATTGNCTCC 240
ATTGTCTTTG TCCAGAGCCT ATTATTATGG AACCAATAAA NTTAATGGG GTCAAA 296

45 SEQ ID NO:1031
SEQUENCE LENGTH:294
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01170
50 SEQUENCE DESCRIPTION:
GATCCTAGTC CCCTGCCCTC TGGCACAGCT GCTTCCTGCA AGANAGCAAG TTTTGGTCT 60

55

CCCTGAGAAG CCATGTCCTT CGTNCCTGNT CTTGCCTGTC CCACCTGTGC CCTGCCCTCC 120
 AGCTTGATT TAAGTCCCTG GGCTGCCCCC TTGGGGTGCC CCCNGCTCCC AGGTTCCCCT 180
 CTGGTGTNAT GTCAGGCATT TNGCAAGGAA AAGCCACTTG GGGAAAGATG GAAAAGGACA 240
 AAAAAAATTA ATAAATTTC ATTGGCCCTC GGGTGAGCTG AGGGTTTTTG CAAA 294

SEQ ID NO:1032

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01171

SEQUENCE DESCRIPTION:

GATCTTCAAG AAGTGAAAGA GACCGAAAAT CAGACAGGAA AGACAAAAGG CGTTAATGGA 60
 AGAAGCCAGG CTTCTTAGC CATTCTTTC AGCAGAAGAT TTCTTGATAA AAAAGGATTA 120
 CCTTTCCTTG TAAAGAGGAT GCTGCCTTAA GANTTGCATG TNGTAAAANN NCTTTTGGGA 180
 AAATACAGAC TGTTTGTTA CCAGACATTC TNGTACTGNT NGCATAATNN GGTAAGAGTT 240
 ATTNATCAAA ATNATGTGAG GTTCCAAAAT ATGTAAAANT GATATNATAA AAN 293

SEQ ID NO:1033

SEQUENCE LENGTH:293

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01172

SEQUENCE DESCRIPTION:

GATCAGCGGT TCTTTTGGCA GCAAAGCCTG CATCTGTGTT GACTTGCAAG ATTTTGCGTT 60
 TATTCAGGCA AAAACTGGTC AAAATGGTTA CTACATGATT TGTTCCAGG GGTGTGAAAC 120
 ATTCAGTGAA ACTTTTAAA ACTTTGATTG CATGATGTAT TTTTTTTNA GAAAGTTATT 180
 GTTTGAGAAT AATGTCTTTT TATACCAGGA AAATAGTTAT CCNGAATGAC GTTGAAAACT 240
 CCCCCTCCCC TTNATTTTNN TTAAATCANT ACATGTGAAA GTNCCANGC AAA 293

SEQ ID NO:1034

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01173

SEQUENCE DESCRIPTION:

GATCCCAATT CCACATAAGC ACTTTTGGAA GAAAACAGCC AAAAGTTGGC TAAAATTGGC 60
 GCTGGAATTT GGNCTGGGAA AAATCTTGTG GTTATTCCT TAAAAAGGA ACAAACCTTT 120
 AGTATTTAAT TAGTTGATTT ATTTAATGTA ATTNCAACA ATTAAATTAT GAATAATGCA 180
 ATGTACAGTA GAATCAGGTT TTGATTTTAT TAACACTGAC CAAGTTTAAAC TCCATATGAN 240
 GTGTAAGCTT GATATCGTTT ATGATGTCTA TCAACTGTAC CAAAAGTAAA ACATTTAAAA 300
 NCANNAAA 308

SEQ ID NO:1035

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01174

SEQUENCE DESCRIPTION:

5 GATCTCAAGT GACCCGCCTG TCTCGACCTC CCAAAGTGCT ATGATTACAG GCATGAGCCA 60
 CTGCACCCAG CCAACATGA CTTTCCATC CAGAGTAAAT CCAACTAACA AGAATCCACC 120
 CTTGGAGTTC ATGTAAAAAT ACATGACACA GGGTGATGAA AGTGCTTTGA AACTAGATAC 180
 AGGCAGTGGT TCTATAGCAT GGTGAATGTA CTCAAGGCAA CTTCTTTACT TTAAAAATCGT 240
 10 TAATTTTATG CCATGTGAAT TGCATCTCAA TAAAAATTGT TTTCATTTTA AA 292

SEQ ID NO:1036

SEQUENCE LENGTH:363

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS01175

SEQUENCE DESCRIPTION:

20 GATCGGGAAC TCCTGCTTCT CCTTGCCTCG AAATGGACCC CAACTGCTCC TGCTCGCCTG 60
 TTGGCTCCTG TGCTGTGCC GGCTCCTGCA AATGCAAAGA GTGCAAATGC ACCTCCTGCA 120
 AGAAGAGCTG CTGCTCCTGC TGCCCTGTGG GTGTGCAAGT GTGCCCAGGG CTGCATCTGC 180
 AAAGGGACGT CAGACAAGTG CAGCTGCTGT GCCTGATGCA GGACAGCTGT GCTCTCAGAT 240
 GTAAATAGAG CAACCTATAT AAACCTGGAT TTTTTTTTTT TTTTTTTTNN AAAANCCCTG 300
 25 NCCNNTTGT AAAATTTTTT TTTNNNTGAA ATANGNAANG GNAATAATTN ATCNGGNNTN 360
 TTN 363

SEQ ID NO:1037

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS01176

SEQUENCE DESCRIPTION:

35 GATCTTGGAA AGCACTAGAA ACTAAACATC TTCACCAGGT GCTGAAGAAA AGTGTCTTCG 60
 TTTTAATTGC CAAGCAGGGA TGTGGACATT TGGATGGTGA CTTTCCTGGG TGGTTCCCCA 120
 TAGATTACAC ATTGCCTCTA ATGGTGTCTA CACCCGTCAT ACTACCAGCT GAGATGGTGG 180
 TGGGCATAAG GAGAATTTGT GCCTATAACC CTTAGTGTGT TCTGGTTTTT TTTCTTTTAA 240
 40 TTTTAAATT GTCGTAAAAT ACTCATAAAA CATACTGTCT TCACCAAA 288

SEQ ID NO:1038

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS01177

SEQUENCE DESCRIPTION:

55 GATCACCTTG TAGTCTTTAA ATTCTTGGTC CCTGAGGCCA AGTCCACAAC TTGCCTTCTA 60
 GTCACCTTGC TGCCCGCAGT GGTGGTGGAT GTGTTAGCTG GTAGATTGG AATCAGTCAC 120
 CAGTCTTTCT GTACTGTCTT GGTAGCTCT ATATAAGTAG GGGCAGCTTA GCCCTGAGGC 180
 CCAGAGACCT GCTGTCCTTT TTCTCCTTGA GGGAGGAAAT AAAACTGCGG AATACAATGT 240

CCTTCCATAG CATGGGAAGA AGAAAATAAA CATCTCCTTT CCAACAAA

288

5 SEQ ID NO:1039
 SEQUENCE LENGTH:288
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01178

10 SEQUENCE DESCRIPTION:
 GATCCACCCT CCTGTAAATA TGGAACAAAT ATCTGAATGA AATCCACCCT AGGAGACGGA 60
 GCAAACTAAA CTTGTGGTTT TNCATTTAAC TTTTGACTAC AGCATGGCCC CATGGCATCC 120
 ACACCAAGAG GGTGTTGTGA TGAGGTGCCG GTGTGCAAAG GGAACTTTAG TTTTCCACT 180
 15 GGTTCCTATC TGCTAGCCTT TTACATACAT GTGTACTATA TTTGTTTATA GACTGTAGGT 240
 GGATATATAA TTTAAAAGCT TGATTTAATA AACATTTAAC CCCNTAAA 288

20 SEQ ID NO:1040
 SEQUENCE LENGTH:287
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01179

25 SEQUENCE DESCRIPTION:
 GATCTTCAAG TATTTGCNAC TTTGAGTAC AGCTAATTGG ATAATCTCAA ACCCTTTAGT 60
 GAAAATATCT TAAATGCATT GAGAATATTT CCTAATTACC TGTGTATGCT ACAGTACAGA 120
 CATTAATTCT ATAAACATGT TCATAGGTCT TCCCCCTCGC CCCGNCCGTC TTCTAAGGGC 180
 ATTTCTGTT TCTNTNAGT GAGTTCATGN ATGTTTACCG GTTCTGGCGN AANGTTTCTT 240
 GCATNCTGAG CATAAAAATA NTAAAACCNA CTGATANTTG CTTGAAA 287

30 SEQ ID NO:1041
 SEQUENCE LENGTH:289
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 35 CLONE:HUMGS01180

SEQUENCE DESCRIPTION:
 GATCTGCACA CGCATAATAA TCAGCATTGA GGGCAACAAA ATGCCATTGT GACCTTGCCT 60
 GGAATGTGTC CCCATCTCTA CTCTAAGAAA TCGCAATGG ACTCTTTGGA GAAAGAAGAT 120
 40 ATTTAAAAAC ATTTTATAGT TGTCTGTAAA TGGTTCAGCG TGTATCAGAT GTTGTCTAG 180
 GACTCACATT TCTCTCAGTT ATATTTAAAA CCGTTGTGTA CTTTGTACAA NGGAATACTA 240
 GTCATACTTC TATAAACTTT NCACAATAAA ATTNTCATTG TGGGTTAAA 289

45 SEQ ID NO:1042
 SEQUENCE LENGTH:287
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01181

50 SEQUENCE DESCRIPTION:
 GATCGCACCA CTGCACTCCA GCCTGGGNAA CACAGTGAGA CCCTCTCTCA AAATAAATAC 60

55

AGNCAGGCAT AGTGGCTCAT GCCTGTAATC CCNGCATTTT GGGNGGTAGA GGTGGGTGAA 120
 TCACCTGAGG TCAGGAGTTC ANGCCCAGCC TGGCCAACAT GGC GAAACCC CATCTCTACT 180
 AANTATACAN AANTTAGCCA GGTGTGGTGG CCTGCACCTG TAATCCCAGC TACTCAGGAG 240
 GCTGAGGTAG CTTGANCCCN GGAGGCANAN NTTGCAGTTA NGCCAAN 287

SEQ ID NO:1043
 SEQUENCE LENGTH:286
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01182
 SEQUENCE DESCRIPTION:
 GATCTCTCCT GGAGTATGAA GACCTCCAAG GACTCACTTT CCCTCCCTTC TGATGCCAGA 60
 GCAGACCAAG CTGTCACACT CCAGTCTCAT GCTGAAGTCT CCAGCTTCTC AAGCTTAGAA 120
 GAGTTTTTNG AAGAGTCACT TTCAGCTCAT GCAGCTCTCA CAAGTGTGAA GGGAGTGGAT 180
 TGGGGGTGTT TTCCTTGCCA TTTTCGAAAA GAAAAAATT ACCTGGTGAT TGGTGGAAAG 240
 ATACAACTGT CAAAAATGCA TGATTGAAGC AATTAGGTT GGGAAA 286

SEQ ID NO:1044
 SEQUENCE LENGTH:286
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01183
 SEQUENCE DESCRIPTION:
 GATCAATAAA TNATACAAA TATATGTTA CAGTATGATT TAAAGTCTGA TTCAGACCAG 60
 GGACTCTATT TTAAGTTCAA CTGAAATAAC ACTGGGTTTT AATTATATCA CAGGAAAAAA 120
 AAAGTGCAAT TAAGTATTGT NATCGTGGAC TTTATAAAAG CAAAGGAAAT TGAAAGTAAC 180
 TTTNGATTCT GTATCANGAA TCATATTNC ATACAGTCAT AACTGTCTTN CTGTGACCCT 240
 TTCACAGGGC ACTGTAGGAT GGATTAAAGG TGGCAATTA CTGAAA 286

SEQ ID NO:1045
 SEQUENCE LENGTH:439
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01184
 SEQUENCE DESCRIPTION:
 GATCATACCG GTAAAGCAGG AATNACAAAG CTTGCTTTTC TGGTATGTNC TAGGTGTATT 60
 GTGACTTTAA CTGTTATATT AATTGCCAAT ATAAGTAAAT ATAGATTATA TATGTATAGT 120
 GTTTCACAAA GCTTAGACCT TTACCTTCCA GCCACCCAC AGTGCTTGAT ATTCAGAGT 180
 CAGTCATTGG TTATACATGT GTAGTTCCAA AGCACATAAG CTAGAAGAAG AAATATTCT 240
 NGGNGCACTA CCATCTGTTT TCAACATGAA ATGCCACACA CATAGANCTC CANGAGCATC 300
 ANTTNCATTG CACAGACTGA CTGTNGTTAA TTTNGTCACA GNGTCTATGG ACTGANTCTA 360
 ATGCTTCCNA AANTGTTGGT TTGTTTGCAN GTTTTCGANC CGTTGTTATG GCANGANGTT 420
 NGTTTAGTTT CNGNTTGTN 439

SEQ ID NO:1046

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01186

SEQUENCE DESCRIPTION:

GATCTGGAAA CAGTTGAAAA CGAGACAATA TAGCCGGAGA CGCCTTATAT GATGATGCAG 60
TATCGACTAC ATTAATGAAA GTAATGCCAA ATNCAACAAG AAAGCTGAAG ATTCTATGGG 120
AATACACAGC TGAATTAACA GATTGGAAG AGAACANCTG NTAATCCTTC AGGACTGTTA 180
TAGAGTTNAG ATGGGTAAAT TCTCCTANAA ATCAAGTCTT TTGAATTTNC AGAATCAGAN 240
TTAGAGCCNG CTCTACTAGA TTGNATAANT GNGGTCTAAC GAAAA 285

SEQ ID NO:1047

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01187

SEQUENCE DESCRIPTION:

GATCCGGGNG GACCCCTTTG CCCTTCCCTC GGCTCCCAGC CCTACAGACT TGCTGTGTGA 60
CCTCAGGCCA GTGTGCCGAC CTCTCTGGGC CTCAGTTTTC CCAGCTATGA AAACAGCTAT 120
CTCACAAAGT TGTGTGAAGC AGAAGAGAAA AGCTGGAGGA AGGCCGTGGG CCAATGGGAG 180
AGCTCTTGT ATTATTAATA TTGTTGCCGC TGTGTGTG TTGTTATTAA TTAATATTCA 240
TATTATTTAT NTAATACTTA CATAAAGATT TTGTACCAGT GAAAA 285

SEQ ID NO:1048

SEQUENCE LENGTH:283

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01188

SEQUENCE DESCRIPTION:

GATCGAAGTG ACAAAGTGTG TTTTCANTCA CAGTGGAGGC TACATCAAGC AAGGGGAGGT 60
CCAGCCCTCT TGCAAGTGTG GTGAGAGGCT CTACTAGCAA AGACATGGGC ACCGGAGTAG 120
GTCCCGTGTA GCATGCGGGT GCTGTAGAGA AAATTCAGTG ACGTACATGG CTCTGGTTCT 180
GGACACAAAA TCTGTACTGG AGAGGAAATG ACTGCTGAAA TAAGGCGATT GTATGAATAT 240
TTAAATGCC TGGAACTA AAGTAAAGTA ATGATATTTT AAA 283

SEQ ID NO:1049

SEQUENCE LENGTH:283

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01189

SEQUENCE DESCRIPTION:

GATCCTCGCA GCTTCTNCG AGCGGGGTGT CGCAGTCTTG TGCACAGAGT AAACCTTNCT 60
AGCTGCCCTT TTCTGTAATA GTGAAAGTTG GTATTTAACA TTTATNCATT TTTAAAAATAT 120
TTGGAAGGTC TGANCTTGTG AAAAGAAAGT GGTGGNCTG AGGTTGGAGG NAGCTGAATG 180
GAATCTNACG GTTGGNAGTG GTGGAAATTG GAAGGATACC AGGAGGTATT TGGGAAGGCC 240

AATGGCGTGG CTCCTTTGAG GAAATAAAAC ACTAAGCATG AAA

283

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SEQ ID NO:1050

SEQUENCE LENGTH:281

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01191

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SEQUENCE DESCRIPTION:

GATCCTTTTC ATACCTNATT TGGGAATTGCT GGATTGTAAC TTTTGGNAGA AGAACAGATT 60

AAACCTGTGA ATCCTGTCTT TTGCATGCCT GAAGAAGTGC TTCAAAGAGT GAATGTTTTCAG 120

CCTGAGCTAG TGAGCTAGAT TCATTGAATT GAAAGTTGCA TAGTATAGTT TTGCCATTTT 180

15

AACATTTCTG TATTTNAAGT GCTTATCGAA TCTAAAAGTG ACTACTGTNA ATATTNNGTA 240

TATNGTGTNA AATTAATTNN ANTAATNAT ATAATTNTAA A 281

SEQ ID NO:1051

SEQUENCE LENGTH:226

20

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01192

SEQUENCE DESCRIPTION:

25

GATCAATGAC AGAGCCTTCT GGAGGACATT CCAAGACAGT ATACAGTCCT GTGGTCTCCT 60

TGGAAATCCG TCTAGTTAAC ATTTCAAGGG CAATACCGTG TTGGTTTGA CTGGATATTC 120

ATATAAATT TTTAAAGAGT TGAGTGATAG AGCTAACCT TATCTGTAAG TTTTGAATTT 180

ATATTGTTTC ATCCCATGTA CAAAACCAT TTTNCCTACA AATAAA 226

30

SEQ ID NO:1052

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01193

35

SEQUENCE DESCRIPTION:

GATCACAGCA TAAAAGAATC ATAAGATAAA ACATCAAACCT ACCCAGCAAC CTGAGAAGCA 60

CAGAGTGTTA AAGCCTCCAC CGTGTGAGAA ACTAAATTAG GGTAAGTAGC TATTGAGTAT 120

ATTGAGTACC TTCAAAGCAC TCAACTGACA GGTTTTACAG ACTGGAAATT ATAATACTTA 180

40

TGACATTTCT ACCTTTTATA TAACCAATAA TCTACCATAG AATGTAGTAT TTTTANAGCT 240

ATTAGCANGC AATATATTAN NNTANTANTG NATTTAA 277

SEQ ID NO:1053

SEQUENCE LENGTH:277

45

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01194

SEQUENCE DESCRIPTION:

50

GATCCAACCC GAATAAGATT AGAAGCTTTC CATCAGTAAA AGGATGTTTT CTTTTTTCAC 60

ACAGTAAAAA TTCTTATCAT TCAAGGATAT TGAACCACA GGACTATTTG GATAAAAAAC 120

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ATTATTGCA AATTAATGCG CATAGGCCAT CTTACTTTTA TTGCAAAATG GCATGTGCTG 180
CCATCTATTA TTCAITTTTA AATGGTCATT TCTTATTCAG TGAGTGCTTT AGTGTTTTAA 240
ACTATATGGA TAAGAATGCA GGTAGGATAA TATTCTN 277

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SEQ ID NO:1054
SEQUENCE LENGTH:283
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

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CLONE:HUMGS01195

SEQUENCE DESCRIPTION:

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GATCCTGAGG ATTACAGCTG TGGAAATTTT GTCCATGCTT CAAATAATTT TGAAAGAAAT 60
TTTCCCATAT NAAAAAAGGA GAGAACACTN GCATCTGTTG AAATTTGGAA NTTCTGAAAT 120
NATAGTATTT TAAAAAATTG CACTGAAGTG TATACACATA AAGCAGGTCT TTTATCCAGT 180
GAACAGGATG TTTTGCTTTA GCAGCAGTGA CATAAANTTC CATGTTAGAT AAGCATNTGT 240
TNACTTACCT NGTTATTAAA TATTTNTTGG AAAAGCAGTG AAA 283

20

SEQ ID NO:1055
SEQUENCE LENGTH:277
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

25

CLONE:HUMGS01196

SEQUENCE DESCRIPTION:

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GATCTGTGTA TGCTGTTGGG TCGGAGTGCC AGTNACTGCT TTGGAAGTCT GNGTTCTGGG 60
GCTGCAGAAT GACAAACGTG TCATGGGATT AAAACCAATC AACTGTGAAT TGTGAAATG 120
AAGCTACTCT TTCGGTTTTA TTTTCTTTAG CATATTGAGT ATAGAAATCT GAAACTTATT 180
TAAATTTTAT ACTGCTTTTG TTGATGGCTC ATTTTGGCTG TGTATCCTCA CTTATGTACT 240
GATTTCTGAT AAAGGCTTGA CATTATTATA ACANAAA 277

35

SEQ ID NO:1056
SEQUENCE LENGTH:103
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

40

CLONE:HUMGS01197

SEQUENCE DESCRIPTION:

GATCGACCTT NTCTGTTTTN TTTTGTTTTN NTTCTNTTT CCTGGCCATG AGGACAAAAA 60
TTACTGAGTG GCCCTTAAAG AGGGAAGTTT GTTTTCAGCT GTN 103

45

SEQ ID NO:1057
SEQUENCE LENGTH:291
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

50

CLONE:HUMGS01198

SEQUENCE DESCRIPTION:

GATCGACCAC ATCTGTGATG CCCTGTAGCC CCTGCCCACA TCCTCCAGGG GGCCAGGGT 60
GCCTGCACTT TNCTGTGGCA GGCAGATTGG GTGGTAGTGG GAGGTTGTGC ATGGAGGCCA 120

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5 GTNAAAGCTG ACATCTGTAA AAGGCCTTCA AGGAAGAGAA ACCAGGCCCT GCGTCAGGCA 180
 GTGTGAGTTT GCCGTTTGT CTTAACTTTC TTTTTTTTTT TTTAAAAAAN GGAAANNTTT 240
 AAAAAANCTC CCTTTAAAC CAAANCATNT TTGNNTTTNN NCCAAGGGAA A 291

10 SEQ ID NO:1058
 SEQUENCE LENGTH:276
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01199
 SEQUENCE DESCRIPTION:
 15 GATCCCGCTC TGTNTTTC AGGTTTGTGC TATTCTNATT ACATTATCGA CTAGTCTGAA 60
 GCAGAGCTGA TATCTCTTTA CCTGGGGAGT CAGCTTCACC AGCCACAGCT GCTGAAAGAA 120
 TAGCTTGGAG ATTCACCCA CTGCATTCT GTNGCTCAA CTTTTGACC TTTGTGCTAT 180
 TTGAGAAATC TTTGAAATGC TGAAGGTATG ATTCTCCTC AGGGGGAACA TGCTTTGGGA 240
 AAAACGCCCA CTTAATAAAA TGTATTCNT TTCAA 276

20 SEQ ID NO:1059
 SEQUENCE LENGTH:276
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 25 CLONE:HUMGS01200
 SEQUENCE DESCRIPTION:
 GATCTGTATA TGGTAAACAG GGGTTTAACC ACATGTGGTT AACATGGATT AATGTGGGAN 60
 TTTGGCTTCA AGAACACAAC CTTAGGACCT TGGNCCCAA AAGCTGGTGG TGAAATGAGA 120
 GGNCCCAATT TAAGAAGACC CTTATGGAGA CCTGAGGCTG CAGAACTGG TAGGTTTCAT 180
 30 CAGGTGGTTA AAGTCGCAA AGTTGTAAGT GACTAACCAA GATTATTCA TTTTAAACC 240
 ACAGAATAAA AATGACACCT GAGCTTCTCT NTNAAA 276

35 SEQ ID NO:1060
 SEQUENCE LENGTH:276
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01201
 SEQUENCE DESCRIPTION:
 40 GATCTAGTTC CCCTGGAAAA GCTGCTGTAT TTTAATTTT TAATGGAATG TAGCTTTTNN 60
 AATCCTGTCA CTGGCATCAA CAAAAGGAAT TATACCATGA GACCTTATAG CTGTACTTAA 120
 AAGCCATTCA GTTCAGCTAT TGGGAGTTCA TGATGAATTA GCATATGCCA GAAAGGTTGC 180
 TAACCTTAAC ATCTGAGAGC AGTAACACTG ATTTTATCTG CTGTATGAGA CTTTGTGCAT 240
 45 TTTACTTTGA AATAAAGATT TTTTCCACA CTGAAA 276

50 SEQ ID NO:1061
 SEQUENCE LENGTH:276
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01202

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SEQUENCE DESCRIPTION:

GATCCTGTTT CTNGCTCTGA GTNCTAGCTA GCCAGCTGTN TTCACACTGT AAACATTCAT 60
 CAAGCTGTAC ATTTGGTGCA CTTTCTGTG TCATACCACA ATAAAAAAAA NCCTATCATC 120
 TTACAAAAAC AAGACACCCA AGTCCAGGCC CAAGGAGTAA GTACAAATAT TCCTGTTTCT 180
 GANCCATTAC TGTAAATTGGC TCTNAAGNCT TGAGGTANCC TTATAGGTTA CTCATAGGGC 240
 ATATACAAAT AAACNGTTT GTTTCTTTT TNCAA 276

SEQ ID NO:1062

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01203

SEQUENCE DESCRIPTION:

GATCTTCAAC GGATACTAGA AAATGAAAAA GACTTGAAG AAGCTGAGGA ATATAAGAA 60
 GCACGTTTAG TACTGGATTC AGTGAAGTTA GAAGCCTGAA ACTTTTCTCG TATGGGGTGG 120
 TTTTGCATT AAATCCTGGG GTCCATTTTA CAATCCATTA TTTTGACCA CTGCTATGTG 180
 TTCAAGTAGT ATGAGAATGT GATTGTTTT ATCTGGTTAC ATATATATTT CTTGTCTAA 240
 TTTAATATGT CAAATAAATG AGTTCATCTA ATAAA 275

SEQ ID NO:1063

SEQUENCE LENGTH:274

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01204

SEQUENCE DESCRIPTION:

GATCTCACCT CTTCTCAGG ATGGGGAGCT CACTCCGAGA ACAGGAGAAA TCAACATTGC 60
 AGTAACAAGG TAGAATGGTT TTGAAGAAGA AAAACCTGC TTTCTGACTG ATTTTGCCTT 120
 GAAGGAAAAA AGAACCTATT TTTGTGCATC ATTTACCAAT CATGCCACAC ANGCAATTAT 180
 TTTTAGTACA TTTTATTTT TCATAAAATT GCTAATGCCA AAGCTTTGTA TTAAGAGAAA 240
 TANATANTAN AATAAAAAGT CTGTGCTGTT GAAA 274

SEQ ID NO:1064

SEQUENCE LENGTH:274

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01205

SEQUENCE DESCRIPTION:

GATCCAAGTT CCTAGACCTC ATGGCTGTCC CCTCCACCA GTCACCTCCA CTGCACAACT 60
 CGGGCGGGGG TGTGACACCT CTCCCCACC NCCGACTCCG TGGTTTCCGT ATCGTCAACC 120
 CTTACCCGC CGACCCGGA GGGGTCTGGC CTACACTGGT CTCCCCTTC CCATCAACTC 180
 TTTCTGCTTG ACAATGTAGC AACCCAGGCC CCCACCCAC GGTCTCCCC TTTTCCTCT 240
 CCCTGACAAT AAAGTCTGAA TTTGTTCTGC NAAA 274

SEQ ID NO:1065

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01207

SEQUENCE DESCRIPTION:

GATCTATCCA TCCAATGTTG TCATTATATT TGA CTGTGGT TCAACAGTAT TGC GTTGTCA 60
 GACTAGGAAA GTTAAACGAA CAAAATGGTT TTAGTTTTGC TGAAGACTGG CCTTATTAAT 120
 GGACAGCTTT CCTAACAAGA GATTATTAAC TTTTATCAGG TGTTAACATC TGTTTCAGGA 180
 ACATGGCAGT ATGTTTACAT GTCAGAAGTT TTGTTTAATT CTATGGTATT TCTAAATTGA 240
 CTTGTTTAAA TAAATTCAGC AAATGGAAA 269

SEQ ID NO:1066

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01208

SEQUENCE DESCRIPTION:

GATCTGGTTG GCATTTTCTC CCTGATGATG GGAGCGTCAT TCTTTTGTCT TCATGGTTAC 60
 TTGTGTGATA TAACATACAT CTGTNAAAGA AAATCACTTC TTTCTAGGGG AGGGAGGTAG 120
 AAAAGTATCT TTCAAACCTG GTTTTNNAGT TTGTNTCTTG TCTTAACTTT GTGTNGGCTC 180
 TAACTNAAAC ATGCTGATAT GTGTTTNCAN GANTTTTGGT TTAAGGANGT ATTGTATGGA 240
 NGTCCACANA TTGGNAGGTN GTTCATCTN 269

SEQ ID NO:1067

SEQUENCE LENGTH:269

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01209

SEQUENCE DESCRIPTION:

GATCGATTAA GGAAGGTGGT TATGGCTGGG TGGTTCAGGG GTTTTTTTGG GTTTNTTTTT 60
 TTTTTTCTTT GTCTTTTNA CCTAAGCTG TTAAAGTTGA AGCATTCTNA GATGTTTGGG 120
 GGGAAACATC CTCTNAAAT GGGNCCTTGT GCTTGCNTTC TGGGGAGGCG GTCCTGAGCA 180
 GGTGANTCAT ANGGCATTGA TGCATATGTN ATATGNGGAC TGNACCCACC TTTCCCCCN 240
 AGCCTTTGCC TCTTGGGTTG TTGTNCTGN 269

SEQ ID NO:1068

SEQUENCE LENGTH:268

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01210

SEQUENCE DESCRIPTION:

GATCCTCTTT GTTTGTNCAA AGGACCAGTT TTCCTAGGCC AAAGAAGTCT CTNCCCCATG 60
 TAAGNCCTAT GCCTTNAAT ATCATGCACC ATGACCCACA GCCATCTGGT TATGTCTTAT 120
 TTTTTCCTA AAAGATAATG TTTATNNTTA AAAAGGAAGG ANGGAGCAAG TGAAGTTTCA 180
 TTCTGCTCCA GCGGTGGGGG ANGCGCTGA ATCCACCTGN TTCTCCTTTT GCAACCGNCA 240
 GCANGCAGCT TTTCTCCGGG CNNCAGGN 268

SEQ ID NO:1069

SEQUENCE LENGTH:267

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01211

SEQUENCE DESCRIPTION:

GATCTAGAAG GTGAAGAATT TTTTATGTA TATATAGACA TATCTATATA AATNGTCTGG 60
 CTGAGGCAGG GCCTTCANCT ATCATTGGT TAATAAATAC ATTTNAGTAT TTNCATTTCC 120
 TACTGCCTGC AGAGTTTCAG GTGCTGTNG TGTGAAAGTC CTGTAGATGT GTGCAAATTT 180
 AACGAAATGA AATTGTATGT GTAAAANTGT ACGATTTTCC ACTGTGCAAC TGTAAATNAT 240
 AAATAANANA TATTTTNTCT ATTCAAA 267

SEQ ID NO:1070

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01212

SEQUENCE DESCRIPTION:

GATCCTAGTG ATTCAGCCC ATGCATTAAA CAGGAAACAA TAATAAATTT GTAGAATTCA 60
 TATTTTCTA AAGGGAACCT AAAAAGTCT GCTACATGTT ATGTACAAAA CTGGTTTATG 120
 CCACATGGAC AGAGAATCAC ANGTTTGGTT TTGGTACTTT NNGTTCCTCT TTGTATTCAG 180
 TTGTATAGAC CTNCCAAATT CAGAATGAGA NGAAAGCTGT CTGTATCAAA CCATTANGC 240
 ANTAATTGTT ATATNTNANA GCTAAA 266

SEQ ID NO:1071

SEQUENCE LENGTH:266

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01213

SEQUENCE DESCRIPTION:

GATCCAAGTT ATACATGAAT AGAAAAAGAT GGTGTTAAAT TTGTGTGTAG GCTGGGAATT 60
 CTTGCTGAAG GAATTGGAGA AAACCTGTTG CTGCAAAATT TTACATGTTT CAGATGGAAA 120
 GGGAAGTCTA AGCNCCTTTT AAAACAATTT TTTTGTAT TTAATTAAGC AATTNCAGTT 180
 ATCTGGGATT TTTGGGTCAG AATTTTAAAT TCTGTTGAT TCTCCATATT CCAGTNAATA 240
 AAATACAAAA GCATTGTNTT TTAAA 266

SEQ ID NO:1072

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01214

SEQUENCE DESCRIPTION:

GATCTTCAAT TCCTTGAGTC TGAGCTTGTG GGTGGAATTC TAAATTGTA TCATAATCTG 60
 TCTTTTGTGA AACATTTTGA AAATATGTAT ATATAATATT GTATATGCAA ATTGTGTTGT 120

EP 0 679 716 A1

TTCACCTGTA AAGGGAAAAG GCTTATTTN CTTTATATTT CTGATAACTT GTTTTGCATA 180
TGACCAGCAC TGA CTGAAAAG GCATGTGTAG CTGCAAACAC TGTTGCTTTT TTTGTGAAAT 240
GNAATAAAAA GTATTAAAT ACAA 265

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SEQ ID NO:1073
SEQUENCE LENGTH:265
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01215

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SEQUENCE DESCRIPTION:
GATCGTGCCA TTGCACTCCA GCCTGGGTGA CAAGAGCAAA ACTCCATCCC CCCTGCCCAA 60
AAAAAAATN AATTTTCACA GAAAATTAAT AGCATAGGTA TTATNATCCT CATTTTACAG 120
AGAAAGAAAC AGCCATAGAG AAAAATGACT TGCTCACAAC ACAGGCAACT TTGACTCTAG 180
AGATANCACT TATTACAGTA AAATCCCTCT TCAGNCACAA AATACATGAT TATCTTAAAC 240
ACATTCTTAA TAAAANTTTA NCAAA 265

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SEQ ID NO:1074
SEQUENCE LENGTH:268
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01216

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SEQUENCE DESCRIPTION:
GATCAAAGAT TGTAATAATA ATTTTGTAAT TTGTAAGCAA AAAGTTATTT TTATATTATA 60
TACAGTCTAA TTGTTTCATCC TAATTGTTCC TGTTTTCATC TAGTCAGAGA TTCAGTAAAGT 120
NCCTTGGAAC AATATTGAAT TCTCTTAGCT TGTGTGTGTT TCTTTAATAT TTGAACTCAA 180
GTGGGATTAG AAGACTATNA NNNTACATGT ATGTTTCAGG ATATTGACC TGTCATTAAT 240
AAAAACAAAC AGTTTTACAG TGCCTAAA 268

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SEQ ID NO:1075
SEQUENCE LENGTH:305
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01217

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SEQUENCE DESCRIPTION:
GATCTCCATG TAGTCCATAT GAAACCTGCA GAGTGATTTT CCAGAGTGCT CGATACTGTT 60
AATTACATCT CCATTAGGGC TGAAAAGAAT GACCTACGTT TCTGTATACA GCTGTGTTGC 120
TTTTGATGTT GTGTTACTGT ACACAGAAGT GTGTGCACTG AGGCTCTGCG TGTGGTCCGT 180
ATGGAAAGCC TGGTAGCCCT GCGAGTTAAG TACTGCTTCC ATTCATTGTT TACGCTGGAA 240
TTTTTCTCCC CATGGAATGT AAGTAAACT TAAGTGTTTG TCATCAATAA ATGGTAATTC 300
CTAAA 305

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SEQ ID NO:1076
SEQUENCE LENGTH:263
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

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CLONE:HUMGS01218

SEQUENCE DESCRIPTION:

5 GATCCTGTAA GTTGTGTCATCA AAATATGATT TAGAAATATT GGCCAAGGTG TTGCTTTAAC 60
 TGAGGAGAAA AGAAAGCACA CTGCCTAAAT GTGTAAAAGA AAAATGCAGA GGTTATTAAA 120
 ATGTAAAGAA GTAACAATCT TTGGATTTGT CTATACATAT ATATATATAT ATATNGNTTT 180
 GCCTTAATAT ACCCCCTTTT TTGTTTGTGA CTTTCAACTG TAATCAGTTA ATAAAGTATT 240
 TATTCTCTGC ATTCAGGTTT AAA 263

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SEQ ID NO:1077

SEQUENCE LENGTH:354

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS01219

SEQUENCE DESCRIPTION:

20 GATCGACAGC AAGCAATCCT TAAGGGACTT TCAGAACTGA GACAGGGCCT TCTCCAGAAG 60
 CAAAAGGAGT TGGAAAGTAG TCTCCTGCCT TTAGCTGAAA ATCAAGAAGA GAGTTTTGGT 120
 TCTTCATTTT AAATGTAGAA AATCAAAATCC TTCACATTG ATTTGTGTCT TCCAAATTAT 180
 AAAATGTGCT CACTGGCTCA ACTGTATTTT TCAAAATAGCC TAGATTTACT TATTTTTTTA 240
 ANNGNNCATT AAAAATCTGT ATACTATGTA GTAAAATGCT GTACTTGTNC TATACAATAA 300
 ANCAGATACT TCTTTTGTA AAGCTTAGTA GTAAAACNCC ACCNNNNNNN NNTN 354

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SEQ ID NO:1078

SEQUENCE LENGTH:260

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS01220

SEQUENCE DESCRIPTION:

35 GATCGTGCCT GTGAATAACC ACTGCACTCC AGCCTGGGCA ACATAGTAAG TAAGACCTTG 60
 TCTCTTAAAA AAAATACATT CTGAAGAAAG TTCTACTTAT GANTACATTT TATTTATAAC 120
 AAAGTGGTGA AAATTTTAGA CCAAACCATG TCTTTCTGGG TTGTAGTGAT TAAAAAATGG 180
 TTAAGAGAAT GTTCCCTATA CAAGGCATAT GTTATTAANC ATGAAATTTA GGNTTAGTTT 240
 TCTCTTTGAA NNTCCTTTN 260

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SEQ ID NO:1079

SEQUENCE LENGTH:260

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01221

SEQUENCE DESCRIPTION:

45 GATCCCGAGA CTGTGTTTCT CTGGCTGAA NACACTNAGG TGCTCCCATC TGTNCGTGGC 60
 CCATGANCTG GGATGGTCCT CCAGCTGCCC ACAAGGTCCG CCCCTCTNTC TCTGCACCAC 120
 CTGTTTGCAAT AAACACACTT TGCTACAATC TTGCTAGTNC GTTTTCTTAA AAGATAATCT 180
 ATTTACTGTA AAAATAAATT GGACTTTGCA AAAGCTTTTA GAAGGAAAAG AAAGAGGATT 240
 AAAGAGAATT GCTGGTGAAA 260

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SEQ ID NO:1080

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01222

SEQUENCE DESCRIPTION:

GATCCAAATT TCCTTTTGAT ATTATTTTAC TTCTGCCTGA AACATTTTCT TTAACATTTT 60
 TTATAGTGTT GTTTTACTGG TGATGATTTC TTTCAGGTTC TAAGTGCCTG AACAAAATCT 120
 TTATTTCAAC TACATCTTGA AAGATAGTTT CTCTGAGTCT ACAATTCCTA GCTGACAATG 180
 TTTATCTTCC AGTACTTTAA AGATGTTGCT TCATTATCTG CTAATTTNNT TTGTTTCCAA 240
 TAAAATGTTT GCTGGCAAA 259

SEQ ID NO:1081

SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01223

SEQUENCE DESCRIPTION:

GATCTGCGGT GAAGCCAAGC CGCAAGGTTA CAAGGCATCC TCACCAGGGA TACCCGCCTG 60
 CTGCTCCAG GTGGCCTGCG GCATNGCTAT GCTCAAGGAC CTGGAACCC ATGCTTCGAG 120
 ACAACGTGAC TTTAATGGGA GGGTGGGTGG GCCGCAGACA GGCTGGCAGG GCAGGTGCTG 180
 CGTGGGGCCC TCTCCAGCCC GTCCTACCCT GGGCTCACAT GGGGCCTGTG CCCACCCCTC 240
 TTGAGTGTCT TGGGGACAGC TCTTTCCACC CCTGGAAGAT GGAATAAAC CTGCGTGTGG 300
 GTGGAGTGTT AGGAAA 316

SEQ ID NO:1082

SEQUENCE LENGTH:259

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01224

SEQUENCE DESCRIPTION:

GATCCAAATG GATTACCACT GTGCTACAGA CTCTTATTA TAGAACAGCA TTCTATTCTA 60
 CATCAAAAAT AGTTTGTGTA AGTTAGTTT GGTACCATC TAAAATATT TTAATGTTT 120
 TTTACATAAA AATTTATGTT GTGTTTTAAA ATCCTTAGGG GCTTTATCTA TTTTCTAAG 180
 TCAGTTAACT GTACTTCTAA AAAAAGTATT TTGTATCTAC TTTTGTAAC TCGTCAGAAT 240
 AAAATATATT GAANGCAA 259

SEQ ID NO:1083

SEQUENCE LENGTH:258

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01225

SEQUENCE DESCRIPTION:

GATCGCTTCA CATNTATAAA AAAAATAANA ATACCCGGGC AAGCTTTCTT TGAAGNTGCT 60
 ACAGCATTAA ATATCGAGAA TTTTGGGTGG GAGAGAGCAG TTCAATTTTC TTTACCAGCT 120

EP 0 679 716 A1

GAAGTTCATT TATGATACAA AAGAGATGAA ATGGAAGTGG CAATATAAGG GGATGAGGAG 180
GCATGCTGGC AACCCCTTCTT TTAAGATGTG CTCAATTTGT ATAANTGGTG TTTCATGNAA 240
TAATCATCTT GGAGGAAA 258

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SEQ ID NO:1084
SEQUENCE LENGTH:342
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01226

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SEQUENCE DESCRIPTION:
GATCGCCGCC CAGGGTTTCA CGGTCGCAGC CATCTTGCTG ACGTCTGNCT GNCAGTCTGCTA 60
TGAAGTCTCG ACCCTAAGCC CAGGGTCTGG CCTTGAAAGC TCCGCAGAAA TGATTCCANA 120
ACCCAGGAG CAACCACTGG CCCTACCGTG GGACTTACTC CCTCCTCTCC TTGAGAGGC 180
CCATGTGTCG CTGGGGAGGA AGTGACCNTT TGTGTAAGT TAACCGAAAG TTTTTCAAA 240
AATCCTAGAT GCTGTTGTTT GAATGTTACA TACTTCTATT NNGGCCACAT CTCCCNCTCA 300
CTCCCNCTGCT TAATAAACTC TAAAAATCCA CTTGTATTTA AA 342

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SEQ ID NO:1085
SEQUENCE LENGTH:260
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01227

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SEQUENCE DESCRIPTION:
GATCTAAGAA GANACTAGCC TTGTGGAGTA TATAGATGCT TTTCATTATA CACACAAAAA 60
TCCCTGAGGG ACATTTTGAG GCATGAATAT AAAACATTTT TATTCAGTA ACTTTTCCCC 120
CTGTGTAAGT TACTATGGTT TGTGGTACAA CTTCACTCTA TAGAATATTA AGTGGAGTG 180
GGTGAATTCT ACTTTTATG TTGGAGTGGA CCAATGTCTA TCAAGAGTGA CAAATAAAGT 240
TAATGATGAT TCCAAATAAA 260

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SEQ ID NO:1086
SEQUENCE LENGTH:256
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01228

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SEQUENCE DESCRIPTION:
GATCCTTAAT GTTTTGATTN TTGTTTCTG AAATTGGATT TTATTTTATT TTATCTTATA 60
ATNNCAGTTC ATCTAAATTG TGTGTTCTGT ACATGTGATG TTGACTGTA CCATTGACTG 120
TTATGGAAGT TCAGCGTTGT ATGTCTCTCT CTACACTGTG GTGCACTTAA CTTGTGGNNT 180
TTTTATACTA AAAATGTAGA NTAAAGACTA TTTTGAAGAT TTGANTAAAG TGNNGNNGTT 240
TGCATTACAC CTCAAA 256

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SEQ ID NO:1087
SEQUENCE LENGTH:254
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

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CLONE:HUMGS01229

SEQUENCE DESCRIPTION:

GATCTTTAAA CTCTGGCTTC TTCCTCCTCA ATCTTGACAG AAAAAGGGTG CAGACGTCTG 60
 GTTCAAAGAG TTGGATATCA ACACTGATGG TGCAGTTAAC TTCCAGGAGT TCCTCATTCT 120
 GGTGATAAAG ATGGGCGTGG CAGCCACAA AAAAGCCAT GAAGAANGCC ACAAAGAGTA 180
 GCTGAGTTAC TGGGCCCAGA GGCTGGGCC CTGGACATGT ACCTGCAGAN TAATAAAGTC 240
 ATCAATACCT CAAA 254

SEQ ID NO:1088

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01230

SEQUENCE DESCRIPTION:

GATCCATCCC ATTCACCCAG TGACTTCTTT TTGCCCAGGC CGGGACTTTT TGCATCAGTN 60
 ACGTTAACCA GATGACTTTG CCTGTAACCA AACCTCATGC ATCCACGTTT GCGTCTGGGG 120
 AGGAATAAAA AGACATCGTT CCCGCTTCTN CGTTTGTNA TTCCTACTGC CGCCATAGGA 180
 ATTATTTCTG TGGCTGANCG TTACCAGCAC CCCGAGANCA CATTTTGATN GANTCAGAGT 240
 AGAGGNCATG GCTGTNTTCT NAAAANGCCN CGCCATGNAA NTGCCAATCC CCTTTN 297

SEQ ID NO:1089

SEQUENCE LENGTH:253

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01231

SEQUENCE DESCRIPTION:

GATCGCATTT TTGTAAAGA ACCATGTGTG TTTATATGTG TTTATATATA TACTTGTGTA 60
 TGCAAAGGTA AAAGTCTGAA AGGATATATG CTAAGTGTTC ACAATGATAA CCCCCAGGA 120
 ATGGGATTGG AGGGGAGGGG GCTTCTGTGT TTGTNATGTA TGCTGGGTGG GANNTTGTGC 180
 TTTTATTCT ATATTGTTG AATTTTTTA CAGTATGTAT TATTTTGTGA ATAAAAATTT 240
 TAAAAAATTC AAA 253

SEQ ID NO:1090

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01232

SEQUENCE DESCRIPTION:

GATCTGCCTT GAAATTTAAA AATCTAAATA GCTCTTAGTT GAACAGGGGA GATATAAACA 60
 AAGTTTGCAA AATTCCTAAA ACACGATGAT AATAAACATC ATACATCAGA NTTTTGAGAT 120
 ATAATTAAG CAGTACTTAG AAGAAAATGT ATAGCCTTAA ATATTTAACA TCAGTAAAN 180
 TGANAGGNTG AAAATTGGGA TTAAATTCC CAACTCAAAG AGCTAGAAAN NGANTTACAA 240
 AGCAAGNNGA AA 252

SEQ ID NO:1091

SEQUENCE LENGTH:251

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01233

SEQUENCE DESCRIPTION:

GATCTCATGG GCTTTCCTGG AGGAAAGTTT TTTTGTTCG TTTTTTTTA AGACTTGAAA 60
CTTGTAACGT AGATGCTGTA GTTTTTTGCC ATCTGTAGTG ATGTAAAGAT TTAACCTGA 120
GAGACTTTN CTTGTGTTAGA TTATGAGAAG NACTAGATGC TTAGGTTTC ATTTCCCTT 180
AATTGCNATT CTTGTGCGCT NGTTGGGNGG GAACTGTTAT TTTCCNCAAT AAAAAGTAAG 240
TCTTATCGAA A 251

SEQ ID NO:1092

SEQUENCE LENGTH:250

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01235

SEQUENCE DESCRIPTION:

GATCATTAAA ATCAACGTTA TCTAAGACAG CTGTATCACA TTTTGGGAT ACATCATGGT 60
ACAGTCAGAA GCATATAAAA TTATGGTTCT GCTTGTGAGN CNCATACAGA ATCCAATACA 120
TTTGGACAAA CTGCCCATTC CTGCAAGTTA ATGCCCTTTT TGAAGCTTCA TTTCTCTTG 180
TAAAGTACAG ATAGGAATCA TTATTTGTG GAGTTGCTGT AAAGATTAA TAAAGGTGAA 240
TGAAAATAAA 250

SEQ ID NO:1093

SEQUENCE LENGTH:248

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01236

SEQUENCE DESCRIPTION:

GATCCCAACA AAGATACAAG TGAAAACGCA GAAGGTCAAA GNGATGAGAA CAAGGACGAC 60
TATACAATCC CAGATGAGTA TAGAATTGGA CCATATCAGC CCAATGTTCC TGTGGTATA 120
GACTATGTGA TACCTAAAAC AGGGTTTTAC TGTAAGCTGT GTTCACTCTT TTATACANN 180
CNAAGAAGTT GCAAAGANTA CTCATTGCAG CAGCCTTCCT CATTATCAGA AATTAAAGAA 240
ATTTCTGN 248

SEQ ID NO:1094

SEQUENCE LENGTH:248

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01237

SEQUENCE DESCRIPTION:

GATCACTGNC AAAGTGGGAG CACTAAGGGG TGGGTGGGA AGTGAAATGT TAGGCGATGA 60
ATTCCTGAGC ACCTTGTTT TNTNCCAAGG TTCGTAGCTC CTCTNTGCC TTCCAAGCCT 120
GTAACCTCGG AGGACTATCT TTTGCCTTN ATCCTTTGTN TTGTTTGAGT GGGNCAGCCC 180
CAGAGGAACT GATAAGCAA TGGCAAGTTT TTAAGGAAG AGTGGAAGN NCTGCAANTA 240

AAANNCCN

248

5 SEQ ID NO:1095
 SEQUENCE LENGTH:246
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01238
 10 SEQUENCE DESCRIPTION:
 GATCTCCATG CGGTCCCTGG AAGTACCCAT TGAACATGC GTATTTGTGT ATAGCAGAAC 60
 TCTGAAATAA TATTCTGACA GCAGTTATCT CTGAGGAATT GGGTTATAGG TGATTTTCCC 120
 TTTCCGCATG ATAAATTTAT GTAATATTTG ACTGACTTGA CCGTAAGTAT GTTACTTGTA 180
 15 TAATAAAAGG AAAAAAGGTA CTTCTATTTT GAAAAATAA AAATAAAAGC CTTTGGGTTC 240
 TTGAAA 246

SEQ ID NO:1096
 SEQUENCE LENGTH:315
 20 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01239
 SEQUENCE DESCRIPTION:
 25 GATCTGTCA GGGNGTCCCC CATGCCTGGA AGAGGAGCTG GTGGCTGCCA GCCCTNGGGC 60
 CCGGCACAGG CCTGGNCCTT CCCCTTCCCT CAAGCCAGGG CTCCTCCTCC TGTCGTGGGC 120
 TCATTGTGAC CACTGGCCTC TCTACAGCAC GGCCTGTGGC CTGTTCAAGG CAGAACCACG 180
 ACCCTTGACT CCCGGGTNNN NNGTGGCCA AGGATGCTGG AGCTGAATCA GACGCTGACA 240
 GTTCTTCAGG CATTCTATT TCACAATCGA ATTGAACACA TTGGNCAAT AAAGTTGAAA 300
 30 TTTTACCACN TGAAA 315

SEQ ID NO:1097
 SEQUENCE LENGTH:245
 35 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01240
 SEQUENCE DESCRIPTION:
 GATCCCGGGA GCCTTGCCGC ACTGCCTTGT GGGTGGCTTG GCGCTCGTAA TTGCTTCCTG 60
 40 TGAACGCCTC CCAAGGACGA GCCCAGTGTA GTTGTGTGGC GTGAACCTCG CCCGTGTGTT 120
 CTCAAATTCC CCAGCTTGGG AAATAGCCCT TGGTGTGGGT TTTATCTCTG GTTTGTGTTC 180
 TCCGTGGTGG AATTGACCGA AAGCTCTATG TTTTCGTAA TAAAGGGCAA CTTAGCCAAG 240
 TTAAG 245

45 SEQ ID NO:1098
 SEQUENCE LENGTH:245
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 50 CLONE:HUMGS01241
 SEQUENCE DESCRIPTION:

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EP 0 679 716 A1

5 GATCTGCAGC AGCCGAAAAT GCGTTNTGGT AAACCTGGCC TCAAATTCAT ACTACCATAA 60
CTGTTTTTAT ATATTGCCAC TAATTTTGAC TGGATTAAAT AGCACTTTAT TGTACANCTA 120
CAAAAAAAAA TATATNCCTA GAATNGTNNC CAGTGTAATT CCTCTAATGT CCTGGTGCCT 180
TTTCATATAT TTCCAGNATT TTNATACTAT ATNGGTATTT CCTTTGTATA AATNGATNGA 240
TNAAN 245

10 SEQ ID NO:1099
SEQUENCE LENGTH:251
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01242
SEQUENCE DESCRIPTION:
15 GATCTTAGGC TTTTCACTTT TTTTGTGTTT TTTTGTGTTT GAAAGAAAGA AAAAAATACA 60
ATTAACAAGC CTCTTTTGTA AATGGGTTTC CTTTCTATGT ATAAAATCGT GGTGGTCCCT 120
TGTTTTTACA TGTTTCATGCT GTGTAATTTT GAGATGTTAC TGAGATATGT TCTGAACATA 180
ATGTGCATTT TTTNCTGTAC AGATGAAATG GGAGANTTTA ATAAAGAGTT TGCAGGTTTT 240
TNCTTGTTAA A 251

20 SEQ ID NO:1100
SEQUENCE LENGTH:247
SEQUENCE TYPE:nucleic acid
25 TOPOLOGY:linear
CLONE:HUMGS01243
SEQUENCE DESCRIPTION:
GATCCAGCCC TGAGCATCAC CCAAGTGCCT GATGCCTCAG GTGACAGAAG GCAGGACGTT 60
CCATGCCGAG GCTGCCCCCT CACCCAGAAG TCTGAGCCCA GCCTCAGGAG GGGCCAAGAA 120
30 CCAGGGGGCC ATCAAAAGCA TCGGGATTG GCATTGGTTC CAGATGAGCT TTAAAGCAA 180
ACATAGCAGT TGTTTGCCAT TTCTTGCACT CAGACCTGTG TAATATATGC TCCTGGAAAC 240
CATCAAA 247

35 SEQ ID NO:1101
SEQUENCE LENGTH:266
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
40 CLONE:HUMGS01244
SEQUENCE DESCRIPTION:
GATCTTCCCT AAAGAGCAGN GGACCANATA NGAAGAGGAA AATTTCTACC TTGAACCGTA 60
TCTGAAAGAG GTTATTCGGG AAAGAAAAGA AAGAGAAGAA TGGGCAAAGA AGTAATCATG 120
TAGTTGAAGT CTGTGGATGC AGCTGTTATG AAGATGGTTA AACTTGAANC AAACAATTTT 180
45 AAGANTTATT TNGTCTGAAN GATGTTTTAC TTAAATAAA TGTCTCNTTG NAATGGCTGG 240
AGGTTTTTGG GNGCCAAACC NTTAAA 266

50 SEQ ID NO:1102
SEQUENCE LENGTH:256
SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS01245

SEQUENCE DESCRIPTION:

5 GATCCCAGGT CCCAAGGAGT GACAGGGGCT TCCTCCCACC TTCTGTCCTT GTCCAGTNAT 60
 GTAAATAATG TGCTTTTCCT CTCCCCGAGT CTTTTTTTTT AAAACCTACC GTGGTTCCTN 120
 AGCTAACTGC ATTCCTTACC CAGGCAGAGA CTGTCCTATG CCTCGNGCTT CCAAACGAGA 180
 CTCAGACCGC GACANAGCCA CCGTATTTAT GGATTGCCAA ANTAANTAAN GCCCAAANCC 240
 10 ATCGGTCTCT GTGAAA 256

SEQ ID NO:1103

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

15

TOPOLOGY:linear

CLONE:HUMGS01246

SEQUENCE DESCRIPTION:

20 GATCCTGGTG CTGGACAACG CTGCCATTGT CTGCAACTTT GGCAGTGAGC TCAGCCTGGT 60
 GTATGTGCCC TCTGTGCTGG AGAAGCTGGA CTGAGCGCAG GGCCTCCTTG CCCAGGCAGG 120
 AGGCTGGGGT GCTGTGTGGG GGCCAATGCA CTGAACCTGG ACTTGGGGGA AAGAGCCGAG 180
 TATCTTCCAG CCGCTGCCTC CTGACTGTAA TAATATTAAT CTTTTTTAAA AAACCATAAA 240

SEQ ID NO:1104

25

SEQUENCE LENGTH:245

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01247

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SEQUENCE DESCRIPTION:

35 GATCTGGGCA GTNAGATAGT GCTCTATGCC TAAGGTGAAG CCACACTAGG NTGAAGCCTC 60
 ACTTCCCTGT TTAAGCAATG CAGTGCCTGC TGCCCGTGTG CANGAAGGTA CAGCCATTCA 120
 GATAAGTGGA ACTATTGAGT TACATAAAGA AAGTAGATT GCANTNNTCN GGCAGACGTT 180
 TATACANCAC CACGGTGCTT TTATACATTG TNCTNATTTT AATAAACTG ANGTTCTATG 240
 TGAAT 245

SEQ ID NO:1105

SEQUENCE LENGTH:240

40

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01248

SEQUENCE DESCRIPTION:

45 GATCTGGCTT CCATTGGGCC CCCTCATTTC CCAAATGTTT AAATGTATTG GATTGGATT 60
 CTCAATGTAT AAGTTGCCTT ATCTGTTAAT GTCTATCTTC TGTCTCTTA ATTTGTATA 120
 TCTGCTGTTT TGCTTTTGA TACATTTTCT AATTAGAAGT CACATGATAA ATATAATCAG 180
 TATAGTAATA ATACCATAAT GTGCACATAC TCAATAAATA AATGACTGCA TTGTTGTAAA 240

SEQ ID NO:1106

50

SEQUENCE LENGTH:240

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01249

SEQUENCE DESCRIPTION:

GATCCATTN TCCNTGTAAC TNGGAGAAAAG GCCAGTCCCT GTAACGGGGC AGCCCTCTCT 60
 TTCCCTCGGT CAGCTCGTGT NAATCCTGGN ACCTCTTCCG GTCGGCTCTG CCCGCTGTTT 120
 TGGGGTCGAC TGCCACGACT TTNNATTCAA GAAGCTTCCT CCAGGCGGNA GCGGCTATTT 180
 TCCCTAAATN AGAATTGTTA CATTGCAAAAT NGTTGAATAA AATATTTNGC GGTCTTAA 240

SEQ ID NO:1107

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01250

SEQUENCE DESCRIPTION:

GATCTGAAGA AATGATGGAA TGGGGAGTGT AGAGAAATGA GAGTCTGTAT GATTCTGGAA 60
 CAGAGACATC AGAAGGAAAG ACTGGTGAAA AGATGTATCT TTGTATATTA ATAGCTGTAA 120
 TGTAGCTTCC TGATGCTTGA CTAATTGAGG TGTTAATTCT GACTTGAGAA TCTTTTCAT 180
 GAATGATTTT AAAGAAAAAT TTGGATTTTA AAGGTATTAA AATATTTTNG TTTTGTA 239

SEQ ID NO:1108

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01251

SEQUENCE DESCRIPTION:

GATCCGCAGT CGAAAAAGAA CAAGCCACAG AAACGGGCTC GTCGTGCCAG GACACAGCAG 60
 TGTCTTTCAA AAAATCAAAA CCAGAAGNTT TATCANCAGC AGGAAGNATG TGGGCTCTGT 120
 CAAGTTCACC GTCACCATCA AGCCACTGCT GTGGAAGAGT TTGNCAACAG GNCAGTGTCA 180
 CAGCACANCT TCAGANGCAG CATCCGNGTG TCGTCCAACA GANGNCCTNG TCCGGTCAN 239

SEQ ID NO:1109

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01252

SEQUENCE DESCRIPTION:

GATCTATGTC CGGTGTGGGT TTTTGTCTC TCGAGTTTG TCTTAATAA AGGCCTTTTT 60
 TGTTTCAAAT TACATACGCT TTTTACTGCA CAATTTTGT ATTGACCTTA TTCAACTGA 120
 AGCGATTATT TCCAGCAGGT TTAATTCGA CAATAAGATA TATTTNAATA GTTTTACCTT 180
 TCGCTAGAAT TTTGTATTGT TTAACAAGT AAATGAATAA NTTTGCTGAT GATTCAA 238

SEQ ID NO:1110

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01253

SEQUENCE DESCRIPTION:

5 GATCAATGAA ATGCACATAA ATNAACTGGT TCCATCAAGA CTGTGCACCC AGGCCTTACA 60
 GTCCAACCTT TTTCTGTGTC TGGCTAATAT TTAATACTAG AAAAATATT CCTAATCAAC 120
 ATGGAGTGGA GAGTTTATTC ACTGTCTTAT CTGCAGAAAT TTGCTGTCAA TATATAACCC 180
 GCCTGCAGTG GAAAGTGTAT AGTGTTTTGT AATAAATGGC CTGATGCTAA TGTGTAAA 238

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SEQ ID NO:1111

SEQUENCE LENGTH:237

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS01254

SEQUENCE DESCRIPTION:

20 GATCTACCGG GGGCTATTAG TTTCAATGTA GTGATGAACA CAACTATAT TTTGAGTTCT 60
 CTGCAGCAAG TGGAAATGTGG TATGAAAATA TCTGATATTT ACAAAGATGA TACTGCTAAG 120
 TCAGAGTCAC GTTTATTGCT AATATGATGG TGGAGTGTG TCTTCATTCA TAATGAAGGG 180
 AAATGTTATT TTTAATAGNG GTTAGTGAAA TAAAANTAAN CCTATTTTCT AANCAAA 237

SEQ ID NO:1112

SEQUENCE LENGTH:268

25

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01256

SEQUENCE DESCRIPTION:

30 GATCTGGAGC ATTTGAGCAA GTTATAGAA GAACATGCCA CAAACTGAG CAGGACCAAG 60
 GAAGAGCTTT GAAGGCCTGA GGTCTGCGNA AGGTGGGAGG AGGCAGACGC CCTGCGTGGC 120
 CCATGGTCGG GGCCTCCACG CCGAGGCCGG CAACAAACGA CAGTATCTCG GATTCTNTT 180
 TTTTTTTTT AAATTTTNA AACTNNGGGG TTNCACTNCA NGNTCTGAAT ACTGANTANC 240
 CATGAATNCC TGAATAGTTT AGNCCAGN 268

35

SEQ ID NO:1113

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40

CLONE:HUMGS01257

SEQUENCE DESCRIPTION:

45 GATCAGCGCT GAGGACGGNC TCAAGCATGA GTATTCCGC NAGACCCGNN NCCCCATCGA 60
 CCCCTCCATG TTCCCACGT GGCCCGCAA GAGCGAGCAG CAGCGTGTGA AGCGGGGCAC 120
 CANCCCGAGG CCCCTGAGGG AGGCCTGGGC TACAGCCAGC TGGGTGACGA CGACCTGAAG 180
 NAGACGGGCT TCCACCTTAC CACCACGAAC CAGGGGCCTC TNCNGCGGGN CCNGGN 236

SEQ ID NO:1114

SEQUENCE LENGTH:235

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SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS01258

SEQUENCE DESCRIPTION:

GATCTGTTGA CTTCCCTGGG TAGGACACTG CCACCTCTGG GCTCAGGTCC TNATGCCTCC 60
 AAATGGCATC TAGAGTTTGA GCAGCCTTCT TGGCTGCAAG GCAGGCCTAG CCTGTGGCAG 120
 CGGGCTAGGG CCCGCAGAGC ATTTGGTGCC CCTCCATGTT GCAATGCAAA CACCTTCACC 180
 ACTGGGGCAG TGGGGAGAGA TGGCTATATT AATAAAATAA CGTGTGTCTT TCAAA 235

SEQ ID NO:1115

SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01259

SEQUENCE DESCRIPTION:

GATCATNATT TTTNCTGCGT AGTTGACAGA CTTAGCATAT TAGTTTTTNN TACTCCTACA 60
 AGTGTAATTT GAAAAATCTT TATATTAAAA AAGTAAACTG TTATGAAGCT GCTATGTACT 120
 AATAATACTT TGCTTGCCAA AGTGTGTTGN NTTTTTTGTN GTTTGTTTGT TTGTTTGT 180
 TTGTTTCATG AACAACAGTN TCTAGAAACC CATTTTGAAA GNGGAAANTT ATTAN 235

SEQ ID NO:1116

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01260

SEQUENCE DESCRIPTION:

GATCACAATT NGCTTCATGA ATCAAGGTGT GGAAATGGTT ATATATGGAT TGATTTAGAN 60
 AATGGTTACC AGTACAGTCA AAAAAGAGAA AATGAAAAAA ATACAATAA AAGGAAGAAA 120
 CACAATTCA AAGATTTTTC AGTGATGAGA ATCCACATTT GTATTCAAG ATAATGTAGT 180
 TTAATAAAAA AAAANGGNAA AACNTTGTT GNAANTNCCN CCTTNCCTC NGGN 234

SEQ ID NO:1117

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01261

SEQUENCE DESCRIPTION:

GATCCCCGN TCAGCNCCNA AAGTGCTGGG ATACAGGCAT GAGCACCACG TCCGNCTAGA 60
 CTTTACCTTT CTAAAGAAAT TGTTTACTGG ATTTATAAGA AGTTAATTTT TGAAATNAC 120
 ATATTTTGT NTGATAGAAA GAATGGAGCA AGTNGTGCCT ATTTCTCCA AGTCAGATAA 180
 GGTTTCTAAA ATAAATAAAT TTCTAGCATA TAAAGGGTAG AGATAAACTC NNNN 234

SEQ ID NO:1118

SEQUENCE LENGTH:233

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01262

SEQUENCE DESCRIPTION:

5 GATCACAGGT CTTCCCTGTG AACTTTGGTT TCTTTCTATA AATGTGTGTG GTTTTCAGCG 60
 CTCAACTCCT GTCTTCAAAT GGTAGTAAGT NCTACTTCTA CTTCTGTCAT TCAGAACATT 120
 TTATGTCAAA TGATGTAATG CAGAAATNCT TGTGCATATT TGTAAGTGAA GGAAGCTTTT 180
 TAGATTTATT TNNGTTTTTA ATAAAATTCA GATTCCTATT CTAAGCTGGT AAA 233

10 SEQ ID NO:1119

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15 CLONE:HUMGS01263

SEQUENCE DESCRIPTION:

20 GATCTNCTAT GCAGTTCTGC CATGCNTCCT GTTGGTCTCT CTGTGTTCTT TGTTACTTGG 60
 GTGCAATAGC AACTTCCCTA CCCCGTGCAT TCCATCTTNN ATGTTGTGTA AAGTTCTTCA 120
 CTTTTNNNTC TGAGGGCTGG GGGTTGGGGG AGTCAGCATG ATTATATTNN AATGTAGAAA 180
 ATGTGACATC TGGATATAAA ATGAAAATAA ATGTTAAATT AAATGGAAAA 230

SEQ ID NO:1120

SEQUENCE LENGTH:237

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01264

SEQUENCE DESCRIPTION:

30 GATCTAAGTT AGTCCAAAAG CTAAATGATT TAAAGTCAAG TTGTAATGCT AGGCATAAGC 60
 ACTCTATAAT ACATTAAATT ATAGGCCGAG CAATTAGGGA ATGTTTCTGA AACATTAAAC 120
 TTGTATNTAT GTCATAAAN TTCTAACACA AACTTAAAAA ATGTGTCTCA TACATATGCT 180
 GTACTAGGCT TCATCATGCA TTNGTAAATT TGTGTATGAT TTGCNNNTNT GNNNGNN 237

35 SEQ ID NO:1121

SEQUENCE LENGTH:234

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS01265

SEQUENCE DESCRIPTION:

45 GATCTGGCCA GTTGTACTTT TAGCTCCCAG AGGGAGAGTT GGTGGTATTA TGAGTTGAGT 60
 AAAAACCATC CAGGGGAACT TGAGGGAGCA GTCTGTTGCC AGTAATGTTT CTTGTGTGCC 120
 ATTAAACCAC CTCCAGATGA GTGGAGGAAC ATCACTTTTT AATTTTTTAA TTGTATTTGG 180
 AATTGTTGCC GTGTACTAAG AACTTGACCT AAATAAAATC CCACAAAGTA TAAA 234

SEQ ID NO:1122

SEQUENCE LENGTH:232

50 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01266

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SEQUENCE DESCRIPTION:

5 GATCCTCAGG ACGCAGGTCA CATTACCTG TGGGCAGAGG GACAGGTCAG ACACCCAGGC 60
 CCACCCAGG GACCCCTCCAT GAACTGTGCT CCCAGCCTTC CCGGCAGGTC TGGGAGTAGG 120
 GAAGGGCTGA AGCCTTGTTT CCCTTGCAAG GGGGCCAGCC ATTGTCTCCC ACTTGGGGAG 180
 TTTCTTCTG GCATCATGCC TTCTGAATAA ATGCCGATTT TATCCATGGA AA 232

SEQ ID NO:1123

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SEQUENCE LENGTH:235

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01267

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SEQUENCE DESCRIPTION:

GATCAGGAGG CATCATTGAG GCCAGGAGCT CTGCCCCGTA CCTGTATCCC ACGTACTCTA 60
 TCTTCATTCT CTGCCCCTGC CCCAGAGGC CAGGAGCTCT GCCCTTGACC TGTATTCCAC 120
 TTACTCCACC TTCCATTCTT CGCCCTGTCC CCACAGCCGA GTCCTGCATC AGCCCTTTAT 180
 CCTCACACGC TTTTCTACAA TGGCATTCAA TAAAGTGTAT ATGTTTCTGG TGA AA 235

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SEQ ID NO:1124

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS01268

SEQUENCE DESCRIPTION:

GATCGATGCC ACGTTCTGTAA GGTCTTAAGT CCTTCTTGGC TCCTNATGTG GTCCCTCTCC 60
 TCGGAAGAAC TGCCAGCCA CGGGTTTNA ACCCACCTGT TGCTCCTNAG GTCGTCACTA 120
 TATCAACAGT CACAAACCCA ATGGCAATAA AGGCACTGAC GATAGCTGGC GCGCGCNACG 180
 CCACACACCA TTTNAGATG CCGTTGCAAT TAAATCTTGC CACACTGTCC TCCTGAAA 238

30

SEQ ID NO:1125

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SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01269

SEQUENCE DESCRIPTION:

40 GATCCCTGGC TGGAAATGTCA TACCATTGAC CCATTTGAAG AGTTAAAGCT GGATTTGACT 60
 GCTCTATTCT ACCAGGAATA TTGTTAGGGT AGCCTTTTAC CAGTTTCTAA ACANTNGTAA 120
 TCATTTATTG ACTCAGCAAT TCCTCAGATA ACAGGTCAAA AGATGTACAG ATACATTNN 180
 NAGTTTCTT GCTATTAAG GCACAAGAGT TTCCTTGAT TTTGACTGAA A 231

45

SEQ ID NO:1126

SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS01270

SEQUENCE DESCRIPTION:

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5 GATCTACAGT CATGCTTTAG CATGGCTATG GAGCTAATTA TCAAGCTTAA AGGGTAACTT 60
 TGGGAGGACT CCTCCCTTCA CTCCTAGTCT CCCTTGGAAG AGCAGTCCAG GCTCAGGGAA 120
 GGGAAATGGAT AGGATGACAC AGTAAGTACA GAAACTGAAG CTGTCAATAG TGAAGGAAAA 180
 AGGGGAATTC TTCGTTGCTT TGGCATTNAC ACATAAGTAC TTTGATTAAA 230

10 SEQ ID NO:1127
 SEQUENCE LENGTH:229
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01272
 SEQUENCE DESCRIPTION:
 15 GATCCAAAAT TTATAGCATT CTTCTACCAC CACAGGGGCT CATATGACAT TAACAGACAA 60
 GACACTTTTC AGAAAGACAG GTTGTTCCTT TGGGCCACAT CTAAGAAATC TTTGTCTAGC 120
 CAAAAGCCAC AAATAATTC TCATTTTTTG GCTTCTGGAA GATGTACAGT TAAATGTTAT 180
 ATTTGGGACT GTTATCTAAT TTGATTAAAT TGCACTCTAC AATATGAAA 229

20 SEQ ID NO:1128
 SEQUENCE LENGTH:229
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 25 CLONE:HUMGS01273
 SEQUENCE DESCRIPTION:
 GATCAGGGCT GAGGGTAAGG AAAAGAAGAG ACTAGGAAAG CTGGGCCCAA AACTGGAGAC 60
 TGTTCGTNTT TCCTGGAGAT GCAGAACTGG GCCCGTGGAG CAGCAGTTTC AGCATCAGGG 120
 CGGAAGCTTA AAGCAGCAGC GGGTGTGCCC AGGCACCCAG ATGATTCCCTA TGGCACCAGC 180
 30 CAGGAAAAAT GGCAGCTCTT AAAGGAGAAA ATGTTTNAGC CCAGTCAAAA 229

35 SEQ ID NO:1129
 SEQUENCE LENGTH:227
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01274
 SEQUENCE DESCRIPTION:
 40 GATCCTTACT ACTGGAATTA CCGGGTTAAA AGGAAATGCT TACCACTAAG ATGTCAGTAT 60
 TCTCCTCATG GATATTTTCA ATCTCAATGT TGCCAGTCTA ATAGTATAGT ATGTGGTTGC 120
 TTTACTGCTG TTCTCCCCAC CCCCGTGGAG TTGTGTCATT ATTTAATGA ATGTGAGCTC 180
 TTGACTTACT CTAGAATTCT AATACAGATA CTTTCTGCAC TAGTAAA 227

45 SEQ ID NO:1130
 SEQUENCE LENGTH:227
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01276
 50 SEQUENCE DESCRIPTION:
 GATCCGCTTG GTGACGGGCG TCTTCCCAGA TGCTGGCGTC ACCGCTAGAC CAAGGAGCCC 60

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TCTGGTGGCC CTGTCCAGGC ATAACAGAAG GCTCGCACTC CTGTCTTCTG GTCACCTTCTC 120
 ACTATGTCCC CTCAGCTCCT ATCTCTGTAT GGCCTGGTTT TTCCTAGGCT ATGATTATTG 180
 AGTGAGGATT ATCATAATAT TGAATAAAAA AGTAATTGCT ACCCAAA 227

SEQ ID NO:1131

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01277

SEQUENCE DESCRIPTION:

GATCAGGATT GTCCTACAGT TGTAAATAAG ANTAGGTCCT GTTTATTTTG ACATCTNITT 60
 ACAAATGCAT TGTATTAGGG TGTGAATATT CTGAACCATC CTCTTGTTA AAGTTTGGAA 120
 ATTTTATTG TTAATGTAA CATTTTAATG GTTGAATAA TTATTTGTAT AGATATGAAT 180
 ATAGTATTTN ATTTAAGANA ATAACTTTG CATTTTGTCA TNGTAAA 227

SEQ ID NO:1132

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01278

SEQUENCE DESCRIPTION:

GATCTGAAAT TTGTGTATNC TAAAGTAATT TNGTTTTATG TATTGGAAGT TCACTTAAAA 60
 ACTGGAAATA TTTTCTAGAA GGGTACCACA CAAAAGGAAT CATCTTTAAG CTGTTTAATT 120
 AACCTAATAA AATAATNTGA TGGGGAAGGC ATTCTAATTG TTTCTGATTT TNNGAGTGGT 180
 TCCTGCTAAN TCATCANTAT CANTACAGCT TGATTTGATT TAAGAAA 227

SEQ ID NO:1133

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01279

SEQUENCE DESCRIPTION:

GATCTTAAAT GTTATATTGA TAACCATGCT CAGCAATGAG CTATTAGATT CATTTTGGGA 60
 AATCTCCATA ATTTCAATTT GTAACTTTG TTAAGACCTG TCTACATTGT TATATGTGTG 120
 TGAATTGAGT AATGTTATCA ACGTTTTGT AAATATTTAC TATGTTTTTC TATTAGCTAA 180
 ATTCCAACAA TTTTGTACTT TAATAAAATG TTCTAAACAT TGCAAA 226

SEQ ID NO:1134

SEQUENCE LENGTH:225

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01280

SEQUENCE DESCRIPTION:

GATCTTTACC AAATTCCTGA CTCAGAGTTC CTCCCATTTN CTTCTGACTC TCATTTTATT 60
 CTTACCTCTC ATTTTATTCT TATGATGTTT ACCATTTCTN TTCTCCTCAG TGTCCCTCTC 120

TGAGTGGTAA GAGTATGTGA ATAAGCCAGT NCTGAGACCG GAGCACGAGG CAACTGCTCA 180
 ATGTTGGTCA TTGCTACTGT TATTAAATGT AACTTAAGGG NNAAG 225

5 SEQ ID NO:1135
 SEQUENCE LENGTH:224
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01281
 10 SEQUENCE DESCRIPTION:
 GATCTGACTT AAAAACCCAC CAGCATGCTC AATCCCTTGT NATCCTTATG GAATCTGTAT 60
 GTTAACTCTC TGGGTGTTCA GGCTTCTATT TGAATGCTGT TGTNACCCTG TTTGCAAAAT 120
 GAATATGACA CTCTGTGGAT TATTNCTCT GTAAGGCACA AGTNCTTCTN ATGATTANTT 180
 15 TGACGTTTCA NGAGCAAAAG CAAATTNANA CTCTCTTTCAG CAAA 224

SEQ ID NO:1136
 SEQUENCE LENGTH:223
 SEQUENCE TYPE:nucleic acid
 20 TOPOLOGY:linear
 CLONE:HUMGS01282
 SEQUENCE DESCRIPTION:
 GATCCAATAG GAGACACCAG TTCCTTGACT GANCCATGCC CCCACCTAAG TNACAAAATG 60
 25 AGGGAAGTGG GGAGTTAGAT TTCAGAGTCC AGGCCCTAG GTTGGGACCC ACTCCAAATA 120
 ATCTCCTCGG TGTGGGTNGT GGTCTATAG AGGNATANAT GAATAATAAA CATTGTTAAA 180
 NTATACGATA ATGNATAAAG TAATCCTTTC ATCANNTGTG AAA 223

30 SEQ ID NO:1137
 SEQUENCE LENGTH:222
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01283
 35 SEQUENCE DESCRIPTION:
 GATCCATCCG ATGGCCTACC AGCTGCAGCT CCAAGCCGCC AGCAACTTCA AGAGCCCAGT 60
 CAAGACGATT CGCTGATTCC CTCCTCCACC TGTCTGCAG TCTTTGACTT TTCCTTTCTT 120
 TTTTGCCACC CTTTCAGGAA CCCTGTATGG TTTTNAAGTT AAATTAAAGG AGTCGTTATC 180
 40 GTGGTGGGAA TATGAAATAA AGTAGAAGAA AAGGCCATGA AA 222

SEQ ID NO:1138
 SEQUENCE LENGTH:432
 SEQUENCE TYPE:nucleic acid
 45 TOPOLOGY:linear
 CLONE:HUMGS01284
 SEQUENCE DESCRIPTION:
 GATCGACAT CCCTGCGCCC CCATGCCCCC ATGCCCTCT GAGTCACACA GGACAGAGGA 60
 GGCAGAGCTT CTGCCCCTG TTATCTTAC TTTCTTTGTC CAGTCTTTTG TTTTAAATAA 120
 50 GCAGTGACCC TCCCTACTCT TCTTTTAAAT GATTTTNGTA GTTGATTGTG CTGAACTGTG 180

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5 GCNACTGTGC ATTCCTTGAA TAATCACTTG TAAAAATTGT CAGTGCTTGA NGCTGTTTCC 240
TTTACTCACA TTGAAGGGAC TTCGTTGGTT TTTNGGAGTC TTGGTTGTGA CNNCAAGAGC 300
AGAGTGAGGA AGACCCCAA GCATAGACTC GGGTACTGTG ATGATGGCTG CAGTCCAGTT 360
TTTATGATTC TGCTTTTAT GTGTCCCTTG ATACCAGTGG NCTTANCAAT TATACATTNC 420
CTCATANTTA AA 432

10 SEQ ID NO:1139
SEQUENCE LENGTH:220
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01285
SEQUENCE DESCRIPTION:
15 GATCAGACCC AGAGAAAAGT AGTTGTCAGT CATAGCACAC ATCGGACATT TGGAAAACAG 60
CAGTGGCAAC AACTGTATGA CACACTTAAT GCCTGGAAAC AAAATCTGAA CAAAGTGAAA 120
AACAGCCTTT TGAGTCTTTC TGATACCTGA GTTTTATGC TTATAATTTT TGTTCCTTGA 180
AAAAAAGCC CTAATCATA GTAAACATT ATANNCTAAA 220

20 SEQ ID NO:1140
SEQUENCE LENGTH:219
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
25 CLONE:HUMGS01286
SEQUENCE DESCRIPTION:
GATCTTGGGG CCTGTTTTC CATGGGATTC AAGAGGGACA GCCCCAGCTT TTTTGTTTT 60
TAAGCTTAGG AATCGCCTTT ATGGAAAGGG CTATGTGGGA GANTCAGCTA TCTTGNTGG 120
TTTTTTGAG ACCTCAGATG TGTNTTCAGC AGGNCAGAAA NCTTTNTNC TTATAAATG 180
30 AGAAATGTAT ATTTACTAA TAAATTATTN ACCGAGAAA 219

35 SEQ ID NO:1141
SEQUENCE LENGTH:219
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01287
SEQUENCE DESCRIPTION:
40 GATCTAGAGA CAAAGGATAC TCAATGAGGA GCTTTTTTCC CCTCTTGAA CAGGTAAAT 60
GCTTTTCCTT ATTAATATAA TTATAAACA GTATTTATG TAACAGCTAT TCCCATATC 120
TAGGAGTGGC CTAAGAAATG CGTGTTCAG TACTAGATT ATAAATATNC TCTATTGTGA 180
ATAGTTGAAT AAAACAGCTG TTTTTTCTG CTCCTAAA 219

45 SEQ ID NO:1142
SEQUENCE LENGTH:219
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01288
50 SEQUENCE DESCRIPTION:

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5 GATCTGTGAA ATGCTATCTC TCCTGANGCA ATACTGTTGA CCAGAAAGGA CACTCCATAT 60
 TGTGAAACCG GCCTAATTTT TCTGACTGAT ATGGAAACGA TTGCCAACAC ATACTTCTAC 120
 TTTTAAATAA ACAACTTTGA TGATGTAACT TGACCTTCCA GAGTTATGGA AATTTTGTCC 180
 CCATGTAATG AATAAATTGT ATGTATTTT CTCTATAAA 219

10 SEQ ID NO:1143
 SEQUENCE LENGTH:219
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01289
 SEQUENCE DESCRIPTION:
 15 GATCCCTGGA CACTTACGTA CAATGCTTCG TNCTGCCTGA TGACAGCCGG GCCAGCCGCC 60
 AGCNTACAAG GNTTGTNCGA CGCAGCCTCA GCCCTGTNTT CAATCACACC ATGGTGTACG 120
 ATGGCTTTGG GCCTGCTGAC CTGCGCCAGG CTTGTNCCGA GCTCTCCCTC TGGGACCATG 180
 GGGCCCTGGG CAACCGNCAG NTNGGGAGGC ACACGCNTN 219

20 SEQ ID NO:1144
 SEQUENCE LENGTH:218
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01290
 25 SEQUENCE DESCRIPTION:
 GATCTCGGTG CTTCTTCCTG TGCTGTGGTT TACCCCAAAC CTTTAGGTTG TTTATTCATT 60
 CAGATTAGAT AGACTGGAGC CATAAAGTTA ATTTGCACCT AGCTTTTGG AGAATAGCCA 120
 TGATTAACTG CTATTCGTGG TGGGGGTGGG GGGGAACCCT ATGATTACT ATGCAGATGA 180
 AGAGGGTAGG AACTAAATAA AGGACTTTGT AAGCCAAA 218

30 SEQ ID NO:1145
 SEQUENCE LENGTH:218
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01291
 SEQUENCE DESCRIPTION:
 GATCAAGAGG GAGTTCATGC AACACCTGAG AATCTGATTA ATGCACTGAA TAAGTCTGGA 60
 TTAAGTGACC TTGCAGAAAG TCTAACTAAT GACAATGAGA CAAATAGTTA GCTTCTTTT 120
 TTTTCTTTT TATTAAANCT GNGATAGATT TTNTTACCAA GCAGCATTG ATAAGAGGTC 180
 CACTGGTTTT GGTAANCAAT AANCATTTT ATACCAA 218

45 SEQ ID NO:1146
 SEQUENCE LENGTH:218
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01292
 SEQUENCE DESCRIPTION:
 50 GATCCCCAGC TGTTTATGCA TAGATAATCT CTCCATTCCC GTGGAACGTT TTTCTGTTC 60

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5 TTAAGACGTG ATTTTGCTGT AGAAGATGGC ACTTATAACC AAAGCCCAAA GTGGTATAGA 120
 AATGCTGGTT TTTCAGTTTT CAGGAGTGGG TTGATTTTCAG CACCTACAGT GTACAGTCTT 180
 GTATTAAAGTT GTTAATAAAA GTACATGTTA AACTTAAA 218

10 SEQ ID NO:1147
 SEQUENCE LENGTH:217
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01293
 SEQUENCE DESCRIPTION:
 15 GATCCTATCC AGTTGAGGAA TGCTTGCAAT GCTCATTGAA GGGATTTGCT TTGGGACTTT 60
 GTCATCTTCC AGAAAGGAAA CATATTGTAT ATTTGGCCCA GTGTGATTGA TTGCTTTATC 120
 TTTGGTAACT TTACTTGAA TGGGATTGTC TGAATTAATG ACTATTGAAT TAAAACTAA 180
 TTATGAGTTG ACAAATAAAT AAAAGGTAGT GTTTAAA 217

20 SEQ ID NO:1148
 SEQUENCE LENGTH:217
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01294
 25 SEQUENCE DESCRIPTION:
 GATCATAGTC AGAAAGTACT GCAGTTAACA GGAACCTTCT TGTTCAGGCT GTCATAGCCA 60
 CAGTTGCAAA AAGTGCAGTA TTGATTAATG CAATNAGTGC AATNAGTGAC ATCCTGAGTC 120
 TTTTATCTGT TNAGCTTGCT NTNCTNTTCT NTCATACATC AGGATATTGC CTGTAATGTG 180
 GAGTGGACAG GATAAAAATA AGNATTTTAC TTTCAA 217

30 SEQ ID NO:1149
 SEQUENCE LENGTH:124
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 35 CLONE:HUMGS01295
 SEQUENCE DESCRIPTION:
 GATCTGAAGA AAGCTTTTGG TGCTTGCTCT CACAACCACC TCAGTCCTCC CTCCTGTCC 60
 TCCCCTGTCT CCTTCCTCC TCCTGGGTTT ATGTTGTAAT AAAAGAAGAT TGTTGGTGTG 120
 40 TAAA 124

45 SEQ ID NO:1150
 SEQUENCE LENGTH:215
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01296
 SEQUENCE DESCRIPTION:
 50 GATCATAGCT TGTTTTATTT TGTGCTATAA AATTAACAGT ATTAAATGAC TTATATTCTT 60
 AGAATACATC GAGTGTCTTT TCTTAACAGA TTAGTGCCCT TTNATTTTGG TATTCCGTTT 120
 TACGTTACTG GTCCCAGCAT CAAAACCCTT GTTCCATGG CCTGTTTGTA TATTGTCTCA 180

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ATAAACTTG CATCAGCCGG TGGTGGCGGC AGAAA

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5 SEQ ID NO:1151
 SEQUENCE LENGTH:299
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01297

10 SEQUENCE DESCRIPTION:
 GATCATAGTG TTTTGAATC ATTTAATGTC TGCAGCCAAA TTTTAAGGG TAATTTAGAC 60
 CTAATACTGC TCTTGCTGTG TCTTATTAAG TTAAAATTAA TGAATGANTN CTGGTAAAAA 120
 TTCANNNGG CACTCTGTGA GTAGAGAGTA TCATTTAAGC TTATTTNAGT CACATGTAGT 180
 ATATATCTCC TTAAAGCTGT CACTCTCACT TTNCTTACCA TTCTCTTGAT TTNNTCAGAA 240
 15 NCCATCTAGT CATCATCTTT ATACTCTACC TGCTTCTGCA ATTGTATATC ANATNGNGN 299

SEQ ID NO:1152
 SEQUENCE LENGTH:214
 20 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01298

SEQUENCE DESCRIPTION:
 GATCAAAGTT TAATTGCTTC ATTTTGTGTT AAAAAGGGAT ACTGATGTCA GAAAATCTGT 60
 AATATGTTTT ATTCAAAGA TGAAATAAT GTATACAGAC TTGTATGTGA TGGGATGGGA 120
 AATATTTAAA TNCTAGGTGT TTTTTTTTTT TTNAANGNGG AACCNCAATG TTTATAGGAA 180
 AAAANTGATT AANTNGTTC GTTGGCCNT GAAA 214

30 SEQ ID NO:1153
 SEQUENCE LENGTH:214
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01299

35 SEQUENCE DESCRIPTION:
 GATCCCTCTC CTCGCCTGCC TTCTGGAAGA CTTCAGAAGA TTGAGCCTCA CTGGTGCCAG 60
 GAAGCCAAAG CTTACTTTGT AGAACTGACA CTAACTACC CGAAGACTTA GGTGCTTTGT 120
 GTACTTAACC CCAGGACCTN CTTACTTTTT AATATAAAGA GTGATGTTGT ATTCGTGTT 180
 40 CTGCACTTTT TAATATAAAG AGTGATGTTG TAAA 214

SEQ ID NO:1154
 SEQUENCE LENGTH:214
 45 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01300

SEQUENCE DESCRIPTION:
 GATCCCAAAG CCACGCTCAT CCAATCCTGG NGAATCATTT ATTTGAATA TAGACCATTG 60
 AATAGGTGAA AAATGGAAAA GTCACTTTTT GTACATTTGC ATTCCTTCAA TAATGATTAC 120
 50 CATTTGTNCA CATATTTGTT GACCATTGGA ATTGATTTTA GCACAGTGCC TAAAATATAG 180

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TAGGTGCTCA ATAAATATTT GTTAATTGAA TAAA 214

SEQ ID NO:1155

SEQUENCE LENGTH:214

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01301

SEQUENCE DESCRIPTION:

GATCCAAACT AATAAGAATA AGCTGTACAG GAACTAGTGC TCAATATACA TTGTATAAAT 60
 TTGTGGAAAT CTCTTGGATG TNAATTGTTA CTTCAAGTGG CTTTATTAA GATTNCTCA 120
 GACTTACTTG GAGGTTAAAG CAAACCCAAA TGTGTATTAT TTTGTTACAG AGCTCTGCTT 180
 TATAATTTTG TAATAAAGTT TCAATACAGA CAAA 214

SEQ ID NO:1156

SEQUENCE LENGTH:213

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01302

SEQUENCE DESCRIPTION:

GATCGCAGTG GAAGAAGATT AGTGCATCAT TGAGAGAGGA GAAGTGGAGT GTGGGGTGAG 60
 CAAAAGCCAA AATACTAATC ACTAGTACAC CAGAGATGCT CCACAAGGTA TGCTCCCCAC 120
 GGTTTCTTCT CAATTTCAA GGTNAAGATG TTTTTTGTG GTGATATAAA ATTTATTGTG 180
 AATACTTGGT CCATNAAATT GGTACTTGCT AAA 213

SEQ ID NO:1157

SEQUENCE LENGTH:213

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01303

SEQUENCE DESCRIPTION:

GATCTTGTG AGGCATTTAG CTGCCATGCA CCTGTCCCC TTTAATACTG GGCATTTTAA 60
 AGCCATCTCA AGAGGCATCT TCTACATGTT TTGTACGCAT TAAATAATT TCAAAGATAT 120
 CTGAGAAAAG CCGATATTTG CCATTCTTCC TATATCCTGG AATATATCTT GCATCCTGAG 180
 TTTATAATAA TAAATAATAT TCTACCTTGG AAA 213

SEQ ID NO:1158

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01304

SEQUENCE DESCRIPTION:

GATCTCATTT CAATTTCTTT ATTAGAGGGC CTTATTGATG TGTTCTAAGT CTTTCCAGAA 60
 AAAAATATC CAGTGATTTA TATCCTGATT TCAACCAGTC ACTTAGCTGA TAATCACAGT 120
 AAGAAGACTT CTGGTATTAT CTCTCTATCA GATAAGATTT TGTTAATGTA CTATTTTACT 180
 CTTCAATAAA TAAAACAGTT TATTATCTCA AA 212

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SEQ ID NO:1159
 SEQUENCE LENGTH:212
 SEQUENCE TYPE:nucleic acid
 5 TOPOLOGY:linear
 CLONE:HUMGS01305
 SEQUENCE DESCRIPTION:
 GATCTGGTCT GTTCCTGCGT CTGCGGANGG CCCTTGTCTC CCAGCTATCT ATAACCTTAG 60
 CTAGAGTGTG GCCTTGTGGG TTCCTGTTGC TGAGACTTCC TGGATGGAGC CGCCTCACCG 120
 10 CCGGGCCCCG GGCCTGCNCG GANTGTGTCC AATAAAGTTC TTGGATGTGA AAACCTTAACA 180
 ATTTTGTGTA ATAAAAATGG AGAAGCTCTA AA 212

SEQ ID NO:1160
 15 SEQUENCE LENGTH:211
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01306
 SEQUENCE DESCRIPTION:
 20 GATCCTTGGT GTGTAGTTCA GTCTTGCACT ATACAAGCTT TTGTGTATAA ATGTTTTATG 60
 ATATGATTCC CTGTATTTTG CAGGGGTTTT TTTCTCTTTT NCTTTTGA TAAATATGTA 120
 TATCAATATT TTAAATNCAT CTTTGCTTTT TTTAGAGGAG TTTGTAATCA CCTTATAACA 180
 TGAAAATAAA CATTCCTTT TTAACATCAA A 211

25 SEQ ID NO:1161
 SEQUENCE LENGTH:210
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 30 CLONE:HUMGS01307
 SEQUENCE DESCRIPTION:
 GATCCTGTAT ATGTGTGTTT TGGGGGAGCT ATGATAAGTT TTATGGCAA CGGTGGGTAT 60
 TGTTAACTTT TTATTGTCAT CAAAAGTTCA TAAAAGTCCT ATTAATCCCC ATATTCTNNN 120
 35 NCTGCCCTTA ACTCTGGTAT ACACCAAAAA GAAATCTTTA CTTTCCTTGT TTTATCATTA 180
 TAAAAATAAA GTATTTTGCT AGTATGGAAA 210

40 SEQ ID NO:1162
 SEQUENCE LENGTH:210
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01308
 SEQUENCE DESCRIPTION:
 45 GATCCGCCCA TGTNAGCCTC CCAAAGTGCT AGGGTTACAG GCATGAGCTA CCATGCCTGG 60
 CAACAGCTTT CATATTTGTA AGTTTTTTTT CCTAGGTAAC CCAAGGTCTA TTGAAATTNC 120
 ATATAGCTTT CTTTNCATT ACATATTTAA ATAGATTTNN CCTGATTNA GAAAAGCTGT 180
 AGATTTTAT ATGTNAATCT TGTNTCCNTN 210

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SEQ ID NO:1163
SEQUENCE LENGTH:209
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01309
SEQUENCE DESCRIPTION:
GATCTNGGAC TCTNCCTCTC ACGACTGCGC CTTAGTCACT CAGACATACG GCGCANTGCA 60
GGAAAAGCCT ACACAGACGA CCTGGGTGCT GTGGGTGGCG CCTGCNTGGA GGACGAGCCA 120
GCNTCCTGCN CTGGATGAGG ACAGCGAGCA CCCGCCATNA TTCTNCGGAC TGA CTGAACT 180
TNACCTGTGA CCTCTTACCN GTGGAGCAN 209

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SEQ ID NO:1164
SEQUENCE LENGTH:209
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01310
SEQUENCE DESCRIPTION:
GATCACTNCA GGCCAGGNGT CCAAGACCAG CACGNCCAAC ATGGCAAAAC CCAGTCTGTA 60
CTAAAAATAG AAAAATTAGC TGGGCGTGGT GGCCTGTGCC TGCAATACCA GCTACTCAGA 120
AGGCTGNAGC AGGNTAATTG CTTGANCCTG GTAGGTGGAG GTTNCAGTGA GCTGANATCA 180
TGCCACTGNA CTCCAGCCTG GGTNACAGN 209

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SEQ ID NO:1165
SEQUENCE LENGTH:207
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01311
SEQUENCE DESCRIPTION:
GATCCTTACC GTCCTAGAGA GCAGACGCTT TCTGAAAAC ACTTGCTCCA AAAGACCCTC 60
TGAGTTAAGC TTTCAGCTGT ATCATTAGAC TTGTATTTAG AGCGTGTAC TCCCTCTGAA 120
CTGTTACTGC CTGAATGGAG TCCTGGACGA CATTGGGTTT TTCCTCTAGG AGAATACAAG 180
CCTTAATAAA CAATACTATT TAGCAAA 207

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SEQ ID NO:1166
SEQUENCE LENGTH:207
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01312
SEQUENCE DESCRIPTION:
GATCTGAACA AAGTCTGCAT TTNGTTAATA GTGTGGTACC AATGTTGGTT TCATAGTTTT 60
GGCCATTGTG CTGTGATTTT ATAAGATGCT AACATTAGGG ATAGCTGAAT GTGGTATATA 120
TAGGAACTCT GTGCTGAGTT TATAACTCCT CTGTATGTCT AAAACTATTT CAAAATAAAA 180
NGTTTAAAGG TAAAANAAAA GATTAAA 207

SEQ ID NO:1167

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SEQUENCE LENGTH:206
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 5 CLONE:HUMGS01313
 SEQUENCE DESCRIPTION:
 GATCCAGCCA CCACTCTGAA ACTCATCACA TCTTCATTGA CAGGGAGGGA GCCCAGGACA 60
 TATGTGTGGC TCATTGACCA GAAGGCTTTC TTAGTCCCAA CAGCCATGAA CCATGCACTT 120
 10 ATGGATACCC AGCCTTTTAG GGCTACGTGA AATGCATCCT TGTANCACTA TTGTATTCTT 180
 TCAATAAATA GCCTTCTGAG TTGAAA 206

SEQ ID NO:1168
 SEQUENCE LENGTH:213
 15 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01314
 SEQUENCE DESCRIPTION:
 GATCTGCCTG CCTATNAGAG CTTTGAGAAG CTCCGCCACA TGCTACTGTT GGCTATCCAG 60
 20 GAGTGTCTG AAGGCTTTGG GCTGGCCTAA TAAGGCCCTG CCCAACTCCG TGGGGTTTTT 120
 TTAACCATTG TTGGACCTGG GGAGGGGGGA GTTAAAAAAA GAACCAGAAA GAAATTGTCA 180
 AAAACCAATA AATGAAATCC ACCAACTCAC AAA 213

25 SEQ ID NO:1169
 SEQUENCE LENGTH:215
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01315
 30 SEQUENCE DESCRIPTION:
 GATCTAAAGT GACCTTGATG GACAGTGGAA GAAATCACAA CATGGAATTC CTCGAATAAC 60
 AATTTATTGA CTTTAAATAA TTTTGTCTAA TGCTACATAT ACACAATTAA AAAACCTTTA 120
 CACTATTCT AGAAAGTCAG CATGTATTTT TGGCTCGNNG TTTCCNCNG TGTTCCTGT 180
 35 GGAAGGAATA AAAATTTGAG TTTCAGTTGT GTAAA 215

SEQ ID NO:1170
 SEQUENCE LENGTH:349
 40 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS01316
 SEQUENCE DESCRIPTION:
 GATCTGTGAC AGCAGCAGCT TCATGTTGTA TTTTTTTTAC TGAAATTGTA AAATATCCAT 60
 45 CTTAAAGACA TCAACTATTC TAAAANTTGT TTACAGGATA TTCCTTTAGT GGTGGAATTA 120
 AAATNTACGA NTAATTGCTT TTTCAAAAAA ATGTATTTN TGTTAAAAGT TTAAAGATTT 180
 TTGCTATATA TTATGGAAGA AAAATGTAAT CGTAAATATT AATTTNTAC CTATATTGTG 240
 CAATACTTGA AAAAAACGGT ATNGAAAGTA TTTTGAGTCA GTGTCTTACA TGTTAAGAGG 300
 50 GACTGAAATA GTTTATATTA AGTTTGATT AAANTTCTTT AAAATTAAA 349

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SEQ ID NO:1171

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01317

SEQUENCE DESCRIPTION:

GATCCAAGCT GTATATACCA TATATAAACA TTTTACATGA ATCATTAGT TTTTAATTC 60
 ATTTACTAAT GCTATAAAAT TTCCTATATT ACCCCAGTAA TTGTCATCAG CTGGTTTATA 120
 TACTAAAGCA ACATGTTTGG ATGAGTTTCT TACATCCTTA TCGAGGAATT GGGTTAGGAA 180
 AAAATACATA ATTGTAAAC TGAAA 205

SEQ ID NO:1172

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01318

SEQUENCE DESCRIPTION:

GATCTTCAGG NTTCTACAAA TAGGGTAATT GTAAATTAA AGCATTAGCA TTTATTGGTG 60
 AATAATGTAT ATATCCCAT TCCAAGAAAT ATAAGTNAGT NANGTTGAAA TAAATCTTT 120
 AAAATTACT ATATTGCCAG TGGTTTCACA NCAGTTCTCT TGTATTATT TATCAATTAA 180
 ATCAAATAAA AATGATTATG TCAAA 205

SEQ ID NO:1173

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01319

SEQUENCE DESCRIPTION:

GATCCCCTGA CCTGCATTAC CTTGGTAACC ATTTCAATTT TTAATTTAAT TTCATTTTT 60
 AATTTTGGTG TACAAGCTGT AACATTTTCA CTTTCAAAGT GTAACACGCT GATTCCTCA 120
 AATAGAGATA CCCCTTTGAG TGATAAATTT GCAAAATGCT GTCTTCATTT TCTGTATTAA 180
 AATTCATTTC AGTTTTAAAA TAAA 204

SEQ ID NO:1174

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01320

SEQUENCE DESCRIPTION:

GATCAGAGCT GCTGAGTTCA GGATGCCTGN GNGTGGTTAG GGTAGCTTCT TACATGGATG 60
 TCAGGAGAGC TGCTGCCCTT GGCCTGAGTG CGTATTCAGG TGTTTTGCTG CTTGGCAGA 120
 GAGTGTTGA GTGTNGAATC GTTCAGCTCT NAGGTTCTGT NCCCTGTGGT GGAGAGGACG 180
 CAGCAGCNAN NTCTGGGNTC TNAN 204

SEQ ID NO:1175